wwPDB EM Validation Summary Report (i)

Aug 7, 2023 – 05:43 PM EDT

PDB ID	:	5T2C
EMDB ID	:	EMD-8345
Title	:	CryoEM structure of the human ribosome at 3.6 Angstrom resolution
Authors	:	Zhang, X.; Lai, M.; Zhou, Z.H.
Deposited on	:	2016-08-23
Resolution	:	3.60 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:

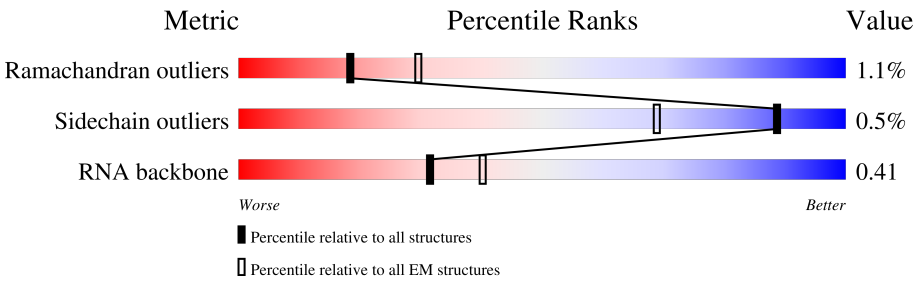
EMDB validation analysis	:	0.0.1.dev50
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	B	121	86% 13%
2	C	157	7% 77% 22%
3	D	257	7% 96%
4	E	403	9% 100%
5	F	427	9% 85% 14%
6	G	297	13% 98%
7	I	203	99%
8	J	160	5% 95%

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Mol	Chain	Length	Quality of chain
9	L	196	24% 95% 5%
10	N	160	15% 99%
11	O	128	25% 78% 21%
12	P	140	11% 94% 6%
13	Q	157	9% 41% 59%
14	S	145	9% 92% 8%
15	T	136	13% 99%
16	U	148	6% 99%
17	V	159	18% 47% 53%
18	X	125	12% 86% 14%
19	Y	135	8% 95% 5%
20	Z	110	7% 99%
21	a	117	12% 97%
22	b	123	18% 99%
23	c	105	28% 97%
24	d	97	89% 11%
25	e	70	44% 97%
26	f	51	16% 98%
27	g	128	7% 41% 59%
28	j	92	11% 99%
29	k	137	8% 91% 9%
30	m	248	6% 91% 9%
31	n	266	41% 91% 9%
32	o	192	12% 99%
33	s	215	7% 64% 35%

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Mol	Chain	Length	Quality of chain
34	t	204	99%
35	h	25	40%, 92%
36	r	211	35%, 97%
37	A	5070	11%, 53%, 21%, 26%
38	H	288	26%, 79%, 16%
39	i	106	12%, 97%
40	K	188	7%, 98%
41	l	217	100%, 98%
42	M	176	6%, 97%
43	p	214	23%, 98%
44	q	178	34%, 96%
45	R	156	13%, 76%, 23%
46	W	115	17%, 85%, 15%
47	AA	1869	41%, 31%, 51%, 12%, 7%
48	AC	83	89%, 95%, 5%
49	AD	143	65%, 96%
50	AE	115	54%, 88%, 12%
51	AF	69	86%, 90%, 9%
52	AH	156	46%, 42%, 54%
53	AJ	293	50%, 74%, 24%
54	AK	249	91%, 92%, 5%
55	AL	194	72%, 94%, 5%
56	AN	151	70%, 97%
57	AP	130	68%, 95%, 5%
58	AQ	133	85%, 95%

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Mol	Chain	Length	Quality of chain
59	AR	125	60% 58% 40%
60	AT	59	86% 93% 5%
61	AV	84	85% 95%
62	An	75	67% 29% 59% 12%
63	Ap	264	64% 78% 19%
64	Aq	243	92% 89% 7%
65	Ar	263	85% 97%
66	At	194	91% 93%
67	Au	208	78% 97%
68	Av	165	59% 58% 41%
69	Ay	146	95% 95% 5%
70	A0	152	92% 91% 7%
71	Ao	295	61% 73% 25%
72	As	204	82% 86% 6% 6%
73	Aw	158	77% 94%
74	Ax	145	66% 56% 10% 33%
75	Az	135	93% 85% 10%
76	AB	119	82% 76% 8% 14%
77	AG	56	93% 89% 5% 5%
78	AI	317	99% 95%
79	AM	132	92% 88% 8%
80	AO	151	78% 88% 5% 7%
81	AU	145	87% 90% 7%

2 Entry composition (i)

There are 81 unique types of molecules in this entry. The entry contains 217989 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 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	B	120	2558	1141	456	842	119	0	0

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

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

- Molecule 3 is a protein called 60S ribosomal protein L8.

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

- Molecule 4 is a protein called 60S ribosomal protein L3.

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

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	367	2919	1835	582	488	14	0	0

- Molecule 6 is a protein called 60S ribosomal protein L5.

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

- Molecule 7 is a protein called 60S ribosomal protein L13a.

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

- Molecule 8 is a protein called 60S ribosomal protein L17.

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

- Molecule 9 is a protein called 60S ribosomal protein L19.

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

- Molecule 10 is a protein called 60S ribosomal protein L21.

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

- Molecule 11 is a protein called 60S ribosomal protein L22.

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

- Molecule 12 is a protein called 60S ribosomal protein L23.

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

- Molecule 13 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	Q	64	534	340	104	87	3	0	0

- Molecule 14 is a protein called 60S ribosomal protein L26.

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

- Molecule 15 is a protein called 60S ribosomal protein L27.

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

- Molecule 16 is a protein called 60S ribosomal protein L27a.

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

- Molecule 17 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	V	75	610	378	130	99	3	0	0

- Molecule 18 is a protein called 60S ribosomal protein L31.

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

- Molecule 19 is a protein called 60S ribosomal protein L32.

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

- Molecule 20 is a protein called 60S ribosomal protein L35a.

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

- Molecule 21 is a protein called 60S ribosomal protein L34.

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

- Molecule 22 is a protein called 60S ribosomal protein L35.

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

- Molecule 23 is a protein called 60S ribosomal protein L36.

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

- Molecule 24 is a protein called 60S ribosomal protein L37.

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

- Molecule 25 is a protein called 60S ribosomal protein L38.

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

- Molecule 26 is a protein called 60S ribosomal protein L39.

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

- Molecule 27 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 28 is a protein called 60S ribosomal protein L37a.

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

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

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

- Molecule 30 is a protein called 60S ribosomal protein L7.

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

- Molecule 31 is a protein called 60S ribosomal protein L7a.

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

- Molecule 32 is a protein called 60S ribosomal protein L9.

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

- Molecule 33 is a protein called 60S ribosomal protein L14.

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

- Molecule 34 is a protein called 60S ribosomal protein L15.

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

- Molecule 35 is a protein called 60S Ribosomal protein L41.

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

- Molecule 36 is a protein called 60S ribosomal protein L13.

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

- Molecule 37 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
37	A	3776	80184	35672	14597	26140	3775	0	0

- Molecule 38 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	H	242	1958	1257	372	325	4	0	0

- Molecule 39 is a protein called 60S ribosomal protein L36a.

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

- Molecule 40 is a protein called 60S ribosomal protein L18.

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

- Molecule 41 is a protein called 60S ribosomal protein L10a.

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

- Molecule 42 is a protein called 60S ribosomal protein L18a.

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

- Molecule 43 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	p	213	1711	1082	329	285	15	0	0

- Molecule 44 is a protein called 60S ribosomal protein L11.

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

- Molecule 45 is a protein called 60S ribosomal protein L23a.

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

- Molecule 46 is a protein called 60S ribosomal protein L30.

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

- Molecule 47 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
47	AA	1742	36900	16458	6595	12106	1741	0	0

- Molecule 48 is a protein called 40S ribosomal protein S21.

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

- Molecule 49 is a protein called 40S ribosomal protein S23.

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

- Molecule 50 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	AE	101	814	507	170	132	5	0	0

- Molecule 51 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	AF	63	498	302	101	93	2	0	0

- Molecule 52 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	AH	71	581	367	109	98	7	0	0

- Molecule 53 is a protein called 40S ribosomal protein S2.

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

- Molecule 54 is a protein called 40S ribosomal protein S6.

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

- Molecule 55 is a protein called 40S ribosomal protein S9.

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

- Molecule 56 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	AN	149	1202	770	228	203	1	0	0

- Molecule 57 is a protein called 40S ribosomal protein S15a.

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

- Molecule 58 is a protein called 40S ribosomal protein S24.

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

- Molecule 59 is a protein called 40S ribosomal protein S25.

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

- Molecule 60 is a protein called 40S ribosomal protein S30.

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

- Molecule 61 is a protein called 40S ribosomal protein S27.

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

- Molecule 62 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
62	An	75	1604	717	298	515	74	0	0

- Molecule 63 is a protein called 40S ribosomal protein S3a.

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

- Molecule 64 is a protein called 40S ribosomal protein S3.

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

- Molecule 65 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 66 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	At	189	1521	969	280	271	1	0	0

- Molecule 67 is a protein called 40S ribosomal protein S8.

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

- Molecule 68 is a protein called 40S ribosomal protein S10.

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

- Molecule 69 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	Ay	146	1158	736	218	200	4	0	0

- Molecule 70 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	A0	150	1235	776	250	208	1	0	0

- Molecule 71 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	Ao	222	1747	1109	306	324	8	0	0

- Molecule 72 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	As	191	1509	943	286	273	7	0	0

- Molecule 73 is a protein called 40S ribosomal protein S11.

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

- Molecule 74 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	Ax	97	804	505	155	138	6	0	0

- Molecule 75 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	Az	132	1072	673	199	195	5	0	0

- Molecule 76 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	AB	102	807	507	153	143	4	0	0

- Molecule 77 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	AG	53	445	278	90	72	5	0	0

- Molecule 78 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 79 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
79	AM	122	952	596	169	179	8	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AM	52	GLN	LEU	conflict	UNP P25398
AM	69	LEU	CYS	conflict	UNP P25398
AM	99	ASN	LYS	conflict	UNP P25398

- Molecule 80 is a protein called 40S ribosomal protein S14.

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

- Molecule 81 is a protein called 40S ribosomal protein S19.

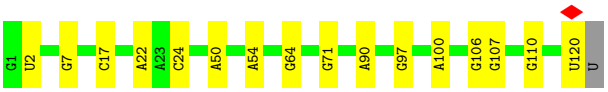
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
81	AU	143	1112	697	214	198	3	0	0

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.

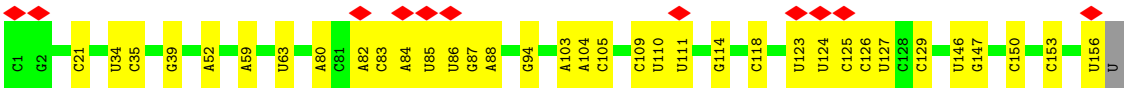
- Molecule 1: 5S rRNA

Chain B:



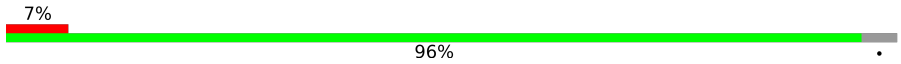
- Molecule 2: 5.8S rRNA

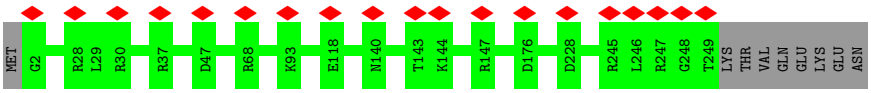
Chain C:



- Molecule 3: 60S ribosomal protein L8

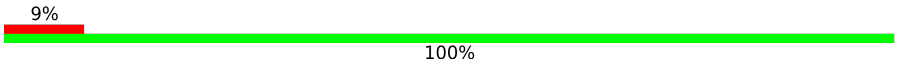
Chain D:

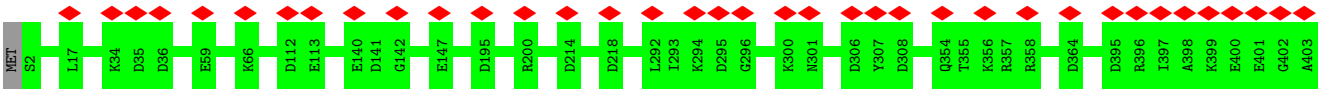




- Molecule 4: 60S ribosomal protein L3

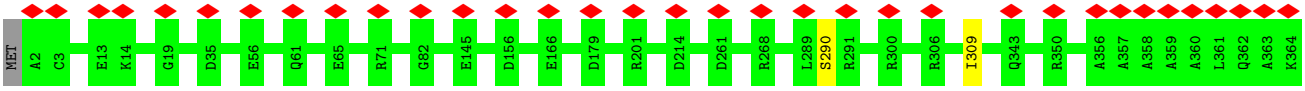
Chain E:

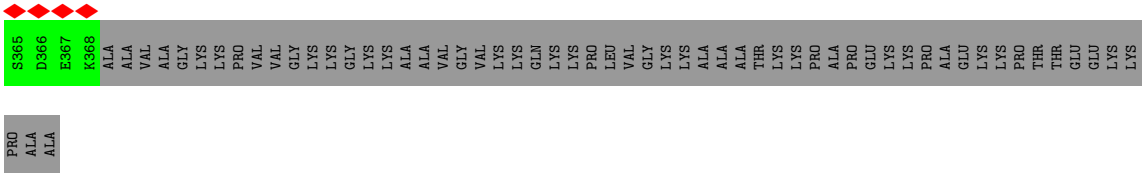




- Molecule 5: 60S ribosomal protein L4

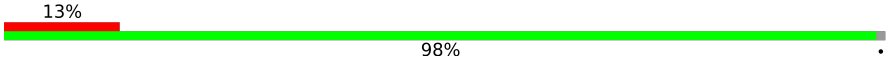
Chain F:

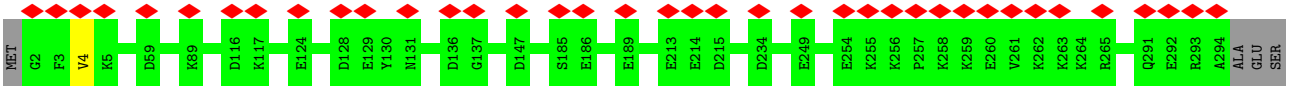




• Molecule 6: 60S ribosomal protein L5

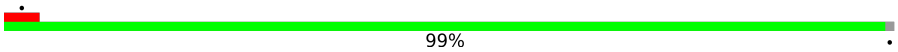
Chain G:

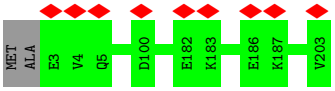




• Molecule 7: 60S ribosomal protein L13a

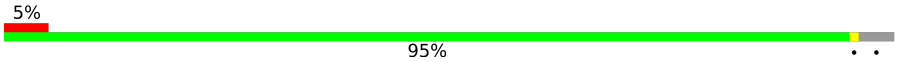
Chain I:

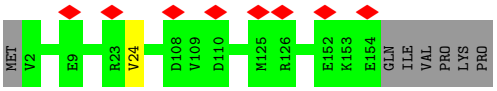




• Molecule 8: 60S ribosomal protein L17

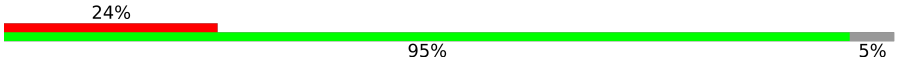
Chain J:

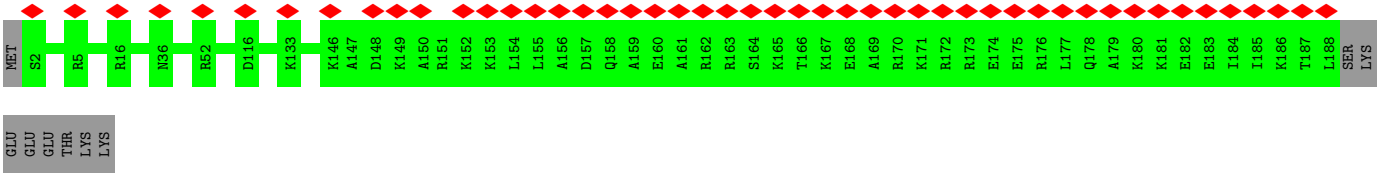




• Molecule 9: 60S ribosomal protein L19

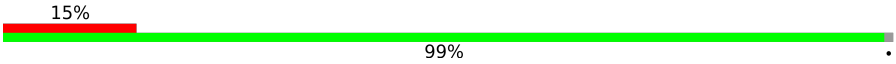
Chain L:

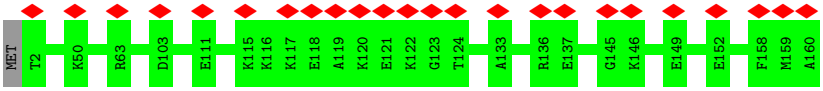




• Molecule 10: 60S ribosomal protein L21

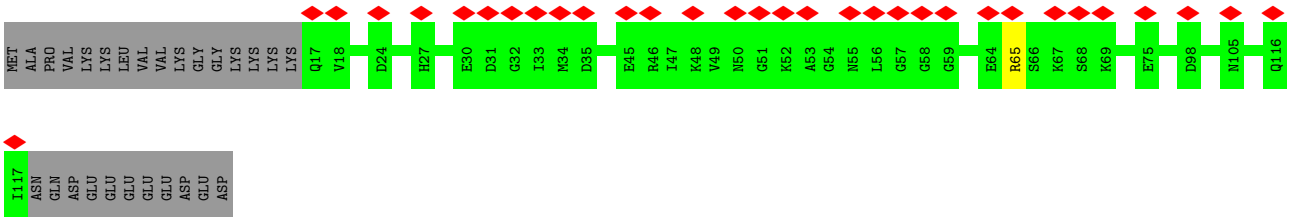
Chain N:





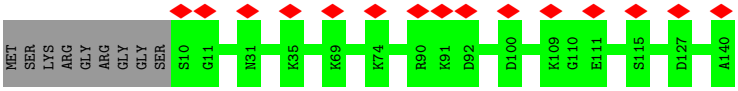
• Molecule 11: 60S ribosomal protein L22

Chain O:



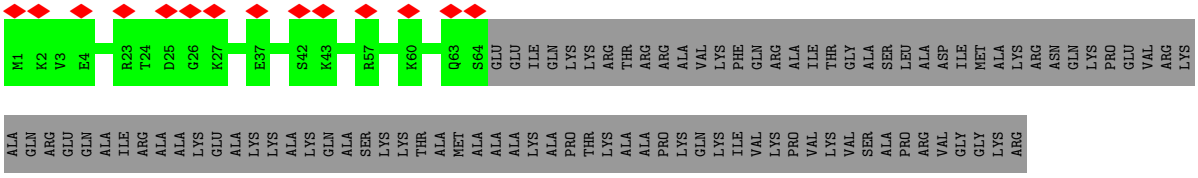
• Molecule 12: 60S ribosomal protein L23

Chain P: 11% 94% 6%



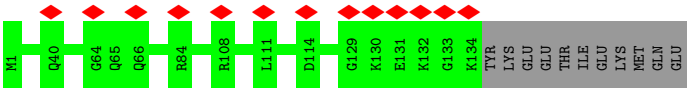
• Molecule 13: 60S ribosomal protein L24

Chain Q: 9% 41% 59%



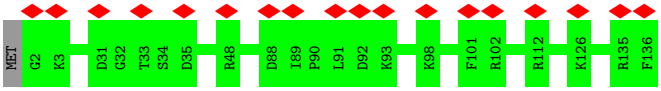
• Molecule 14: 60S ribosomal protein L26

Chain S: 9% 92% 8%



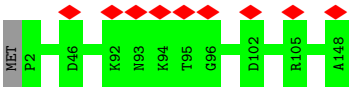
• Molecule 15: 60S ribosomal protein L27

Chain T: 13% 99%



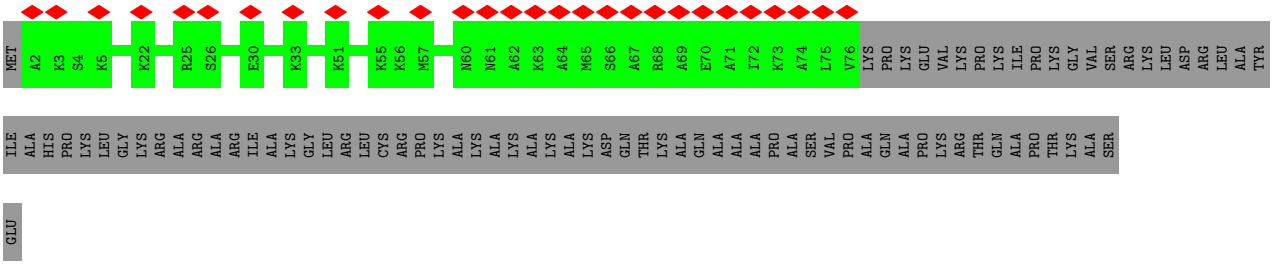
• Molecule 16: 60S ribosomal protein L27a

Chain U: 6% 99%



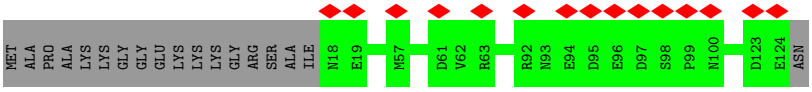
• Molecule 17: 60S ribosomal protein L29

Chain V: 18% 47% 53%



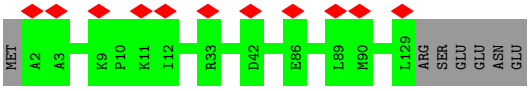
- Molecule 18: 60S ribosomal protein L31

Chain X: 12% 86% 14%



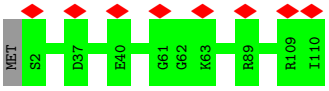
- Molecule 19: 60S ribosomal protein L32

Chain Y: 8% 95% 5%



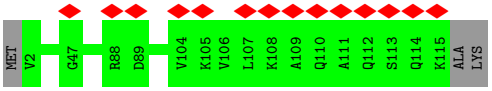
- Molecule 20: 60S ribosomal protein L35a

Chain Z: 7% 99%



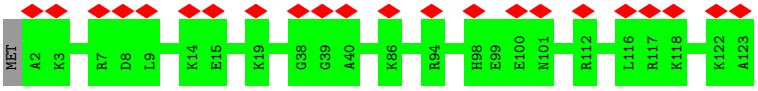
- Molecule 21: 60S ribosomal protein L34

Chain a: 12% 97%



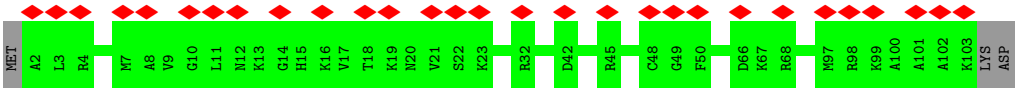
- Molecule 22: 60S ribosomal protein L35

Chain b: 18% 99%



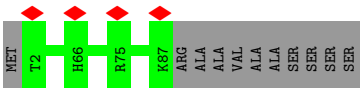
- Molecule 23: 60S ribosomal protein L36

Chain c: 28% 97%



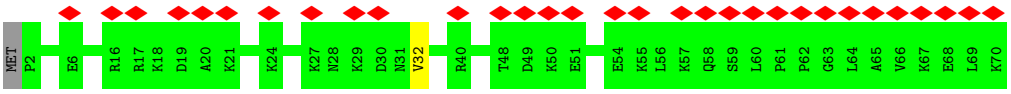
• Molecule 24: 60S ribosomal protein L37

Chain d: 89% 11%



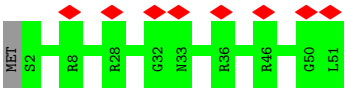
• Molecule 25: 60S ribosomal protein L38

Chain e: 44% 97%



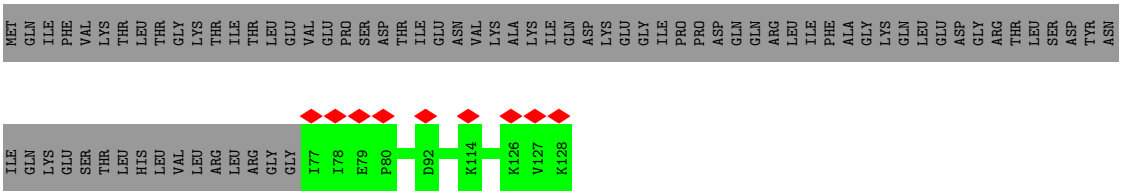
• Molecule 26: 60S ribosomal protein L39

Chain f: 16% 98%



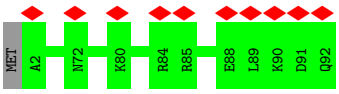
• Molecule 27: Ubiquitin-60S ribosomal protein L40

Chain g: 7% 41% 59%



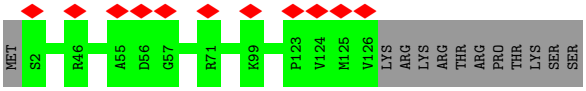
• Molecule 28: 60S ribosomal protein L37a

Chain j: 11% 99%



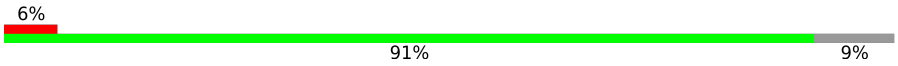
• Molecule 29: 60S ribosomal protein L28

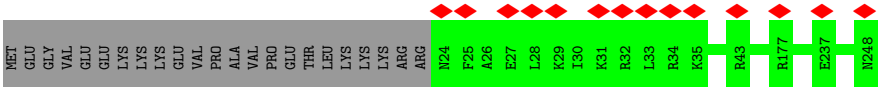
Chain k: 8% 91% 9%



• Molecule 30: 60S ribosomal protein L7

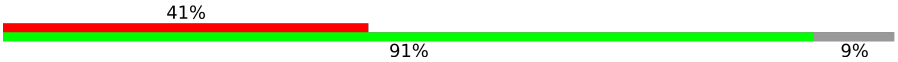
Chain m:

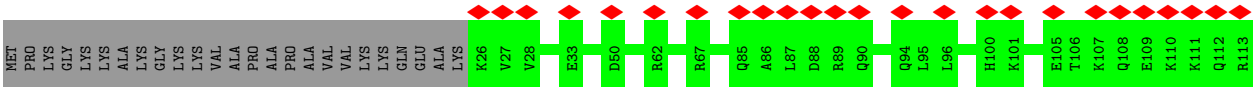


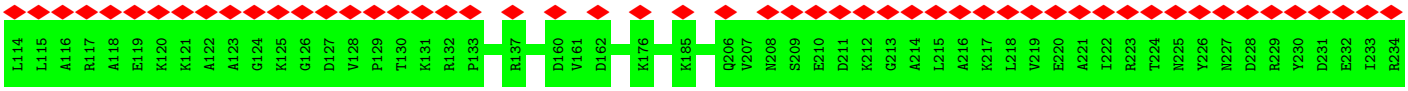


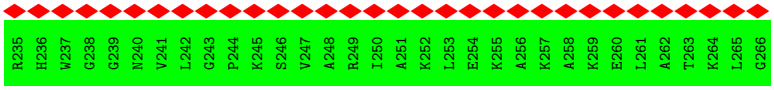
• Molecule 31: 60S ribosomal protein L7a

Chain n:



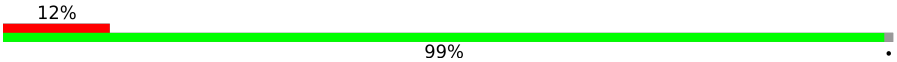


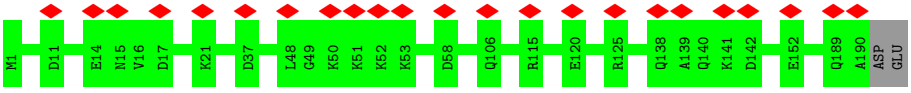




• Molecule 32: 60S ribosomal protein L9

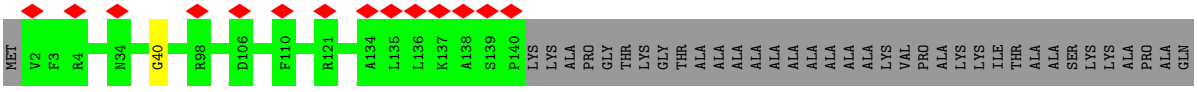
Chain o:

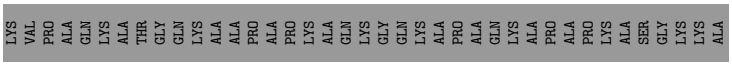




• Molecule 33: 60S ribosomal protein L14

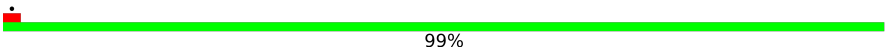
Chain s:

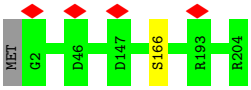




• Molecule 34: 60S ribosomal protein L15

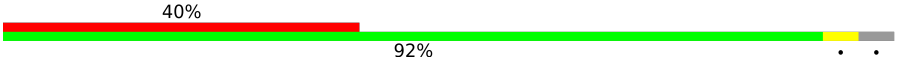
Chain t:

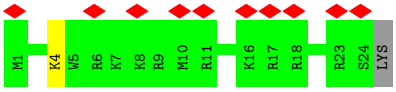




- Molecule 35: 60S Ribosomal protein L41

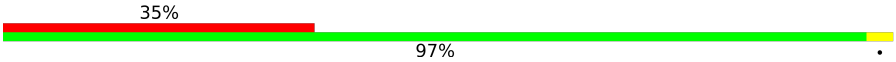
Chain h:

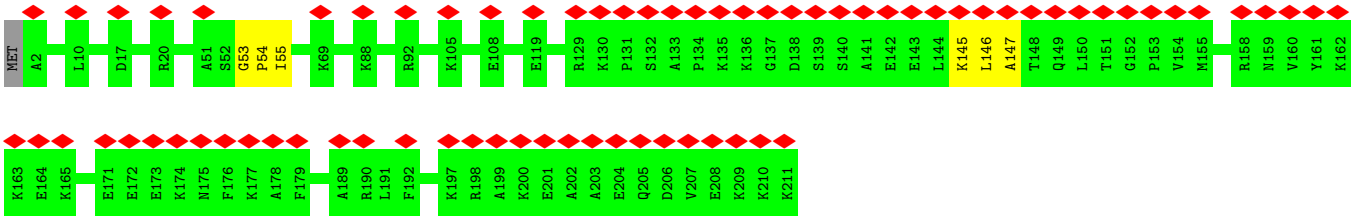




- Molecule 36: 60S ribosomal protein L13

Chain r:





- Molecule 37: 28S rRNA

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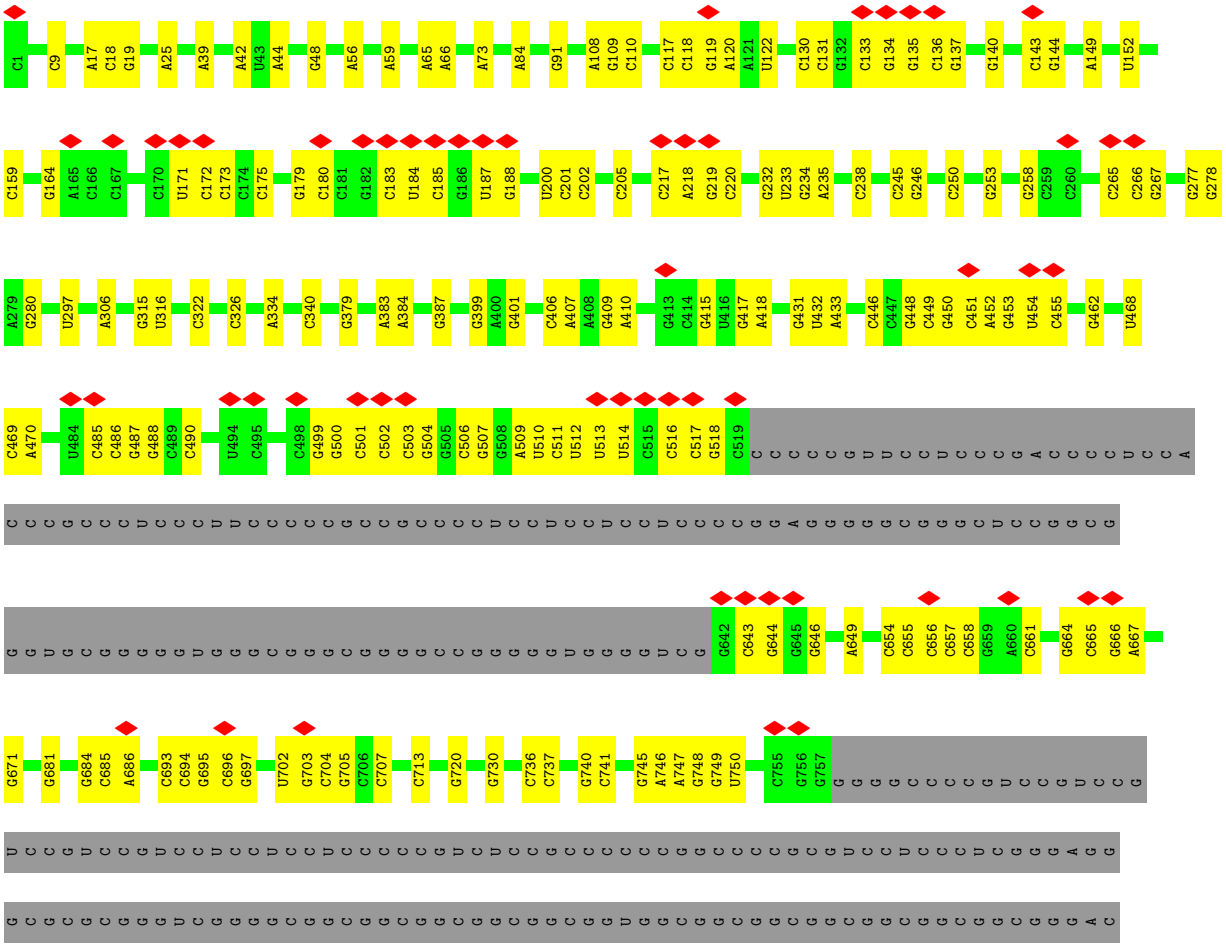

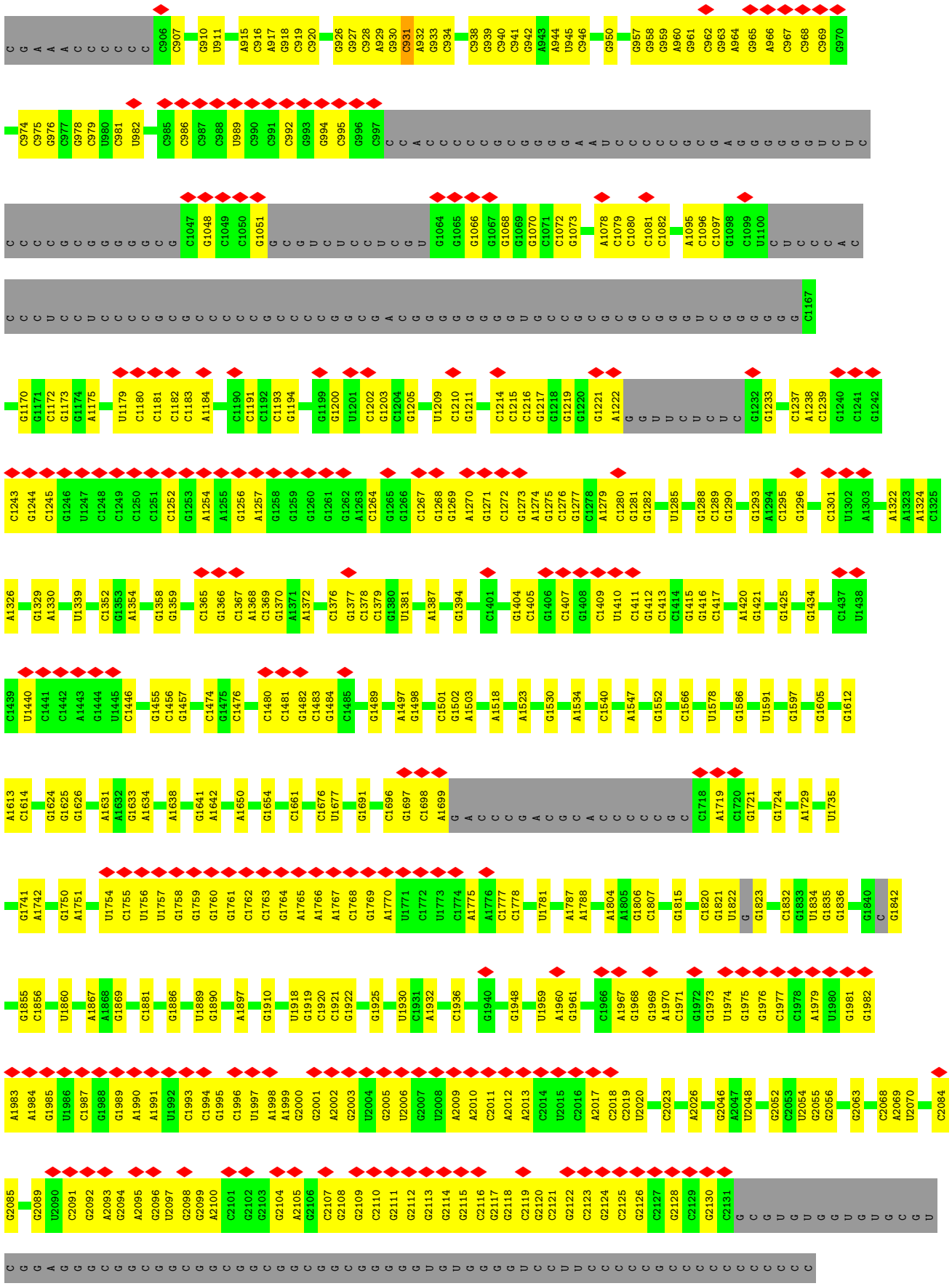
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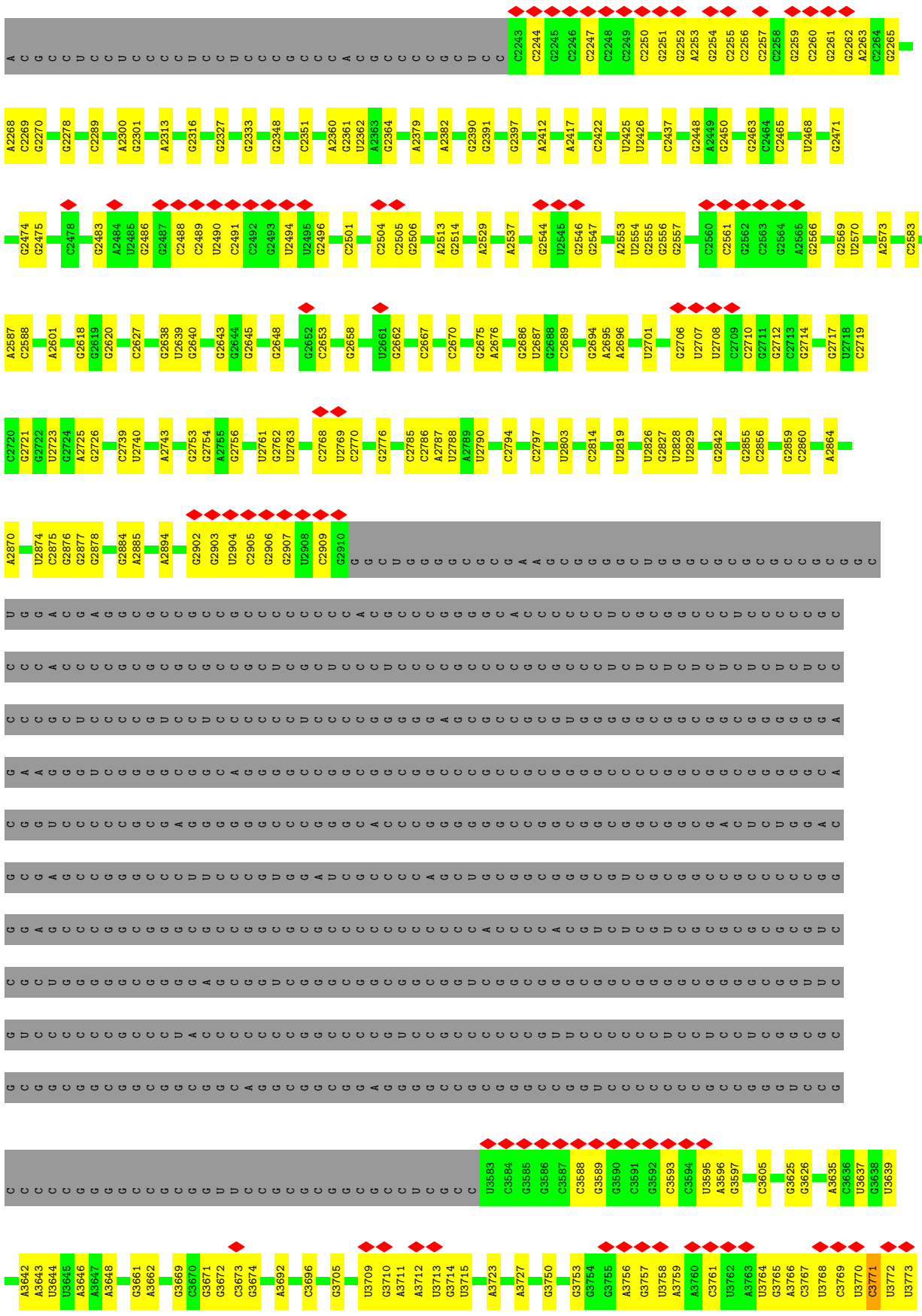
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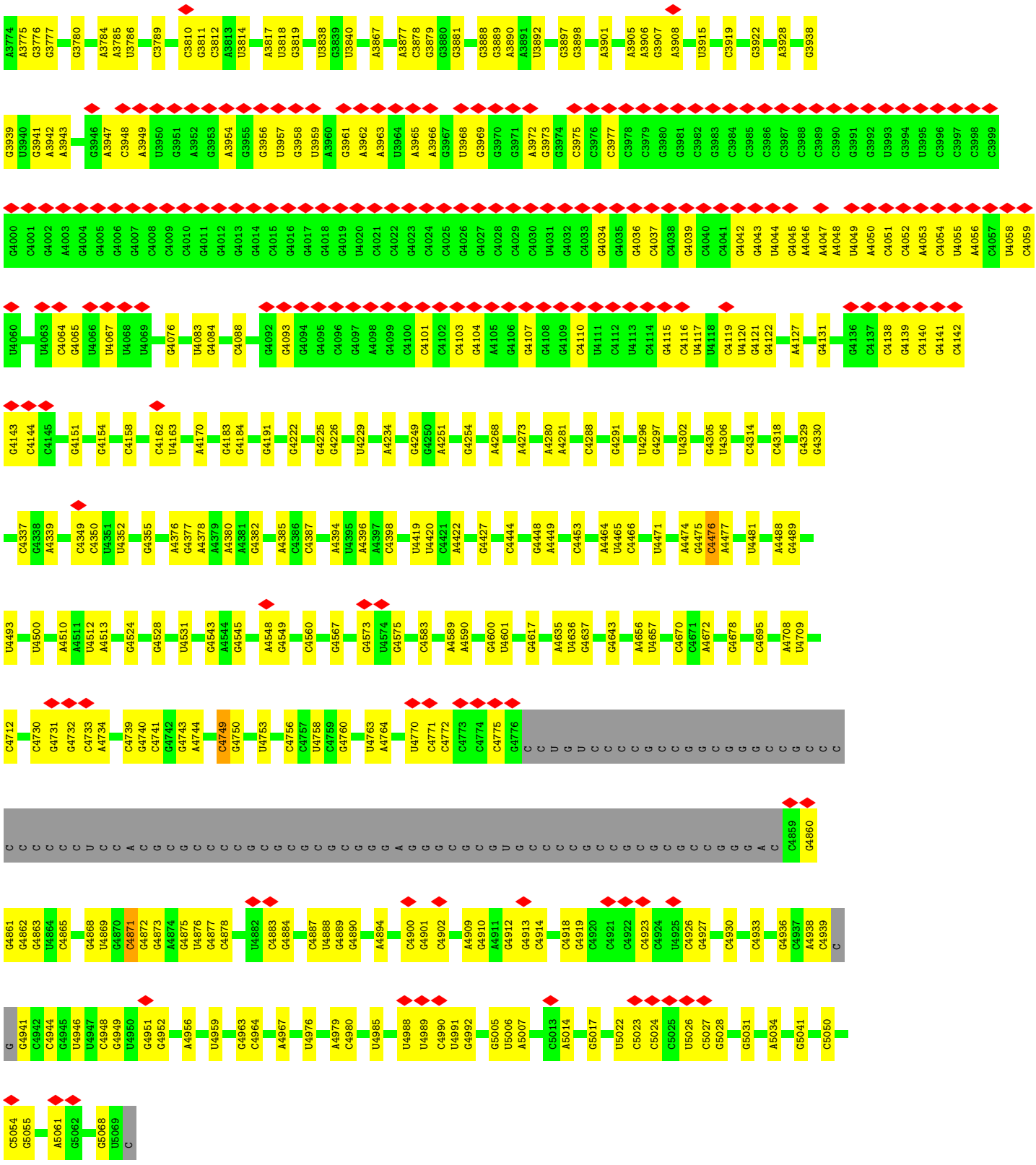
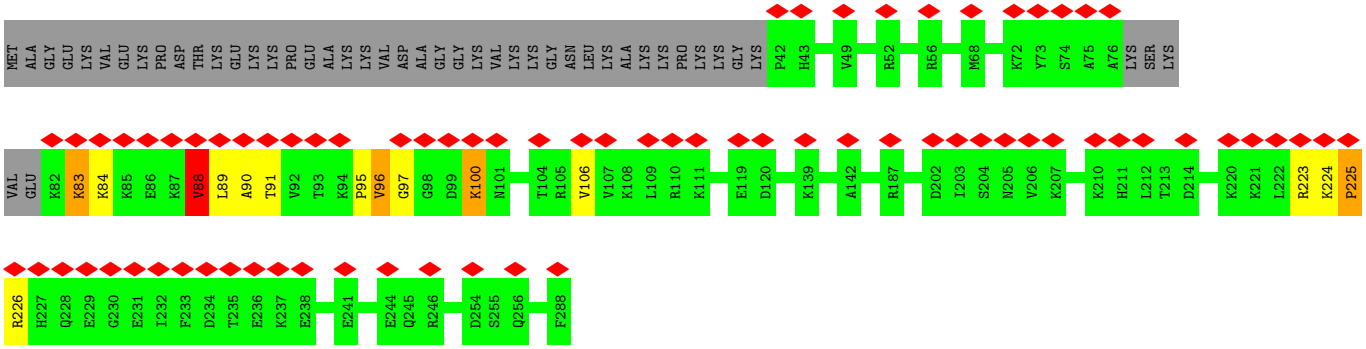


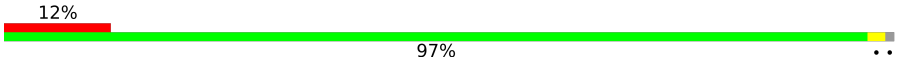
- Molecule 38: 60S ribosomal protein L6

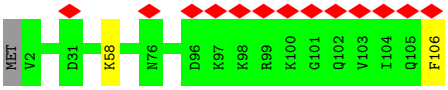
Chain H:



- Molecule 39: 60S ribosomal protein L36a

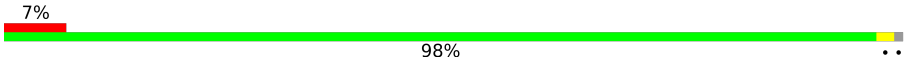
Chain i:

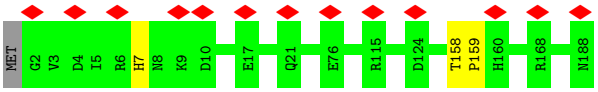




- Molecule 40: 60S ribosomal protein L18

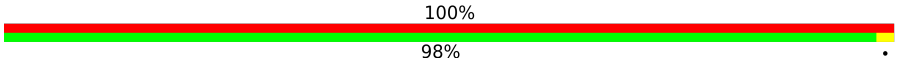
Chain K:

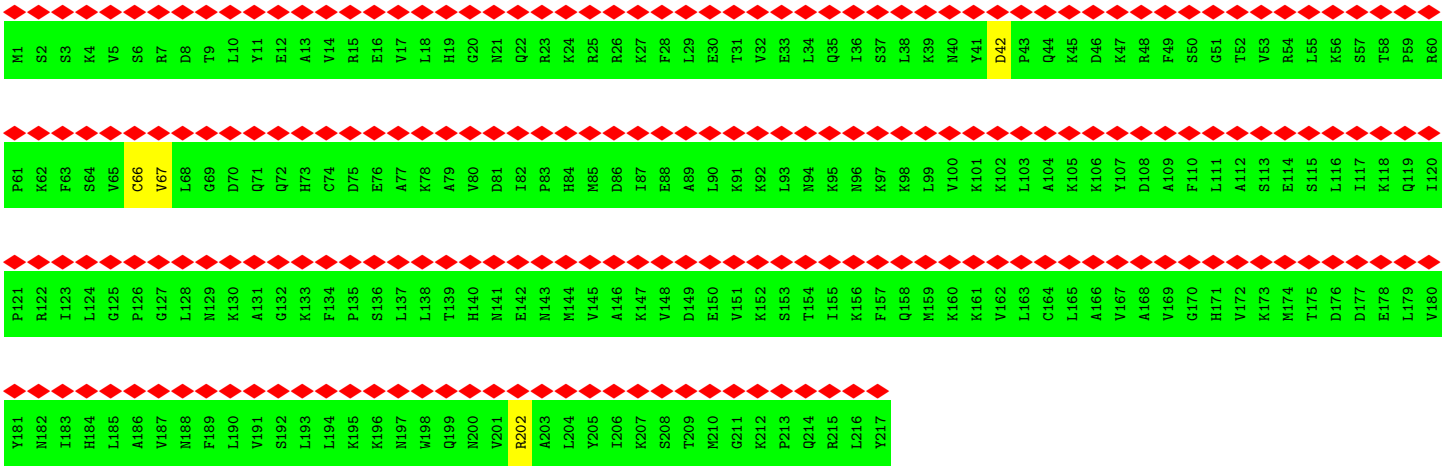




- Molecule 41: 60S ribosomal protein L10a

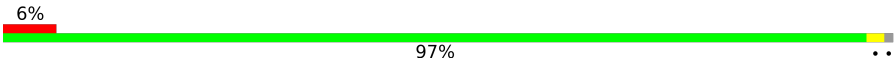
Chain l:

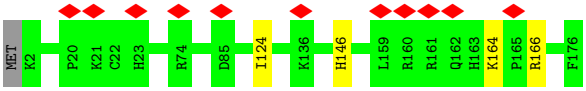




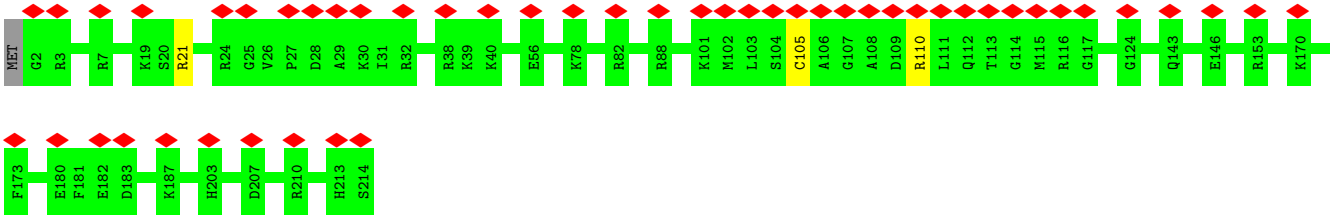
- Molecule 42: 60S ribosomal protein L18a

Chain M:

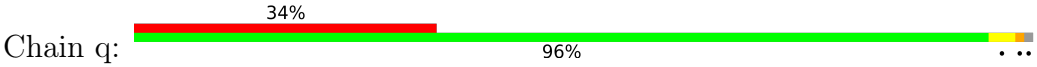


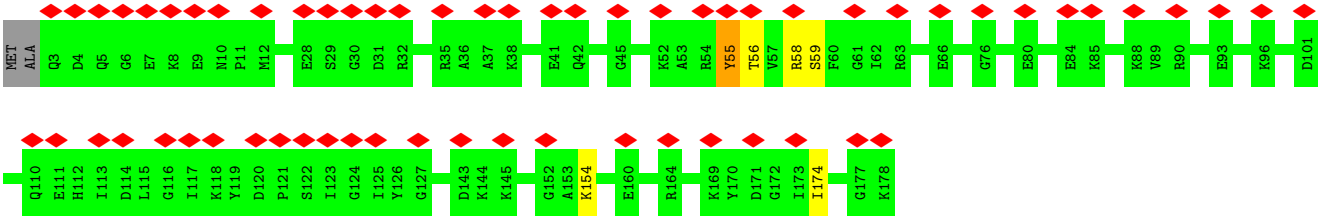


• Molecule 43: 60S ribosomal protein L10-like

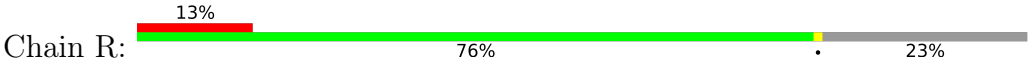


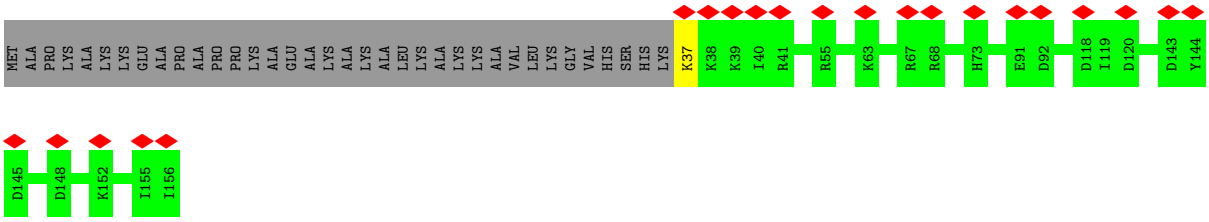
• Molecule 44: 60S ribosomal protein L11



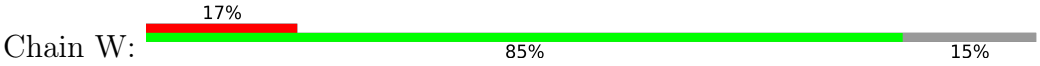


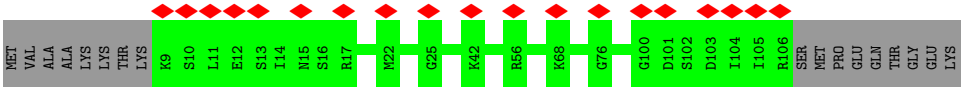
• Molecule 45: 60S ribosomal protein L23a



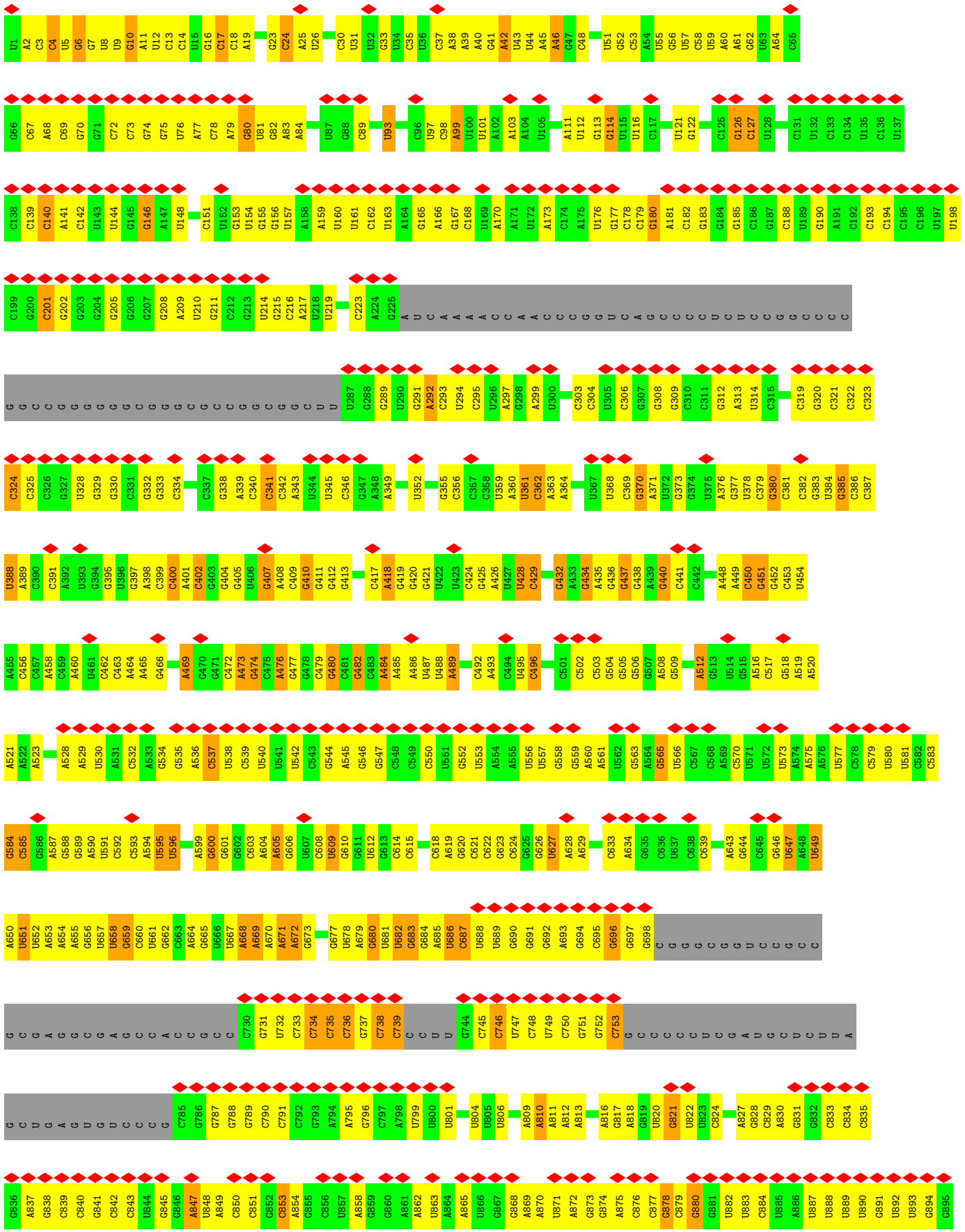


• Molecule 46: 60S ribosomal protein L30





• Molecule 47: 18S rRNA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G66 C67 A68 C69 G70 G71 C72 C73 G74 G75 U76 A77 C78 A79 G80 U81 G82 A83 A84 U87 G88 C89 U93 C96 U97 C98 A99 U100 U101 A102 A103 A104 U105 A111 U112 G113 G114 U115 U116 C117 U121 G122 C125 G126 C127 U128 C131 U132 C133 C134 U135 C136 U137
C138 C139 C140 A141 C142 U143 U144 G145 G146 A147 U148 C151 U152 G153 U154 G155 G156 U157 A158 A159 U160 U161 C162 U163 A164 G165 A166 G167 C168 U169 A170 A171 U172 A173 C174 A175 U176 G177 C178 C179 G180 A181 C182 G183 G184 G185 C186 G187 C188 U189 G190 A191 C192 C193 C194 C195 C196 U197 U198
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G G C C G G G G G C G G G G C G C C G G C G G C U U U287 G288 G289 U290 G291 A292 G293 U294 C295 U296 A297 G298 A299 U300 C303 C304 U305 C306 G307 G308 G309 C310 C311 G312 A313 U314 C315 C319 G320 C321 C322 C323
C324 C325 C326 G327 U328 G329 G330 C331 G332 G333 C334 C337 G338 A339 C340 C341 C342 A343 U344 U345 C346 G347 A348 A349 U352 G355 C356 C357 C358 U359 A360 U361 C362 A363 A364 U367 U368 C369 G370 A371 U372 G373 G374 U375 A376 G377 U378 C379 G380 C381 C382 G383 U384 G385 C386 C387
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G C U G A G U G U C C C G C785 G786 G787 G788 G789 C790 C791 C792 G793 A794 A795 G796 C797 A798 U799 U800 U801 U804 U805 U806 A809 A810 A811 A812 A813 A816 G817 A818 G819 U820 G821 U822 U823 C824 A827 G828 C829 A830 G831 G832 C833 C834 C835
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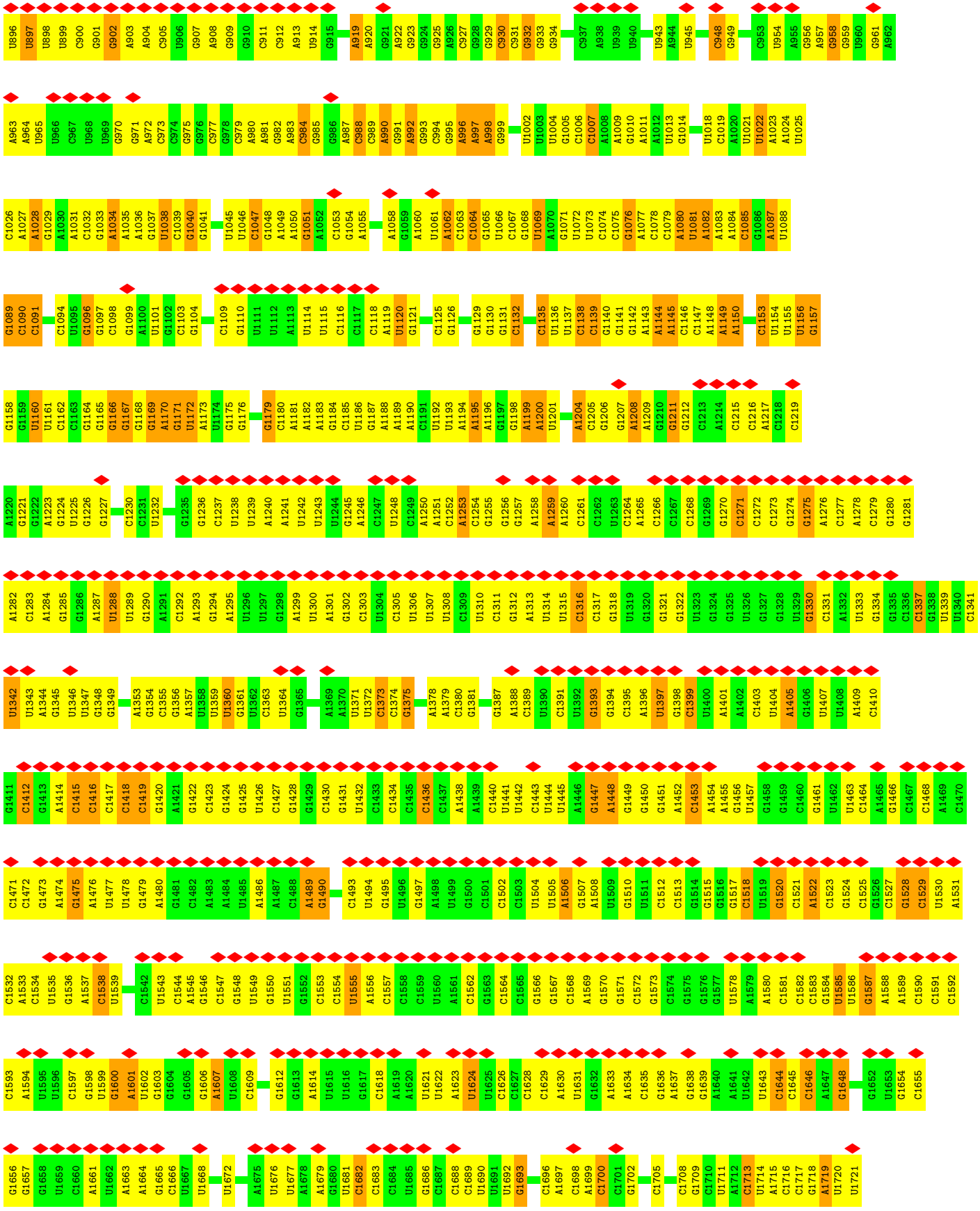
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G1089 C1090 C1091 C1094 U1095 G1096 G1097 C1098 G1099 A1100 U1101 G1102 C1103 G1104 C1109 G1110 U1111 U1112 A1113 U1114 U1115 C1116 C1117 C1118 A1119 U1120 G1121 C1125 G1126 G1129 G1130 G1131 C1132 C1135 U1136 U1137 C1138 C1139 G1140 G1141 G1142 A1143 A1144 A1145 C1146 C1147 A1148 A1149 A1150 C1153 U1154 U1155 U1156 G1157
G1158 G1159 U1160 U1161 C1162 C1163 G1164 G1165 G1166 G1167 G1168 G1169 A1170 G1171 U1172 A1173 U1174 C1175 G1176 G1179 C1180 A1181 A1182 A1183 G1184 C1185 U1186 G1187 A1188 A1189 A1190 C1191 U1192 U1193 A1194 A1195 A1196 C1197 G1198 A1199 A1200 U1201 A1204 C1205 G1206 G1207 A1208 A1209 G1210 G1211 G1212 C1213 A1214 C1215 C1216 A1217 C1218 C1219
A1220 G1221 G1222 A1223 G1224 U1225 G1226 G1227 C1230 C1231 U1232 G1235 G1236 C1237 U1238 U1239 A1240 A1241 U1242 U1243 U1244 G1245 A1246 C1247 U1248 C1249 A1250 A1251 C1252 A1253 C1254 G1255 G1256 G1257 A1258 A1259 A1260 C1261 C1262 U1263 C1264 A1265 C1266 C1267 C1268 G1269 C1270 C1271 C1272 C1273 G1274 G1275 A1276 C1277 A1278 C1279 G1280 G1281
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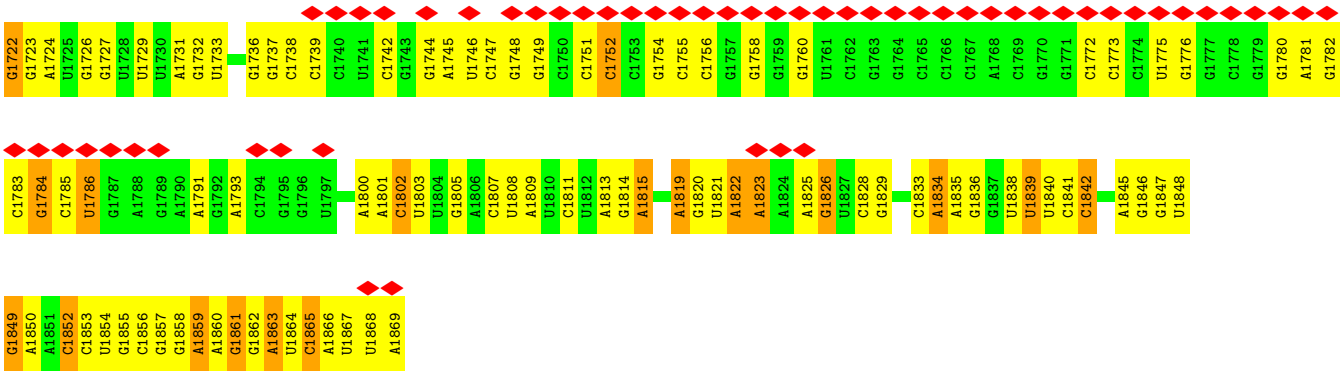
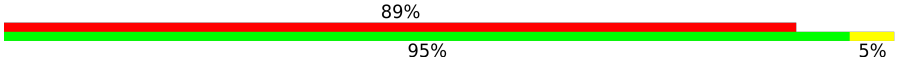
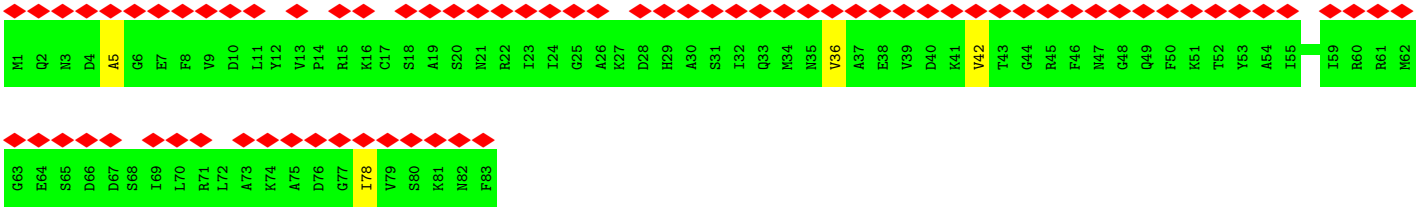
G1411 C1412 G1413 A1414 C1415 C1416 C1417 C1418 C1419 G1420 A1421 G1422 C1423 G1424 G1425 U1426 C1427 G1428 G1429 C1430 G1431 U1432 C1433 C1434 C1435 C1436 C1437 A1438 A1439 C1440 U1441 U1442 C1443 U1444 U1445 A1446 G1447 A1448 G1449 G1450 G1451 A1452 C1453 A1454 A1455 G1456 U1457 G1458 G1459 C1460 G1461 U1462 U1463 C1464 A1465 G1466 C1467 C1468 A1469 C1470
C1471 C1472 G1473 A1474 G1475 A1476 U1477 U1478 G1479 A1480 G1481 C1482 A1483 A1484 U1485 A1486 A1487 C1488 A1489 G1490 C1493 U1494 G1495 U1496 G1497 A1498 U1499 G1500 C1501 C1502 C1503 U1504 U1505 A1506 G1507 A1508 U1509 G1510 U1511 C1512 C1513 G1514 G1515 G1516 G1517 C1518 U1519 G1520 C1521 A1522 C1523 G1524 C1525 G1526 C1527 G1528 C1529 U1530 A1531
C1532 A1533 C1534 U1535 G1536 A1537 C1538 U1539 C1542 U1543 C1544 A1545 G1546 C1547 G1548 U1549 G1550 U1551 G1552 C1553 C1554 U1555 A1556 C1557 C1558 C1559 U1560 A1561 C1562 G1563 C1564 C1565 G1566 G1567 C1568 A1569 G1570 G1571 C1572 G1573 C1574 G1575 G1576 G1577 U1578 A1579 A1580 C1581 C1582 C1583 G1584 U1585 U1586 G1587 A1588 A1589 C1590 C1591 C1592
C1593 A1594 U1595 U1596 C1597 G1598 U1599 G1600 A1601 U1602 G1603 G1604 G1605 G1606 A1607 U1608 C1609 G1612 G1613 A1614 U1615 U1616 G1617 C1618 A1619 A1620 U1621 U1622 A1623 U1624 U1625 C1626 C1627 C1628 C1629 A1630 U1631 G1632 A1633 A1634 C1635 G1636 A1637 G1638 G1639 A1640 A1641 U1642 U1643 C1644 C1645 C1646 A1647 G1648 G1652 U1653 G1654 C1655
G1656 G1657 G1658 U1659 C1660 A1661 U1662 A1663 A1664 G1665 C1666 U1667 U1668 U1672 A1675 U1676 U1677 A1678 A1679 G1680 U1681 C1682 C1683 C1684 U1685 G1686 C1687 C1688 C1689 U1690 U1691 U1692 G1693 C1696 A1697 C1698 A1699 C1700 C1701 G1702 C1705 C1708 G1709 C1710 U1711 A1712 C1713 U1714 A1715 C1716 C1717 G1718 A1719 U1720 U1721



- Molecule 48: 40S ribosomal protein S21

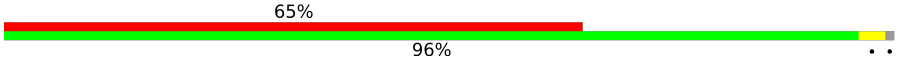
Chain AC:

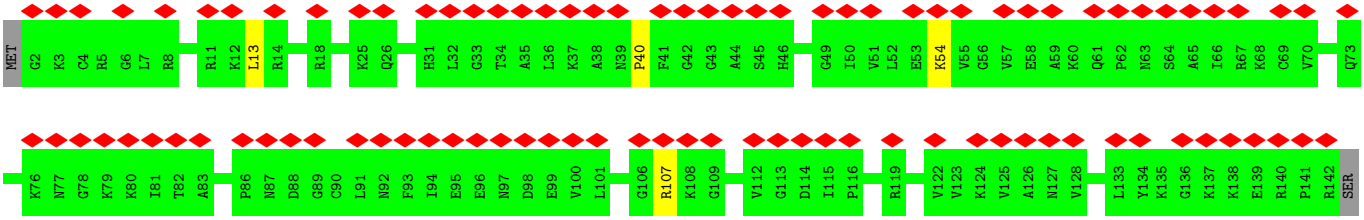




- Molecule 49: 40S ribosomal protein S23

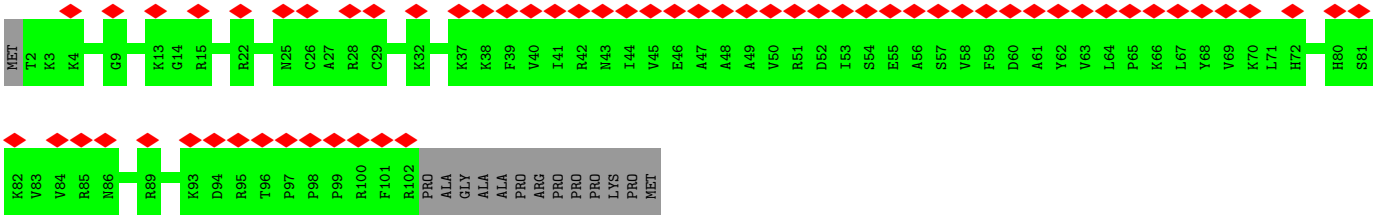
Chain AD:





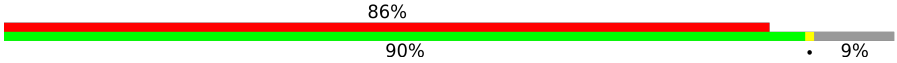
- Molecule 50: 40S ribosomal protein S26

Chain AE:



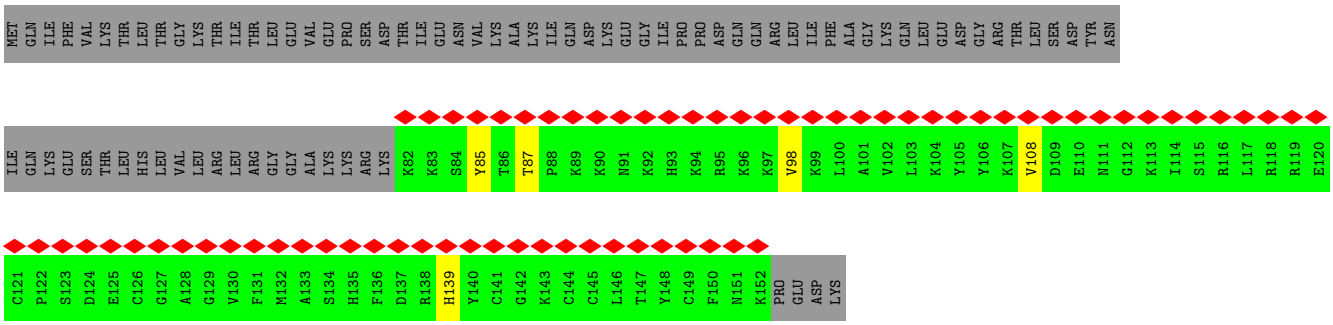
- Molecule 51: 40S ribosomal protein S28

Chain AF:



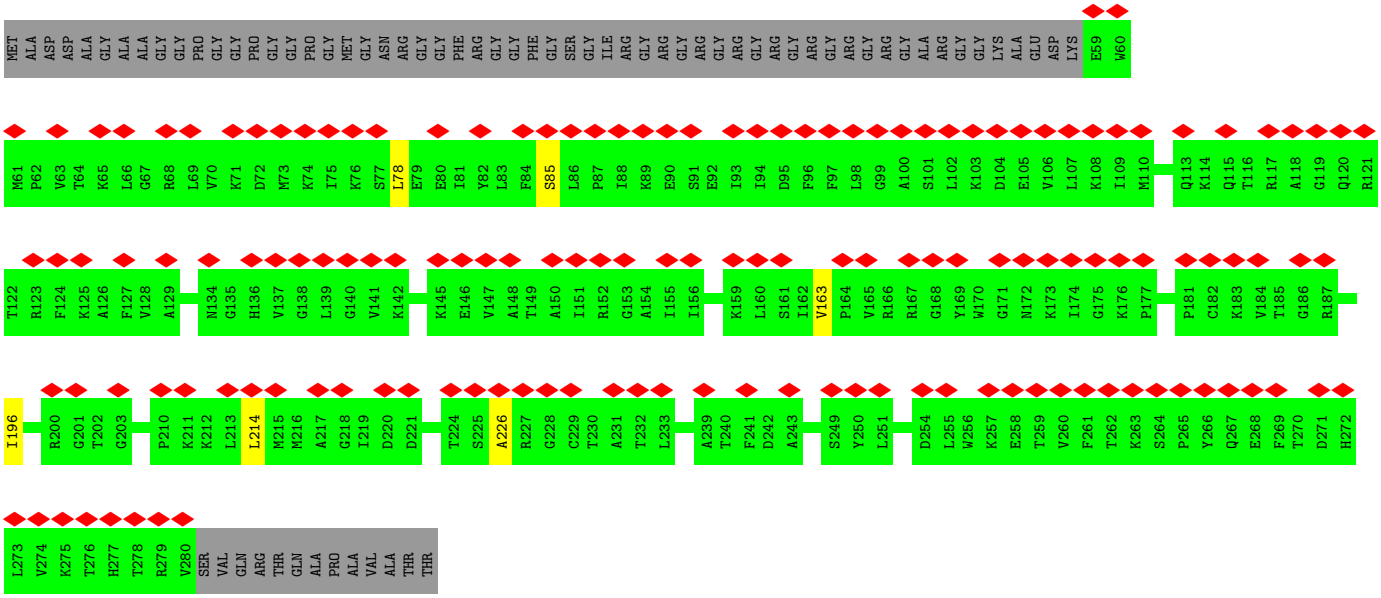
- Molecule 52: Ubiquitin-40S ribosomal protein S27a

Chain AH:



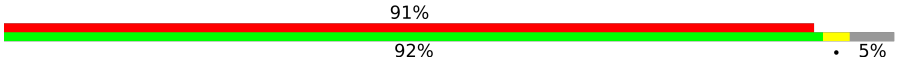
- Molecule 53: 40S ribosomal protein S2

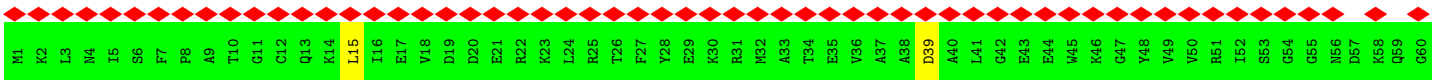
Chain AJ:

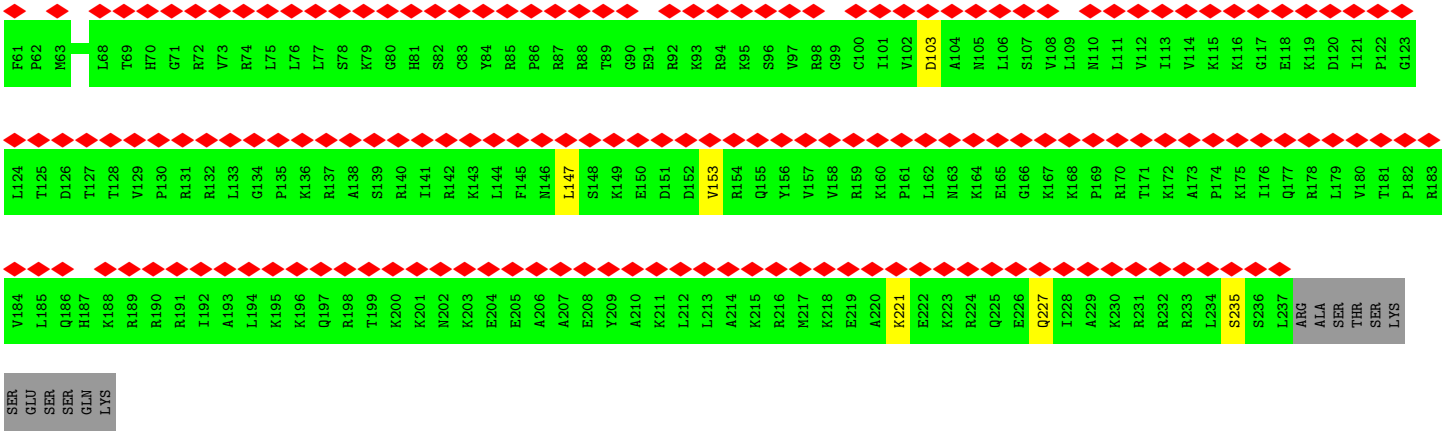


- Molecule 54: 40S ribosomal protein S6

Chain AK:

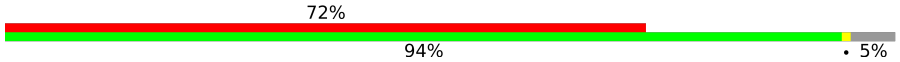


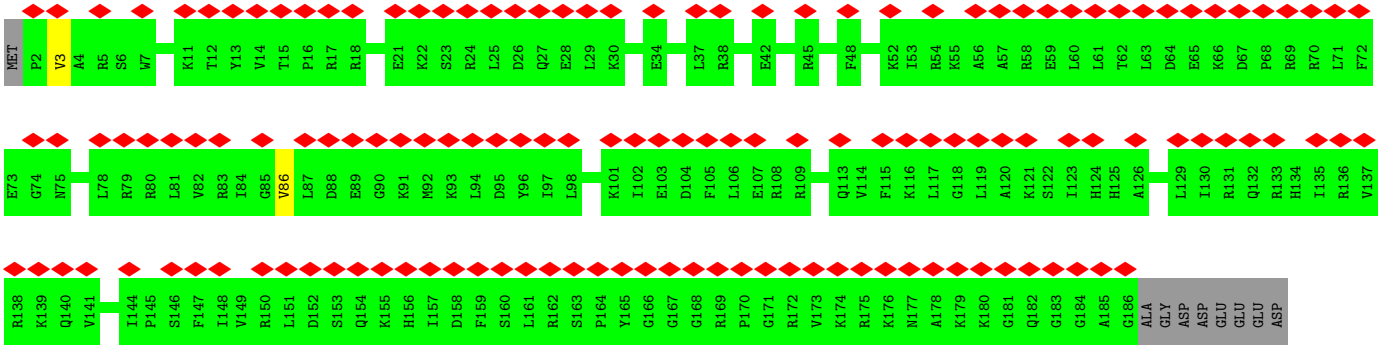




- Molecule 55: 40S ribosomal protein S9

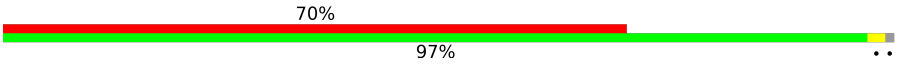
Chain AL:





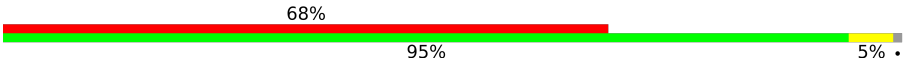
- Molecule 56: 40S ribosomal protein S13

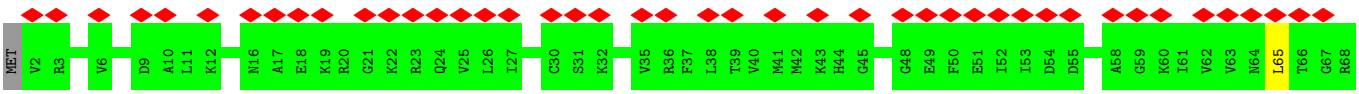
Chain AN:

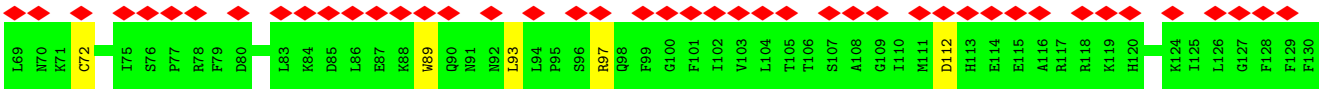


- Molecule 57: 40S ribosomal protein S15a

Chain AP:

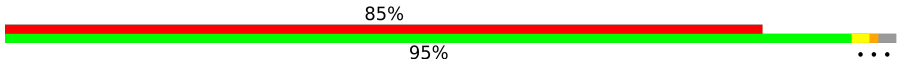






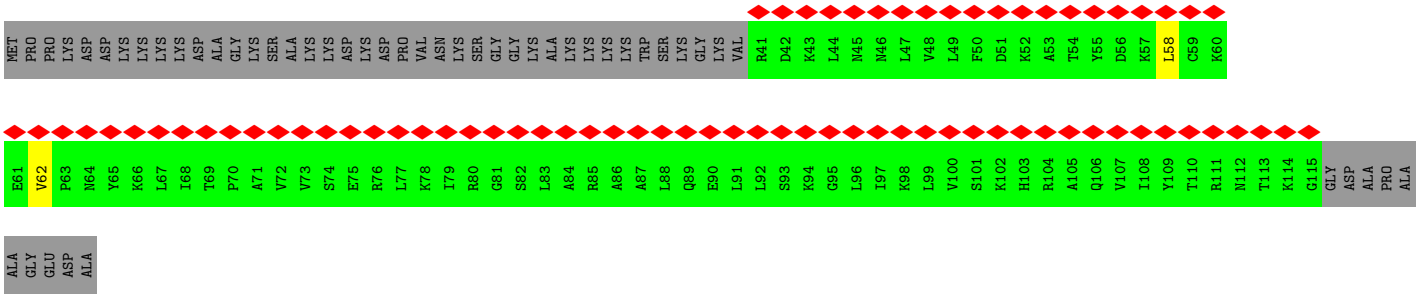
- Molecule 58: 40S ribosomal protein S24

Chain AQ:



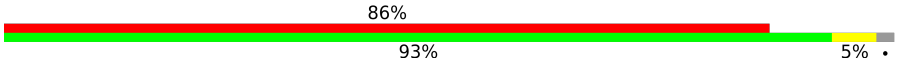
- Molecule 59: 40S ribosomal protein S25

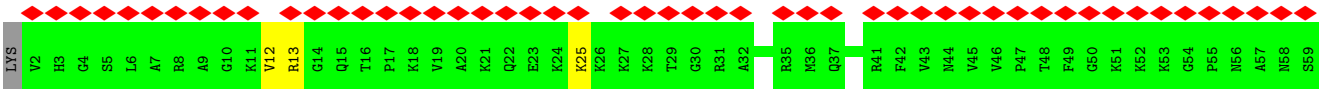
Chain AR:



- Molecule 60: 40S ribosomal protein S30

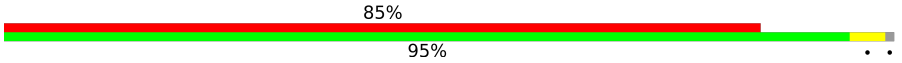
Chain AT:

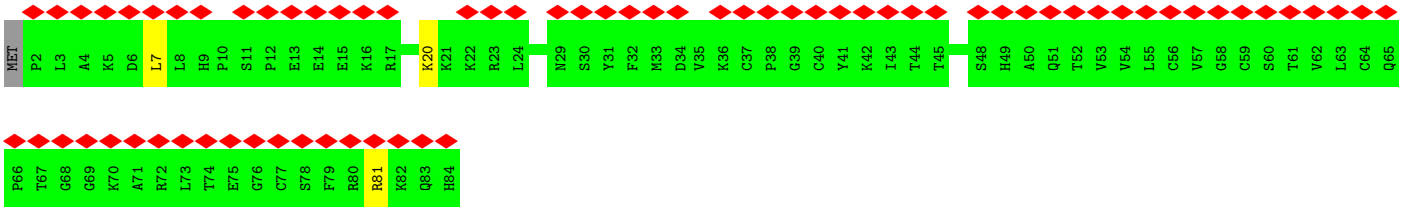




- Molecule 61: 40S ribosomal protein S27

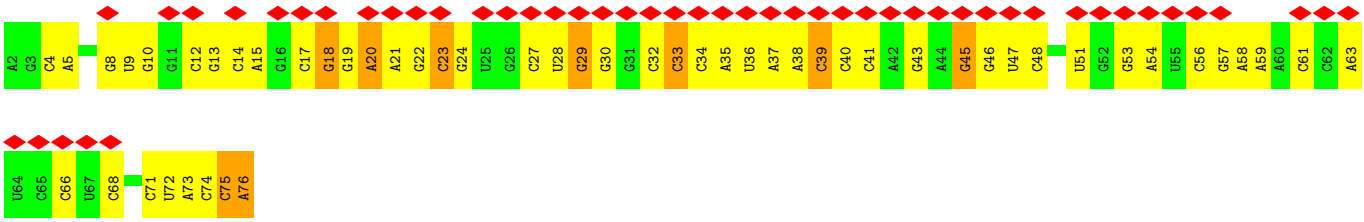
Chain AV:





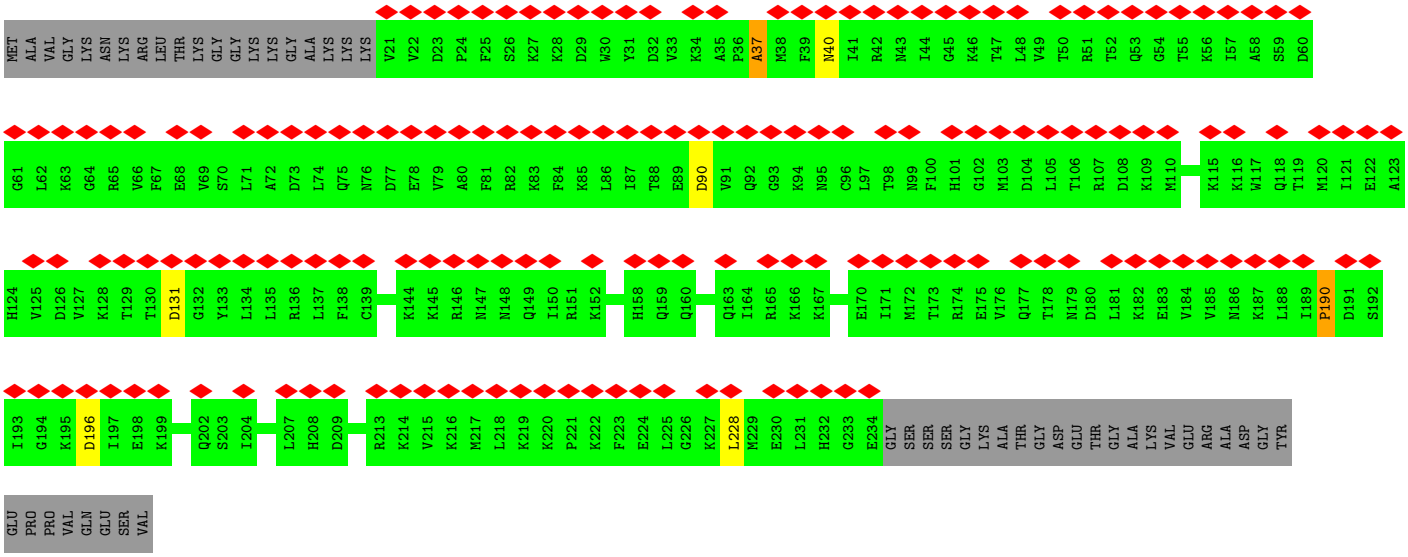
- Molecule 62: tRNA

Chain An:



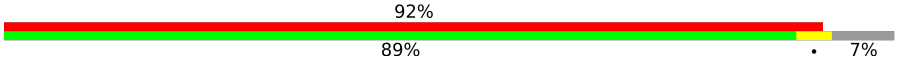
- Molecule 63: 40S ribosomal protein S3a

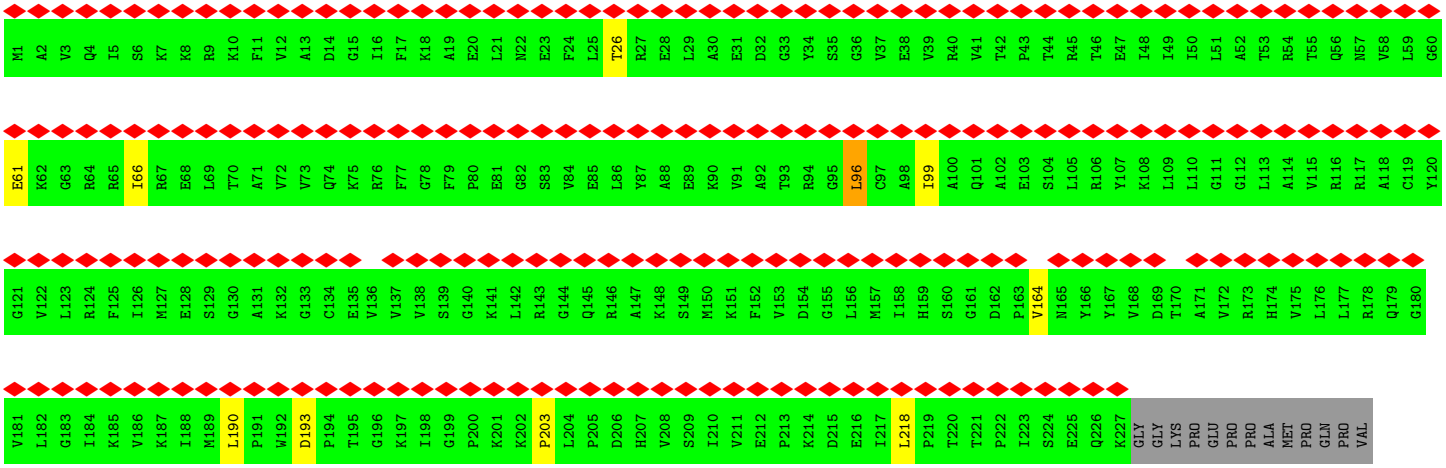
Chain Ap:



- Molecule 64: 40S ribosomal protein S3

Chain Aq:

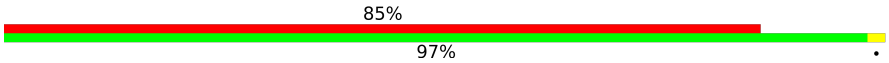




PRO
THR
ALA

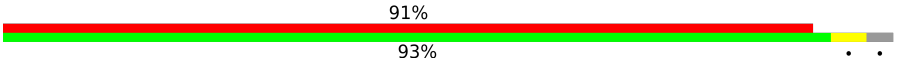
- Molecule 65: 40S ribosomal protein S4, X isoform

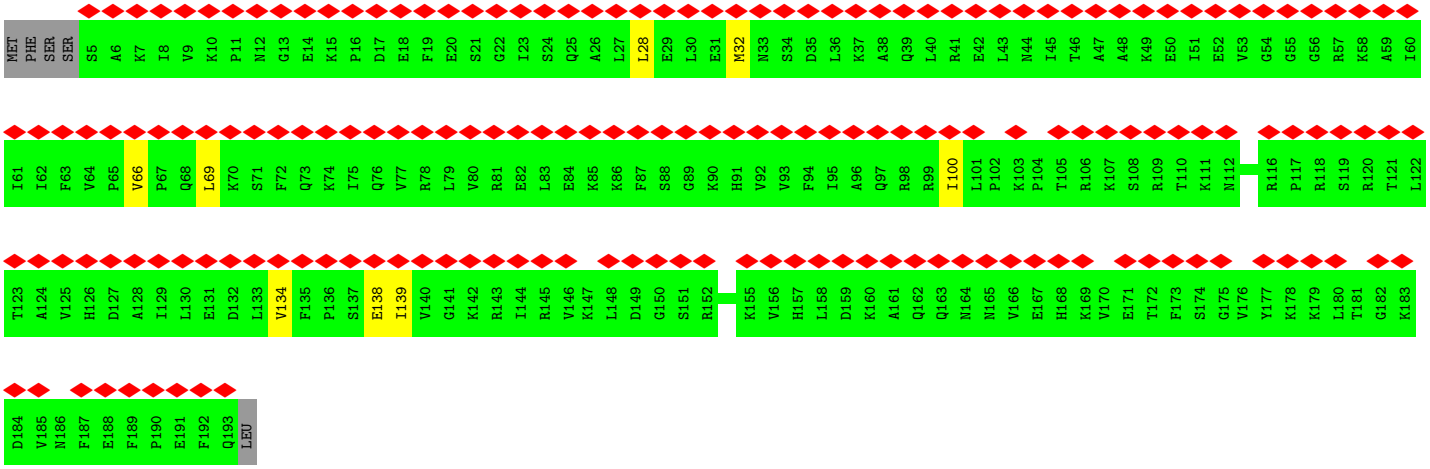
Chain Ar:



- Molecule 66: 40S ribosomal protein S7

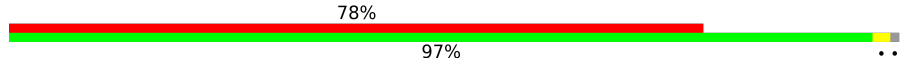
Chain At:

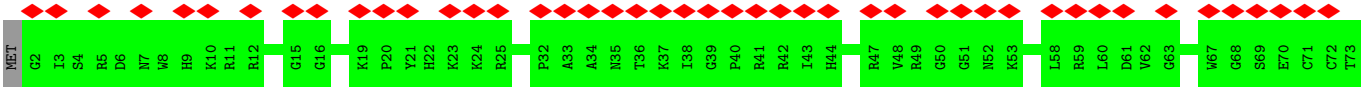




- Molecule 67: 40S ribosomal protein S8

Chain Au:





R74 K75 T76 R77 I78 I79 D80 V81 V82 Y83 N84 A85 S86 N87 N88 E89 L90 V91 R92 T93 K94 T95 L96 V97 K98 N99 C100 I101 V102 L103 I104 D105 S106 Y109 R110 Q111 W112 Y113 E114 S115 H116 Y117 A118 L119 P120 L121 G122 R123 K124 K125 G126 A127 K128 L129 T130 P131 E132 E133 E134

E135 I136 L137 N138 K139 K140 R141 S142 K143 K144 I145 Q146 K147 K148 Y149 D150 E151 R152 K153 K154 N155 A156 K157 I158 S159 S160 L161 L162 E163 E164 Q165 F166 Q167 Q168 G169 K170 L171 L172 A176 S177 R178 Q181 A185 D186 G187 L190 E191 G192 K193 E194 L195 E196 F197 Y198 L199 R200

K201 I202 K203 A204 R205 K206 G207 LYS

- Molecule 68: 40S ribosomal protein S10

Chain Av: 59% 58% 41%

M1 L2 M3 P4 K5 K6 N7 R8 I9 A10 I11 Y12 E13 L14 L15 F16 K17 E18 G19 V20 M21 V22 A23 K24 K25 D26 V27 H28 M29 P30 K31 H32 P33 E34 L35 A36 D37 K38 N39 V40 P41 N42 L43 H44 V45 M46 K47 A48 M49 Q50 S51 L52 K53 S54 R55 G56 Y57 V58 K59 E60

Q61 F62 A63 W64 R65 H66 F67 Y68 W69 Y70 L71 T72 N73 E74 G75 I76 Q77 Y78 L79 R80 D81 Y82 L83 H84 L85 P86 P87 E88 I89 V90 P91 A92 T93 L94 R95 R96 S97 R98 PRO GLU THR GLY ARG PRO ARG PRO LYS GLY LEU GLU GLY GLU ARG PRO ALA ARG LEU THR ARG GLY

GLU ALA ASP ARG ASP THR TYR ARG ARG SER ALA VAL PRO PRO GLY ALA ASP LYS LYS ALA GLU ALA GLY ALA GLY SER ALA THR GLU PHE GLN PHE ARG GLY GLY PHE GLY ARG GLY ARG GLY GLN PRO PRO GLN

- Molecule 69: 40S ribosomal protein S16

Chain Ay: 95% 95% 5%

M1 P2 S3 K4 G5 P6 L7 Q8 S9 V10 Q11 V12 F13 G14 R15 K16 K17 T18 A19 T20 A21 V22 A23 H24 C25 K26 R27 G28 N29 G30 L31 I32 K33 V34 N35 G36 R37 P38 L39 E40 M41 I42 E43 P44 R45 T46 L47 Q48 Y49 K50 L51 L52 E53 P54 V55 L56 L57 L58 G59 K60

E61 R62 F63 A64 G65 V66 D67 I68 R69 V70 R71 V72 K73 G74 G75 G76 H77 Q80 I81 Y82 A83 I84 R85 Q86 S87 I88 S89 K90 A91 L92 V93 A94 Y95 Y96 Q97 K98 Y99 V100 D101 E102 A103 S104 K105 K106 E107 I108 K109 D110 I111 L112 I113 Q114 Y115 D116 R117 T118 L119 L120 V121

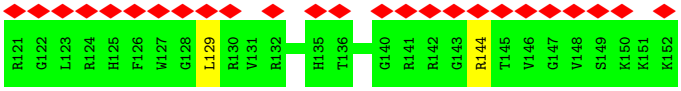
A122 D123 P124 R125 R126 C127 E128 S129 K130 G133 G134 P135 G136 A137 R138 A139 R140 Y141 Q142 K143 S144 Y145 R146

- Molecule 70: 40S ribosomal protein S18

Chain A0: 92% 91% 7%

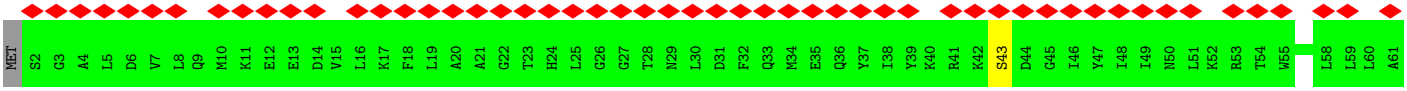
MET SER L3 V4 I5 P6 E7 K8 F9 Q10 H11 I12 L13 R14 V15 L16 N17 T18 N19 I20 D21 G22 R23 R24 K25 I26 A27 F28 A29 I30 T31 A32 I33 K34 G35 V36 G37 R38 R39 Y40 A41 H42 V43 V44 L45 R46 K47 A48 D49 I50 D51 L52 T53 K54 R55 A56 G57 E58 L59 T60

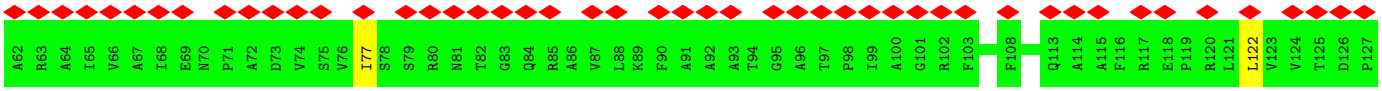
E61 D62 E63 V64 E65 R66 V67 I68 T69 I70 M71 Q72 N73 P74 R75 Q76 Y77 K78 I79 P80 D81 W82 F83 L84 N85 R86 Q87 K88 D89 V90 K91 D92 G93 K94 Y95 S96 Q97 V98 L99 A100 N101 G102 L103 D104 N105 K106 L107 R108 E109 D110 L111 E112 R113 L114 K115 K116 I117 R118 A119 H120

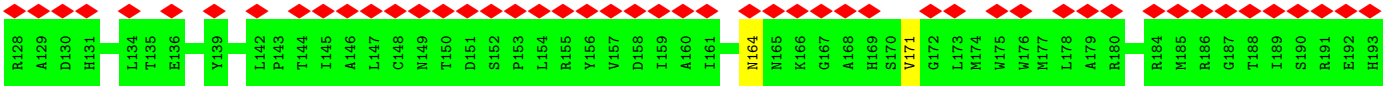


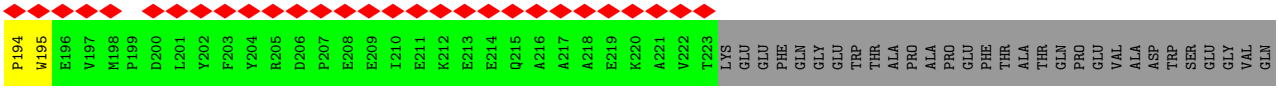
• Molecule 71: 40S ribosomal protein SA

Chain Ao:



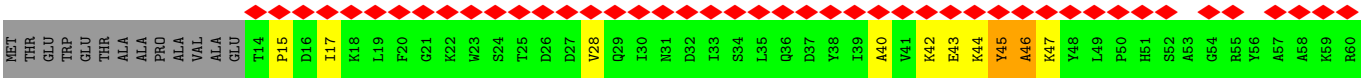


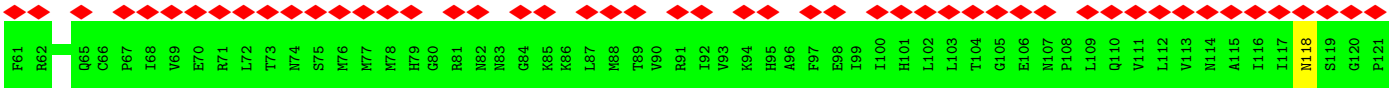


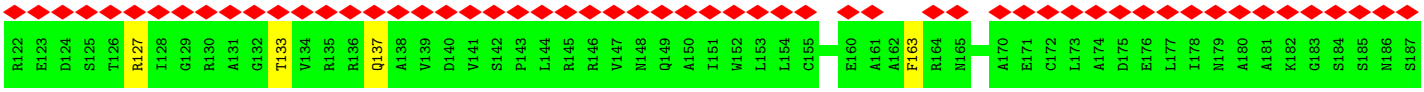


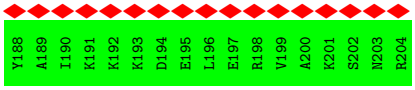
• Molecule 72: 40S ribosomal protein S5

Chain As:



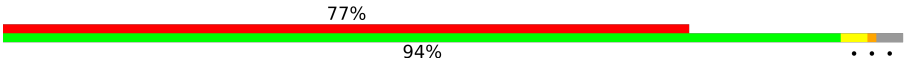


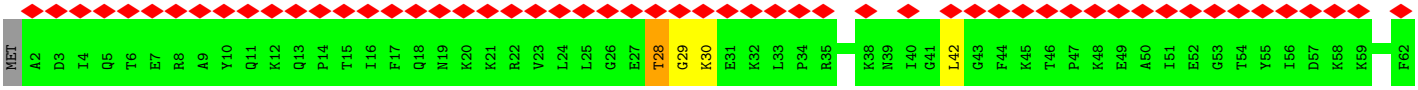


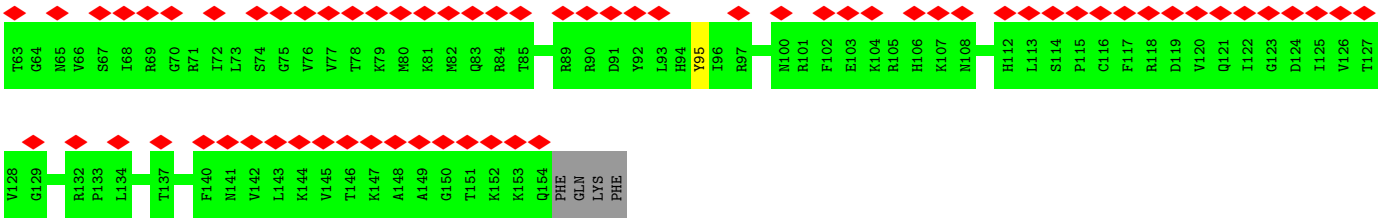


• Molecule 73: 40S ribosomal protein S11

Chain Aw:

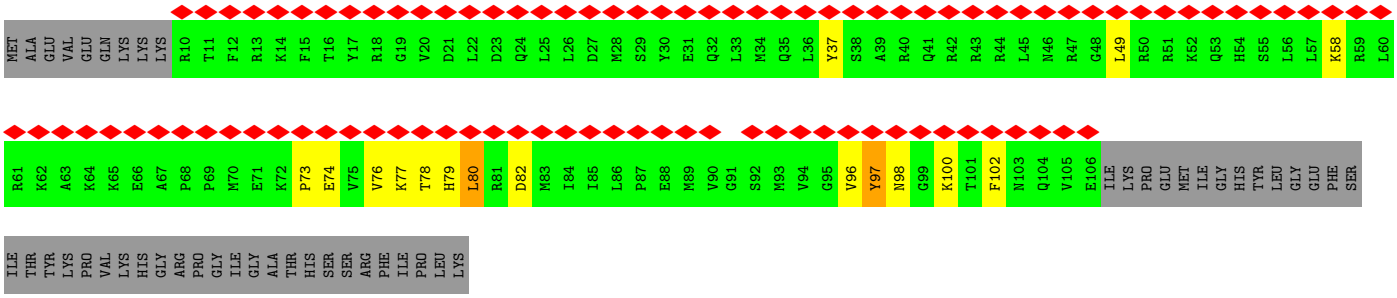






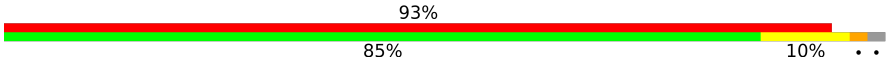
- Molecule 74: 40S ribosomal protein S15

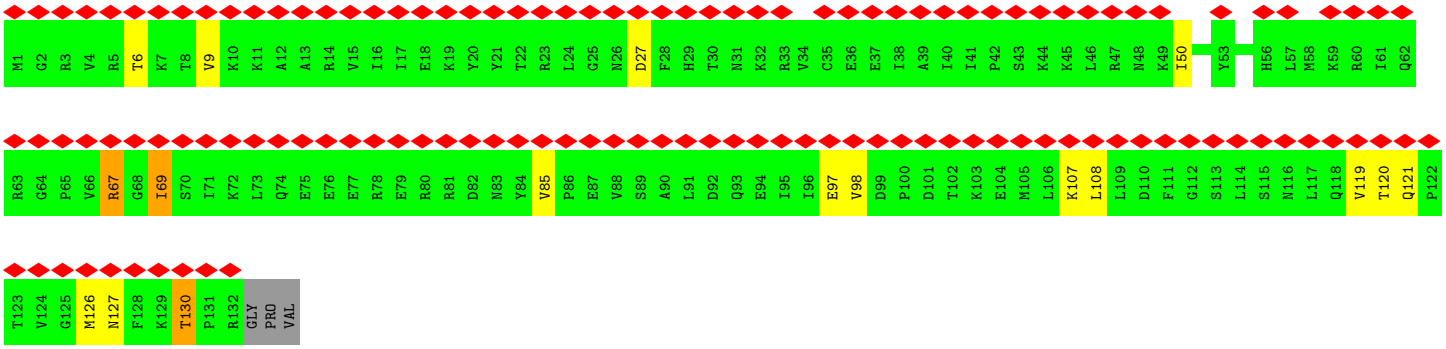
Chain Ax:



- Molecule 75: 40S ribosomal protein S17

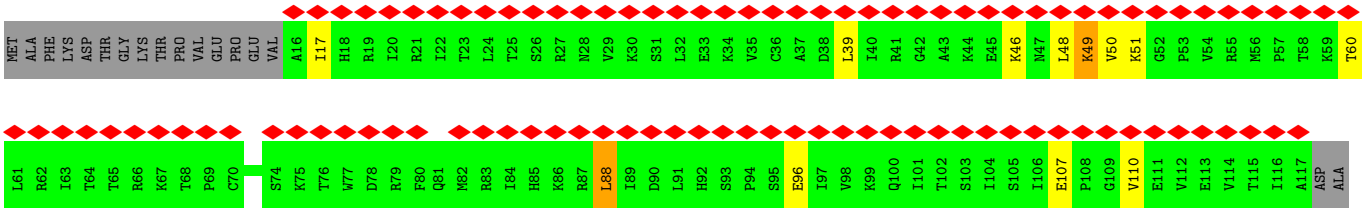
Chain Az:





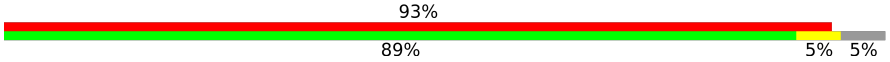
- Molecule 76: 40S ribosomal protein S20

Chain AB:



- Molecule 77: 40S ribosomal protein S29

Chain AG:



MET GLY HIS Q4 Q5 L6 Y7 W8 S9 H10 P11 R12 K13 F14 G15 Q16 G17 S18 R19 S20 C21 R22 V23 C24 S25 N26 R27 H28 G29 L30 I31 R32 K33 Y34 G35 L36 N37 M38 C39 R40 Q41 C42 F43 R44 Q45 Y46 A47 K48 D49 I50 G51 F52 I53 K54 L55 D56

- Molecule 78: Receptor of activated protein C kinase 1

Chain AI: 99% 95%

MET T2 E3 Q4 M5 T6 L7 R8 G9 T10 L11 K12 G13 H14 N15 G16 W17 V18 T19 Q20 I21 A22 T23 T24 P25 Q26 F27 P28 D29 M30 I31 L32 S33 A34 S35 R36 D37 K38 T39 I40 I41 M42 W43 K44 L45 T46 R47 D48 E49 T50 N51 Y52 G53 I54 P55 Q56 R57 A58 L59 R60

G61 H62 S63 H64 F65 V66 S67 D68 V69 V70 I71 S72 S73 D74 G75 Q76 F77 A78 L79 S80 G81 S82 W83 D84 G85 T86 L87 R88 L89 W90 D91 L92 T93 T94 G95 T96 T97 T98 R99 R100 F101 V102 G103 H104 T105 K106 D107 V108 L109 S110 V111 A112 F113 S114 S115 D116 N117 R118 Q119 I120

V121 S122 G123 S124 R125 D126 K127 T128 I129 K130 L131 W132 N133 T134 L135 G136 V137 C138 K139 Y140 T141 V142 Q143 D144 E145 S146 H147 S148 E149 W150 V151 S152 C153 V154 R155 F156 S157 P158 N159 S160 S161 N162 P163 I164 I165 V166 S167 C168 G169 W170 D171 K172 L173 V174 K175 V176 W177 N178 L179 A180

N181 C182 K183 L184 K185 T186 N187 H188 I189 G190 H191 T192 G193 Y194 L195 N196 T197 V198 T199 V200 S201 P202 D203 G204 S205 L206 C207 A208 S209 G210 G211 K212 D213 G214 Q215 A216 M217 L218 W219 D220 L221 N222 E223 G224 K225 H226 L227 Y228 T229 L230 D231 G232 G233 D234 I235 I236 N237 A238 L239 C240

F241 S242 P243 N244 R245 Y246 W247 L248 C249 A250 A251 T252 G253 P254 S255 I256 K257 I258 W259 D260 L261 E262 G263 K264 I265 I266 V267 D268 E269 L270 K271 Q272 E273 V274 I275 S276 T277 S278 S279 K280 A281 E282 P283 P284 Q285 C286 T287 S288 L289 A290 W291 S292 A293 D294 G295 Q296 T297 L298 F299 A300

G301 Y302 T303 D304 N305 L306 V307 R308 V309 W310 Q311 V312 T313 I314 GLY THR ARG

- Molecule 79: 40S ribosomal protein S12

Chain AM: 92% 88% 8%

MET ALA GLU GLU GLY ILE ALA ALA GLY GLY V11 M12 D13 V14 N15 T16 A17 L18 Q19 E20 V21 L22 K23 T24 A25 L26 I27 H28 D29 G30 L31 A32 R33 G34 I35 R36 E37 A38 A39 K40 A41 L42 D43 K44 R45 Q46 A47 H48 L49 C50 V51 Q52 A53 S54 N55 C56 D57 E58 P59 M60

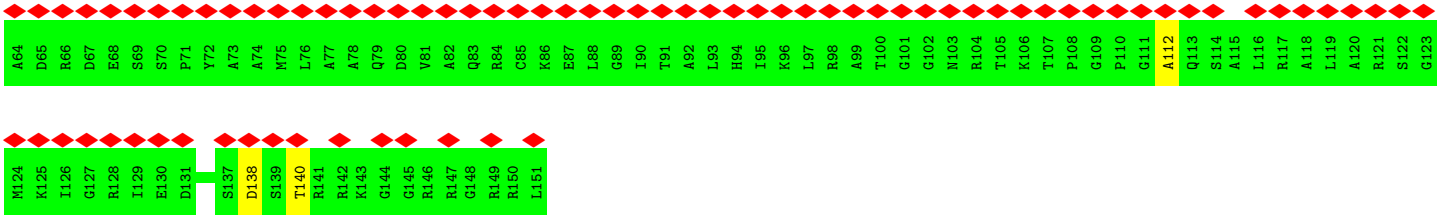
Y61 V62 K63 L64 V65 E66 A67 L68 L69 A70 E71 H72 Q73 I74 N75 L76 I77 K78 V79 D80 D81 N82 K83 K84 L85 G86 E87 W88 V89 G90 L91 C92 K93 I94 D95 R96 E97 G98 N99 P100 R101 K102 V103 V104 G105 C106 S107 C108 V109 V110 V111 K112 D113 Y114 G115 K116 E117 S118 Q119 A120

K121 D122 V123 I124 E125 E126 Y127 F128 K129 C130 K131 K132

- Molecule 80: 40S ribosomal protein S14

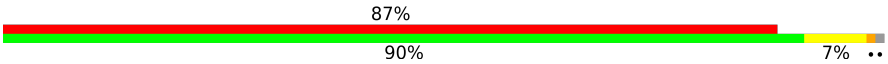
Chain AO: 78% 88% 5% 7%

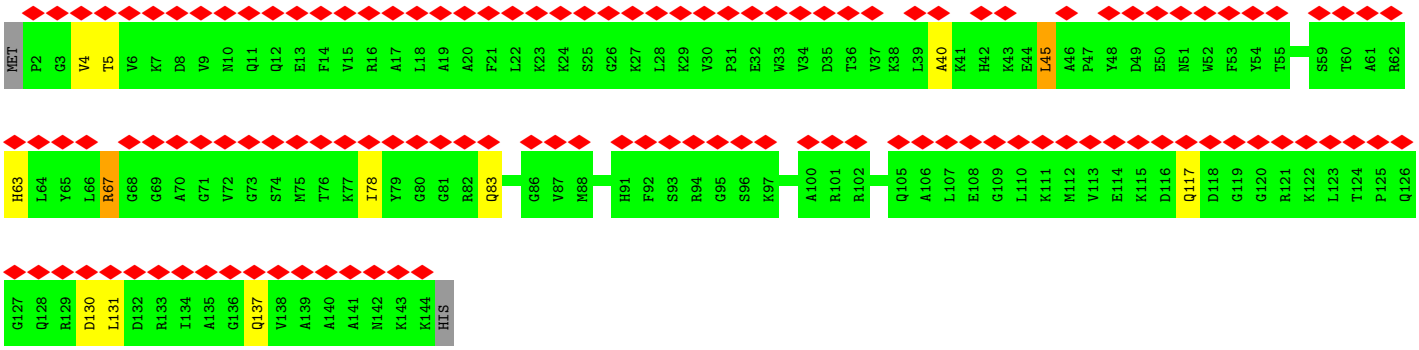
MET ALA PRO ARG LYS GLY LYS GLU LYS LYS GLU E12 Q13 V14 I15 S16 L17 G18 P19 Q20 V21 A22 E23 G24 E25 N26 V27 F28 G29 V30 I33 S36 F37 N38 F41 V42 H43 V44 T45 D46 L47 S48 G49 K50 E51 T52 I53 C54 R55 V56 T57 G58 G59 M60 K61 V62 K63



- Molecule 81: 40S ribosomal protein S19

Chain AU:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	175708	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.127	Depositor
Minimum map value	-0.052	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	374.50003, 374.50003, 374.50003	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	B	0.22	0/2858	0.68	0/4455
2	C	0.23	0/3701	0.71	3/5766 (0.1%)
3	D	0.28	0/1936	0.50	0/2596
4	E	0.26	0/3306	0.49	0/4424
5	F	0.25	0/2973	0.47	0/3992
6	G	0.26	0/2428	0.45	0/3252
7	I	0.26	0/1682	0.45	0/2250
8	J	0.26	0/1268	0.45	0/1701
9	L	0.24	0/1582	0.45	0/2091
10	N	0.26	0/1326	0.44	0/1770
11	O	0.27	0/839	0.46	0/1126
12	P	0.27	0/993	0.47	0/1332
13	Q	0.26	0/547	0.44	0/728
14	S	0.25	0/1132	0.46	0/1504
15	T	0.27	0/1130	0.47	0/1507
16	U	0.28	0/1191	0.51	0/1591
17	V	0.24	0/620	0.41	0/819
18	X	0.25	0/903	0.44	0/1216
19	Y	0.26	0/1071	0.46	0/1429
20	Z	0.27	0/895	0.50	0/1198
21	a	0.25	0/916	0.46	0/1220
22	b	0.24	0/1023	0.43	0/1351
23	c	0.25	0/843	0.44	0/1115
24	d	0.25	0/720	0.48	0/952
25	e	0.26	0/575	0.51	0/761
26	f	0.24	0/454	0.41	0/599
27	g	0.23	0/435	0.44	0/575
28	j	0.29	0/718	0.45	0/953
29	k	0.26	0/1017	0.49	0/1364
30	m	0.26	0/1905	0.42	0/2539
31	n	0.25	0/1960	0.45	0/2637
32	o	0.25	0/1537	0.49	0/2066
33	s	0.28	0/1161	0.45	0/1554
34	t	0.26	0/1746	0.48	1/2338 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	h	0.21	0/231	0.36	0/294
36	r	0.29	0/1732	0.51	2/2315 (0.1%)
37	A	0.24	0/89645	0.73	17/139764 (0.0%)
38	H	0.34	0/1996	0.86	9/2673 (0.3%)
39	i	0.26	0/876	0.47	0/1156
40	K	0.27	0/1537	0.70	1/2052 (0.0%)
41	l	0.29	0/1769	0.52	1/2371 (0.0%)
42	M	0.32	0/1493	0.50	0/2003
43	p	0.26	0/1751	0.48	0/2340
44	q	0.25	0/1432	0.46	0/1912
45	R	0.25	0/1002	0.44	0/1345
46	W	0.26	0/774	0.46	0/1038
47	AA	1.45	406/41243 (1.0%)	1.53	695/64257 (1.1%)
48	AC	0.64	0/643	0.79	0/860
49	AD	0.83	0/1116	0.85	1/1490 (0.1%)
50	AE	0.75	0/828	0.78	0/1109
51	AF	0.50	0/500	0.83	1/669 (0.1%)
52	AH	0.51	0/593	0.80	1/786 (0.1%)
53	AJ	0.75	0/1762	0.83	3/2381 (0.1%)
54	AK	0.48	0/1946	0.75	1/2590 (0.0%)
55	AL	0.61	0/1550	0.77	0/2069
56	AN	0.67	0/1226	0.79	2/1649 (0.1%)
57	AP	0.74	0/1051	0.93	4/1406 (0.3%)
58	AQ	0.59	1/1083 (0.1%)	0.79	1/1438 (0.1%)
59	AR	0.42	0/604	0.80	1/810 (0.1%)
60	AT	0.54	0/465	0.73	0/612
61	AV	0.58	0/665	0.75	1/891 (0.1%)
62	An	1.24	10/1795 (0.6%)	1.64	46/2798 (1.6%)
63	Ap	0.66	0/1765	0.78	1/2362 (0.0%)
64	Aq	0.54	2/1793 (0.1%)	0.77	2/2414 (0.1%)
65	Ar	0.60	0/2118	0.72	0/2849
66	At	0.53	0/1544	0.79	3/2068 (0.1%)
67	Au	0.69	0/1715	0.76	1/2287 (0.0%)
68	Av	0.45	0/851	0.79	0/1147
69	Ay	0.49	0/1177	0.74	0/1575
70	A0	0.50	0/1253	0.84	1/1676 (0.1%)
71	Ao	0.68	0/1784	0.76	1/2424 (0.0%)
72	As	0.48	0/1531	0.76	1/2059 (0.0%)
73	Aw	0.79	1/1268 (0.1%)
74	Ax	0.44	0/815	0.78	1/1087 (0.1%)
75	Az	0.55	0/1086	0.84	0/1457
76	AB	0.47	0/817	0.84	2/1097 (0.2%)
77	AG	0.52	0/455	0.68	0/603

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
78	AI	0.46	0/2493	0.75	3/3394 (0.1%)
79	AM	0.41	0/962	0.80	1/1290 (0.1%)
80	AO	0.61	0/1062	0.83	0/1425
81	AU	0.52	0/1131	0.82	2/1515 (0.1%)
All	All	0.69	420/234319 (0.2%)	0.92	811/344274 (0.2%)

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
5	F	0	1
11	O	0	1
33	s	0	1
38	H	0	1
39	i	0	1
40	K	0	1
48	AC	0	1
49	AD	0	3
52	AH	0	2
53	AJ	0	1
54	AK	0	5
55	AL	0	1
56	AN	0	1
59	AR	0	1
60	AT	0	3
61	AV	0	1
63	Ap	0	3
64	Aq	0	3
65	Ar	0	2
66	At	0	3
67	Au	0	1
68	Av	0	1
69	Ay	0	5
70	A0	0	4
71	Ao	0	4
72	As	0	6
75	Az	0	4
76	AB	0	4
78	AI	0	5
79	AM	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
80	AO	0	2
81	AU	0	4
All	All	0	78

The worst 5 of 420 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	1031	A	N9-C4	-10.37	1.31	1.37
47	AA	1170	A	N9-C4	-9.35	1.32	1.37
47	AA	1815	A	N9-C4	-9.17	1.32	1.37
47	AA	1815	A	N3-C4	-8.95	1.29	1.34
47	AA	1173	A	N9-C4	-8.77	1.32	1.37

The worst 5 of 811 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
40	K	158	THR	C-N-CD	-21.62	73.03	120.60
38	H	96	VAL	N-CA-C	-18.95	59.84	111.00
38	H	89	LEU	N-CA-C	-15.05	70.37	111.00
47	AA	1130	G	N3-C4-C5	12.10	134.65	128.60
47	AA	1861	G	N3-C4-C5	-11.49	122.85	128.60

There are no chirality outliers.

5 of 78 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	F	290	SER	Peptide
38	H	88	VAL	Mainchain
11	O	65	ARG	Peptide
39	i	58	LYS	Peptide
33	s	40	GLY	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	
3	D	246/257 (96%)	227 (92%)	19 (8%)	0	100	100
4	E	400/403 (99%)	378 (94%)	22 (6%)	0	100	100
5	F	365/427 (86%)	331 (91%)	33 (9%)	1 (0%)	41	75
6	G	291/297 (98%)	270 (93%)	20 (7%)	1 (0%)	41	75
7	I	199/203 (98%)	195 (98%)	4 (2%)	0	100	100
8	J	151/160 (94%)	145 (96%)	5 (3%)	1 (1%)	22	61
9	L	185/196 (94%)	177 (96%)	8 (4%)	0	100	100
10	N	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
11	O	99/128 (77%)	94 (95%)	5 (5%)	0	100	100
12	P	129/140 (92%)	122 (95%)	7 (5%)	0	100	100
13	Q	62/157 (40%)	58 (94%)	4 (6%)	0	100	100
14	S	132/145 (91%)	121 (92%)	11 (8%)	0	100	100
15	T	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
16	U	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
17	V	73/159 (46%)	65 (89%)	8 (11%)	0	100	100
18	X	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
19	Y	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
20	Z	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
21	a	112/117 (96%)	109 (97%)	3 (3%)	0	100	100
22	b	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
23	c	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
24	d	84/97 (87%)	79 (94%)	5 (6%)	0	100	100
25	e	67/70 (96%)	62 (92%)	4 (6%)	1 (2%)	10	47
26	f	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
27	g	50/128 (39%)	45 (90%)	5 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	j	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
29	k	123/137 (90%)	110 (89%)	13 (11%)	0	100	100
30	m	223/248 (90%)	212 (95%)	11 (5%)	0	100	100
31	n	239/266 (90%)	228 (95%)	11 (5%)	0	100	100
32	o	188/192 (98%)	172 (92%)	16 (8%)	0	100	100
33	s	137/215 (64%)	124 (90%)	13 (10%)	0	100	100
34	t	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
35	h	22/25 (88%)	19 (86%)	2 (9%)	1 (4%)	2	23
36	r	208/211 (99%)	189 (91%)	17 (8%)	2 (1%)	15	55
38	H	238/288 (83%)	203 (85%)	30 (13%)	5 (2%)	7	40
39	i	103/106 (97%)	99 (96%)	4 (4%)	0	100	100
40	K	185/188 (98%)	177 (96%)	7 (4%)	1 (0%)	29	68
41	l	215/217 (99%)	188 (87%)	25 (12%)	2 (1%)	17	57
42	M	173/176 (98%)	158 (91%)	13 (8%)	2 (1%)	13	51
43	p	211/214 (99%)	196 (93%)	14 (7%)	1 (0%)	29	68
44	q	172/178 (97%)	163 (95%)	6 (4%)	3 (2%)	9	45
45	R	118/156 (76%)	112 (95%)	6 (5%)	0	100	100
46	W	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
48	AC	81/83 (98%)	70 (86%)	8 (10%)	3 (4%)	3	28
49	AD	139/143 (97%)	117 (84%)	22 (16%)	0	100	100
50	AE	99/115 (86%)	93 (94%)	6 (6%)	0	100	100
51	AF	61/69 (88%)	55 (90%)	6 (10%)	0	100	100
52	AH	69/156 (44%)	54 (78%)	13 (19%)	2 (3%)	4	33
53	AJ	220/293 (75%)	195 (89%)	25 (11%)	0	100	100
54	AK	235/249 (94%)	206 (88%)	27 (12%)	2 (1%)	17	57
55	AL	183/194 (94%)	161 (88%)	21 (12%)	1 (0%)	29	68
56	AN	147/151 (97%)	125 (85%)	22 (15%)	0	100	100
57	AP	127/130 (98%)	112 (88%)	15 (12%)	0	100	100
58	AQ	129/133 (97%)	118 (92%)	8 (6%)	3 (2%)	6	38
59	AR	73/125 (58%)	61 (84%)	12 (16%)	0	100	100
60	AT	56/59 (95%)	51 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	AV	81/84 (96%)	73 (90%)	7 (9%)	1 (1%)	13	51
63	Ap	212/264 (80%)	184 (87%)	25 (12%)	3 (1%)	11	48
64	Aq	225/243 (93%)	195 (87%)	26 (12%)	4 (2%)	8	43
65	Ar	260/263 (99%)	226 (87%)	31 (12%)	3 (1%)	13	51
66	At	187/194 (96%)	155 (83%)	30 (16%)	2 (1%)	14	53
67	Au	204/208 (98%)	179 (88%)	22 (11%)	3 (2%)	10	47
68	Av	96/165 (58%)	77 (80%)	18 (19%)	1 (1%)	15	55
69	Ay	144/146 (99%)	123 (85%)	18 (12%)	3 (2%)	7	40
70	A0	148/152 (97%)	121 (82%)	21 (14%)	6 (4%)	3	26
71	Ao	220/295 (75%)	190 (86%)	28 (13%)	2 (1%)	17	57
72	As	189/204 (93%)	158 (84%)	23 (12%)	8 (4%)	3	25
73	Aw	151/158 (96%)	130 (86%)	18 (12%)	3 (2%)	7	41
74	Ax	95/145 (66%)	60 (63%)	21 (22%)	14 (15%)	0	3
75	Az	130/135 (96%)	93 (72%)	26 (20%)	11 (8%)	1	10
76	AB	100/119 (84%)	82 (82%)	14 (14%)	4 (4%)	3	26
77	AG	51/56 (91%)	43 (84%)	6 (12%)	2 (4%)	3	27
78	AI	311/317 (98%)	261 (84%)	44 (14%)	6 (2%)	8	42
79	AM	120/132 (91%)	91 (76%)	26 (22%)	3 (2%)	5	36
80	AO	138/151 (91%)	112 (81%)	21 (15%)	5 (4%)	3	29
81	AU	141/145 (97%)	116 (82%)	18 (13%)	7 (5%)	2	21
All	All	11449/12881 (89%)	10266 (90%)	1060 (9%)	123 (1%)	18	53

5 of 123 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	H	100	LYS
38	H	225	PRO
40	K	159	PRO
44	q	55	TYR
44	q	59	SER

5.3.2 Protein sidechains (i)

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	190/199 (96%)	190 (100%)	0	100	100
4	E	348/349 (100%)	348 (100%)	0	100	100
5	F	305/348 (88%)	305 (100%)	0	100	100
6	G	246/250 (98%)	246 (100%)	0	100	100
7	I	173/174 (99%)	173 (100%)	0	100	100
8	J	134/141 (95%)	134 (100%)	0	100	100
9	L	166/175 (95%)	166 (100%)	0	100	100
10	N	139/140 (99%)	139 (100%)	0	100	100
11	O	91/115 (79%)	91 (100%)	0	100	100
12	P	101/107 (94%)	101 (100%)	0	100	100
13	Q	56/126 (44%)	56 (100%)	0	100	100
14	S	124/135 (92%)	124 (100%)	0	100	100
15	T	117/118 (99%)	117 (100%)	0	100	100
16	U	120/121 (99%)	120 (100%)	0	100	100
17	V	63/126 (50%)	63 (100%)	0	100	100
18	X	98/110 (89%)	98 (100%)	0	100	100
19	Y	114/121 (94%)	114 (100%)	0	100	100
20	Z	88/89 (99%)	88 (100%)	0	100	100
21	a	98/100 (98%)	98 (100%)	0	100	100
22	b	109/110 (99%)	109 (100%)	0	100	100
23	c	86/89 (97%)	86 (100%)	0	100	100
24	d	73/80 (91%)	73 (100%)	0	100	100
25	e	64/65 (98%)	64 (100%)	0	100	100
26	f	47/48 (98%)	47 (100%)	0	100	100
27	g	48/116 (41%)	48 (100%)	0	100	100
28	j	74/75 (99%)	74 (100%)	0	100	100
29	k	109/121 (90%)	109 (100%)	0	100	100
30	m	194/215 (90%)	194 (100%)	0	100	100
31	n	203/223 (91%)	203 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	o	169/171 (99%)	169 (100%)	0	100	100
33	s	118/161 (73%)	118 (100%)	0	100	100
34	t	171/172 (99%)	171 (100%)	0	100	100
35	h	23/24 (96%)	23 (100%)	0	100	100
36	r	176/177 (99%)	174 (99%)	2 (1%)	73	88
38	H	215/252 (85%)	209 (97%)	6 (3%)	43	72
39	i	93/94 (99%)	92 (99%)	1 (1%)	73	88
40	K	164/165 (99%)	164 (100%)	0	100	100
41	l	195/196 (100%)	194 (100%)	1 (0%)	88	95
42	M	156/157 (99%)	154 (99%)	2 (1%)	69	86
43	p	180/181 (99%)	178 (99%)	2 (1%)	73	88
44	q	148/149 (99%)	144 (97%)	4 (3%)	44	73
45	R	108/133 (81%)	107 (99%)	1 (1%)	78	90
46	W	83/97 (86%)	83 (100%)	0	100	100
48	AC	67/67 (100%)	67 (100%)	0	100	100
49	AD	113/115 (98%)	113 (100%)	0	100	100
50	AE	88/98 (90%)	88 (100%)	0	100	100
51	AF	56/62 (90%)	56 (100%)	0	100	100
52	AH	64/140 (46%)	64 (100%)	0	100	100
53	AJ	188/225 (84%)	186 (99%)	2 (1%)	73	88
54	AK	207/218 (95%)	207 (100%)	0	100	100
55	AL	161/168 (96%)	161 (100%)	0	100	100
56	AN	130/131 (99%)	130 (100%)	0	100	100
57	AP	112/113 (99%)	110 (98%)	2 (2%)	59	81
58	AQ	113/115 (98%)	113 (100%)	0	100	100
59	AR	66/103 (64%)	66 (100%)	0	100	100
60	AT	47/48 (98%)	47 (100%)	0	100	100
61	AV	75/76 (99%)	75 (100%)	0	100	100
63	Ap	195/231 (84%)	193 (99%)	2 (1%)	76	88
64	Aq	190/202 (94%)	190 (100%)	0	100	100
65	Ar	224/225 (100%)	223 (100%)	1 (0%)	91	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	At	169/174 (97%)	169 (100%)	0	100	100
67	Au	178/180 (99%)	178 (100%)	0	100	100
68	Av	89/136 (65%)	89 (100%)	0	100	100
69	Ay	121/121 (100%)	120 (99%)	1 (1%)	81	91
70	A0	130/132 (98%)	130 (100%)	0	100	100
71	Ao	184/243 (76%)	184 (100%)	0	100	100
72	As	161/170 (95%)	159 (99%)	2 (1%)	71	87
73	Aw	137/142 (96%)	136 (99%)	1 (1%)	84	93
74	Ax	87/130 (67%)	84 (97%)	3 (3%)	37	69
75	Az	120/122 (98%)	115 (96%)	5 (4%)	30	63
76	AB	93/107 (87%)	89 (96%)	4 (4%)	29	63
77	AG	47/49 (96%)	46 (98%)	1 (2%)	53	78
78	AI	272/275 (99%)	270 (99%)	2 (1%)	84	93
79	AM	104/108 (96%)	103 (99%)	1 (1%)	76	88
80	AO	110/119 (92%)	110 (100%)	0	100	100
81	AU	113/115 (98%)	112 (99%)	1 (1%)	78	90
All	All	9988/10975 (91%)	9941 (100%)	47 (0%)	89	95

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
72	As	45	TYR
75	Az	120	THR
73	Aw	28	THR
74	Ax	97	TYR
75	Az	130	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
56	AN	105	ASN
70	A0	125	HIS
61	AV	19	HIS
66	At	44	ASN
73	Aw	13	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	119/121 (98%)	16 (13%)	0
2	C	155/157 (98%)	34 (21%)	1 (0%)
37	A	3707/5070 (73%)	1071 (28%)	50 (1%)
47	AA	1716/1869 (91%)	906 (52%)	48 (2%)
62	An	74/75 (98%)	37 (50%)	0
All	All	5771/7292 (79%)	2064 (35%)	99 (1%)

5 of 2064 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	2	U
1	B	7	G
1	B	17	C
1	B	22	A
1	B	24	C

5 of 99 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	AA	428	U
47	AA	912	C
47	AA	465	A
47	AA	681	U
47	AA	991	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
44	q	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	q	151:ILE	C	152:GLY	N	2.01

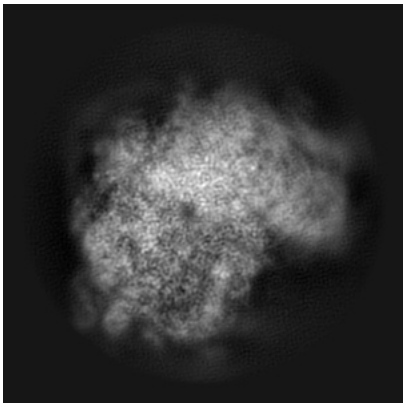
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-8345. These allow visual inspection of the internal detail of the map and identification of artifacts.

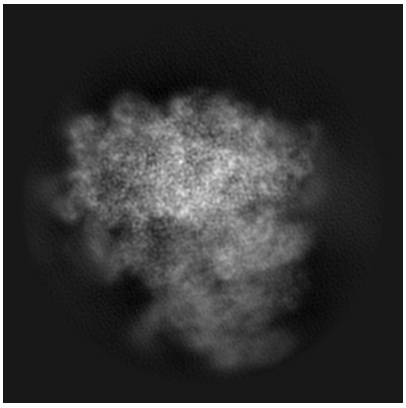
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

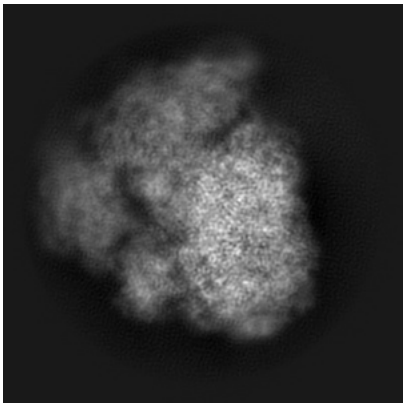
6.1.1 Primary map



X



Y

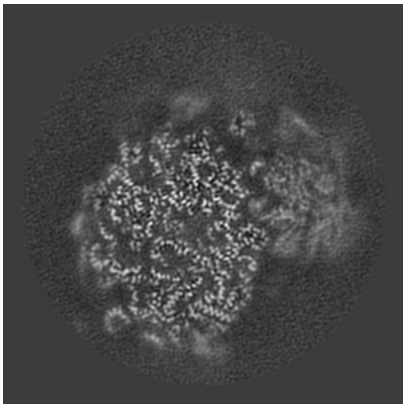


Z

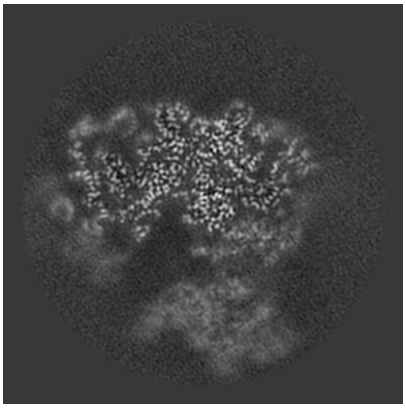
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

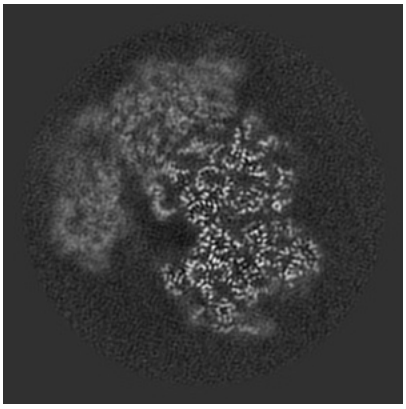
6.2.1 Primary map



X Index: 175



Y Index: 175

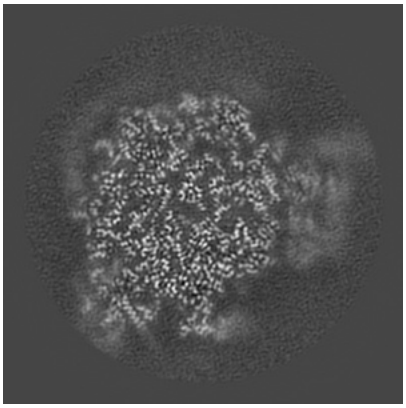


Z Index: 175

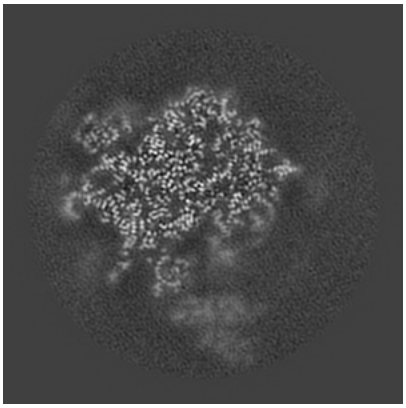
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

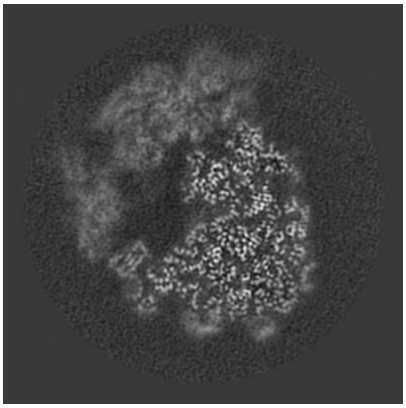
6.3.1 Primary map



X Index: 202



Y Index: 132

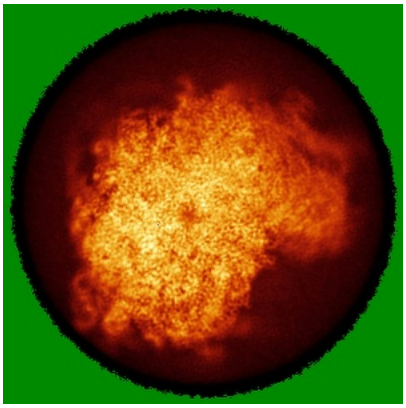


Z Index: 156

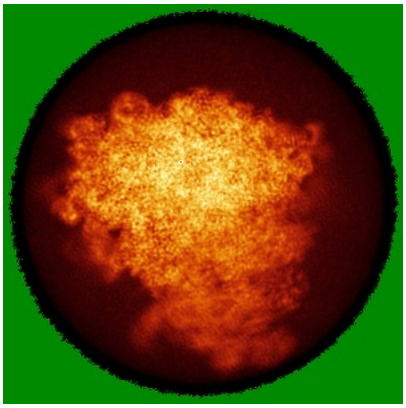
The images above show the largest variance slices of the map in three orthogonal directions.

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

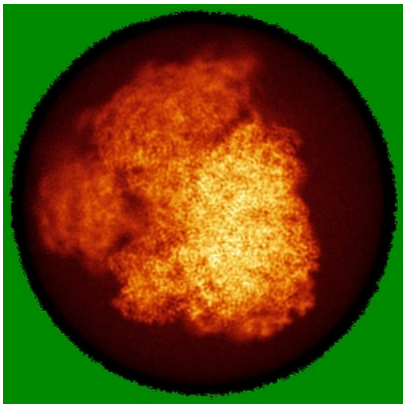
6.4.1 Primary map



X



Y



Z

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

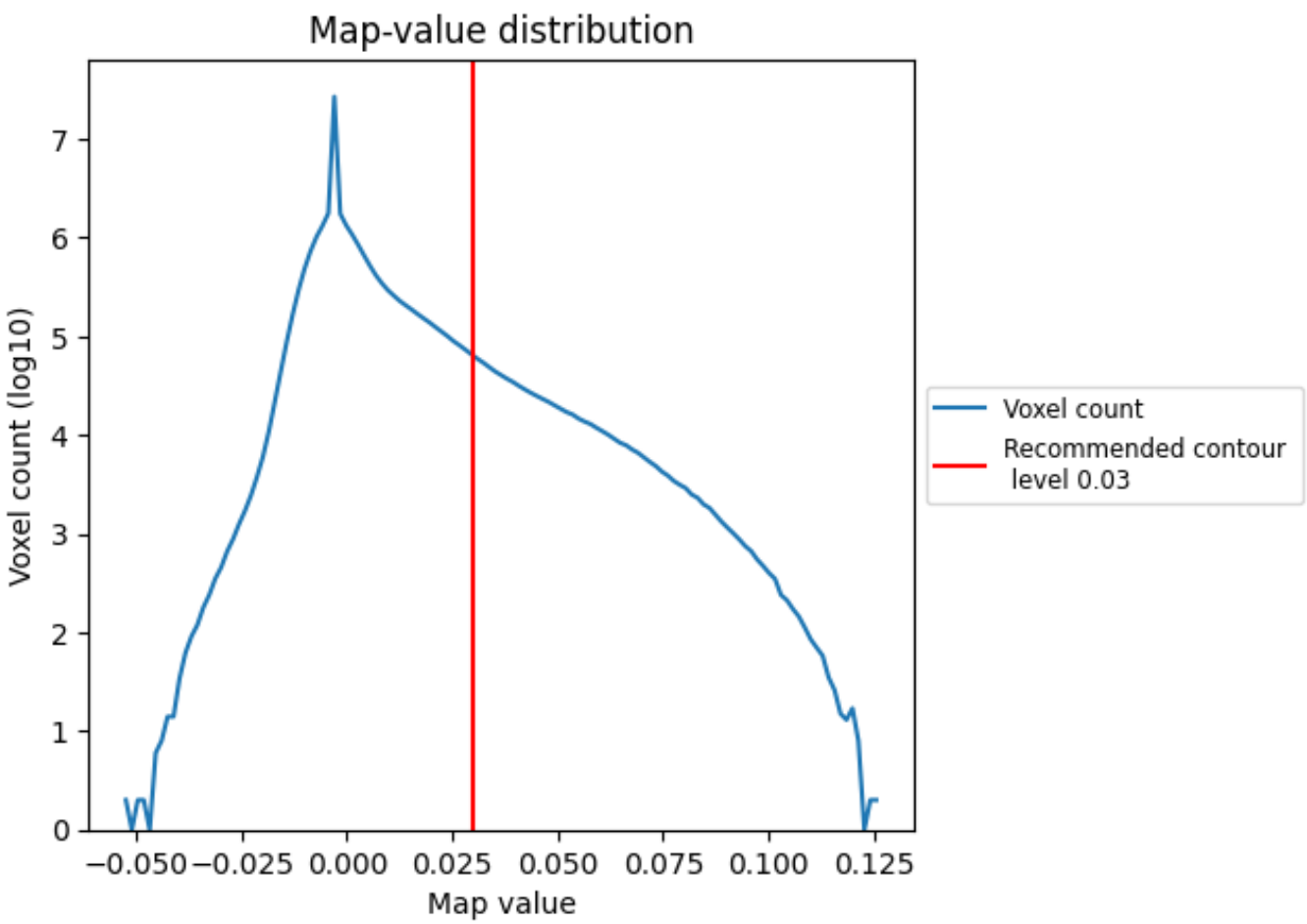
6.6 Mask visualisation (i)

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

7 Map analysis (i)

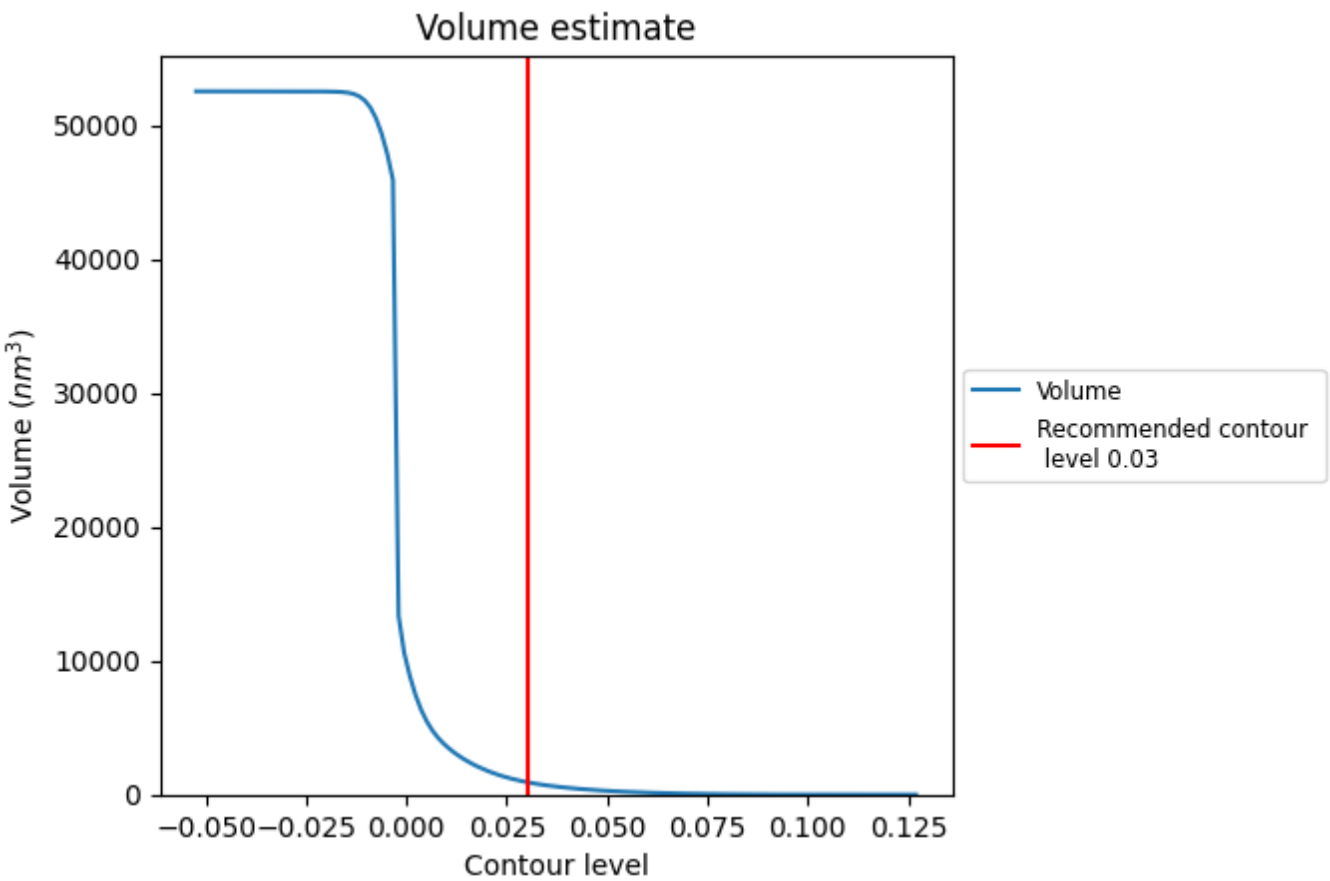
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

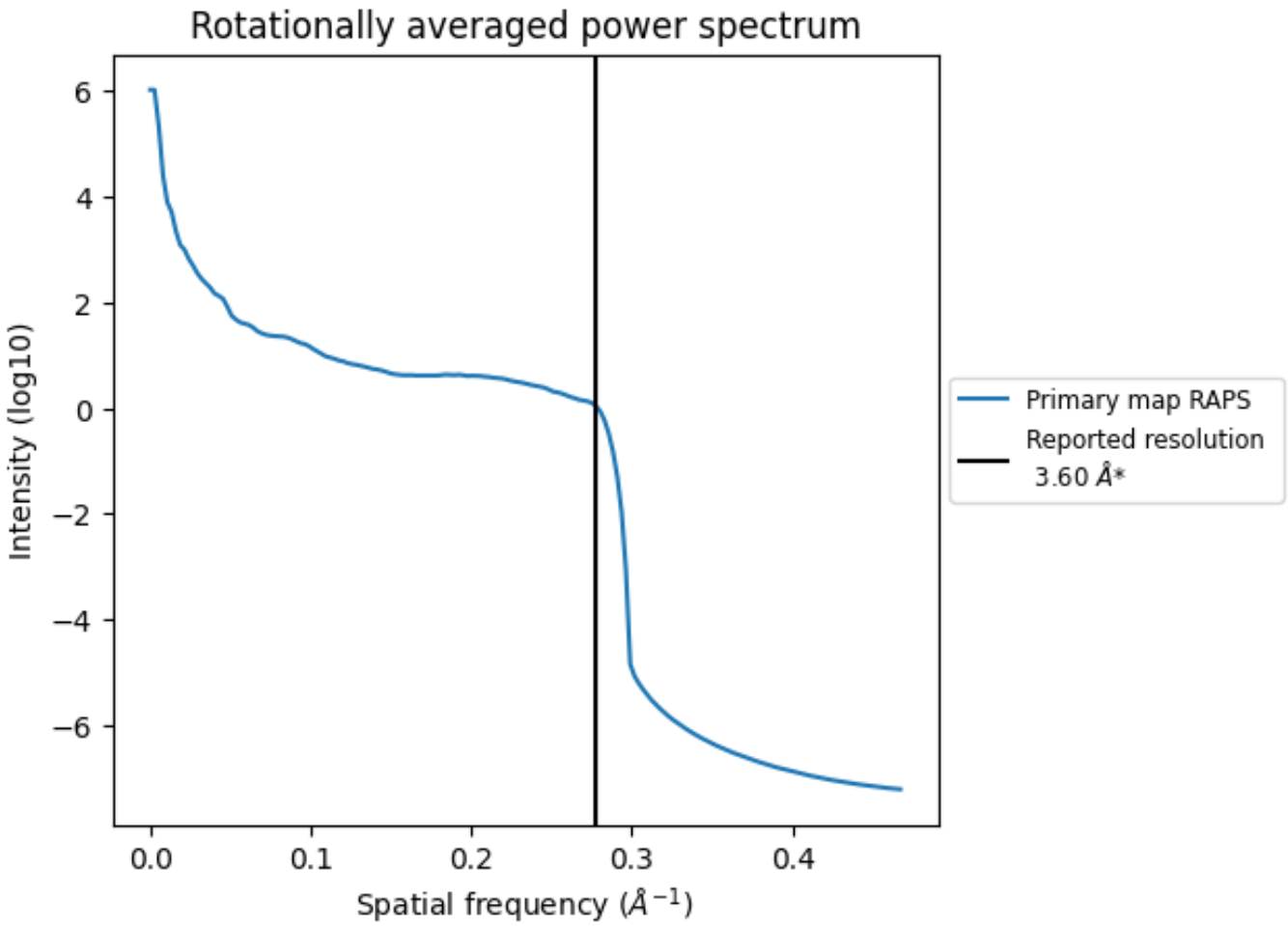
7.2 Volume estimate (i)



The volume at the recommended contour level is 928 nm^3; this corresponds to an approximate mass of 838 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 0.278 Å^{-1}

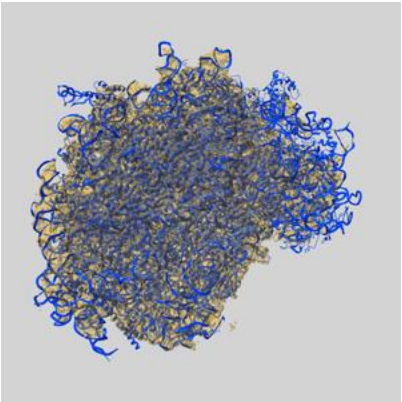
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

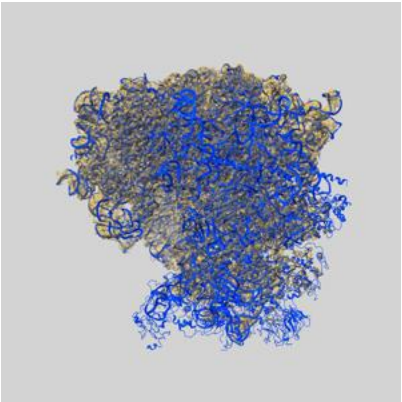
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-8345 and PDB model 5T2C. Per-residue inclusion information can be found in section 3 on page 18.

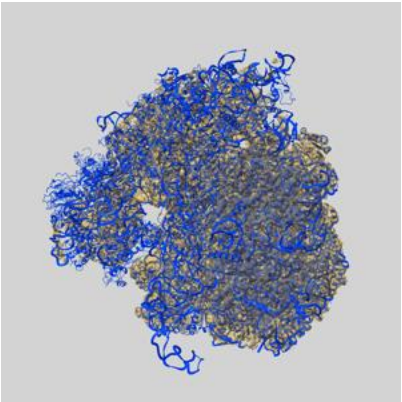
9.1 Map-model overlay (i)



X



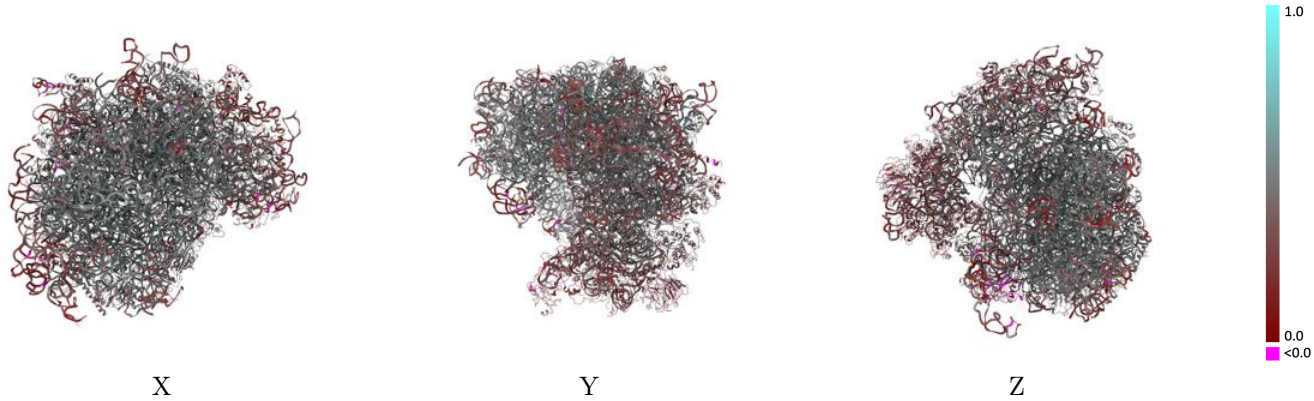
Y



Z

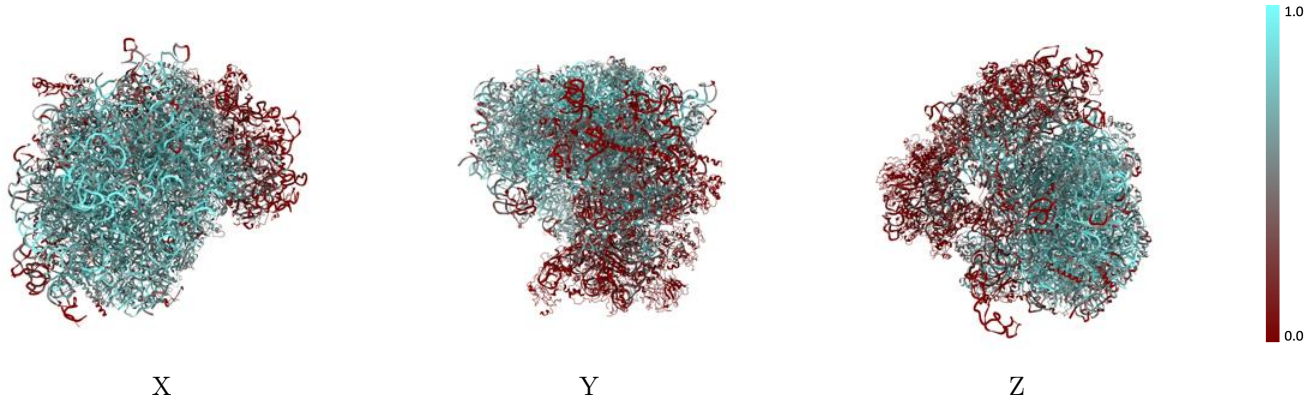
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



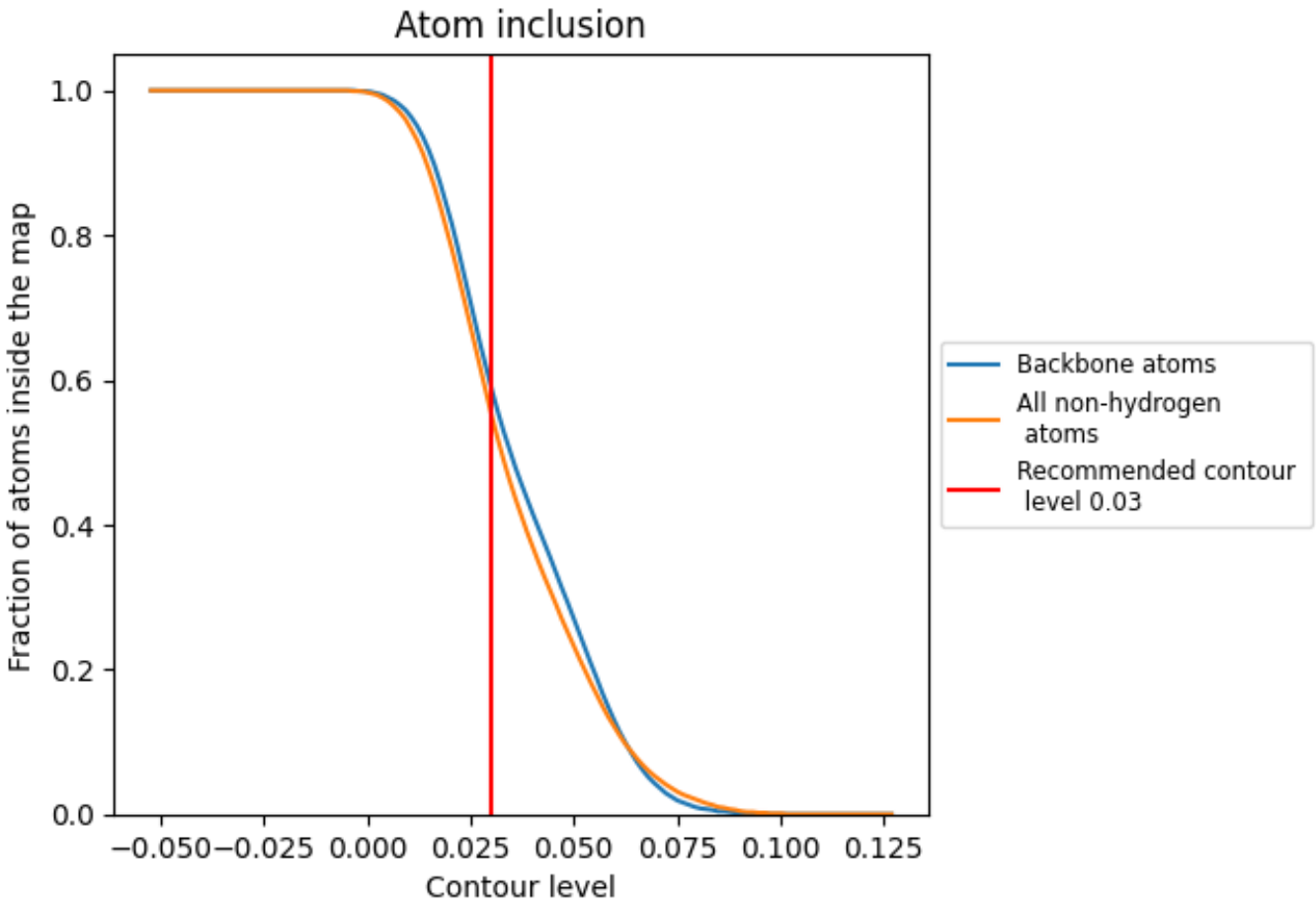
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion (i)



At the recommended contour level, 59% of all backbone atoms, 55% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5530	0.4190
A	0.7530	0.4420
A0	0.0820	0.2900
AA	0.4670	0.3940
AB	0.0480	0.3020
AC	0.1670	0.3780
AD	0.3240	0.4300
AE	0.3230	0.4420
AF	0.0710	0.3370
AG	0.0610	0.3260
AH	0.0040	0.2180
AI	0.0050	0.2700
AJ	0.2980	0.4100
AK	0.0650	0.3290
AL	0.2460	0.3850
AM	0.0000	0.2500
AN	0.2860	0.4450
AO	0.1830	0.4010
AP	0.3010	0.4190
AQ	0.1450	0.3330
AR	0.0070	0.2640
AT	0.1400	0.3800
AU	0.1390	0.2840
AV	0.1450	0.4080
An	0.3200	0.3210
Ao	0.2080	0.3830
Ap	0.1910	0.4150
Aq	0.0240	0.3290
Ar	0.1870	0.4020
As	0.1180	0.3070
At	0.0800	0.3510
Au	0.2030	0.4180
Av	0.0090	0.2770
Aw	0.1960	0.4350
Ax	0.0390	0.2670

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Chain	Atom inclusion	Q-score
Ay	0.0650	0.3010
Az	0.0630	0.3070
B	0.8980	0.4870
C	0.8290	0.4720
D	0.6560	0.4920
E	0.6320	0.4730
F	0.6400	0.4710
G	0.6210	0.4260
H	0.4890	0.3930
I	0.6480	0.4870
J	0.6750	0.4910
K	0.6530	0.4830
L	0.5470	0.4320
M	0.6810	0.4810
N	0.6220	0.4670
O	0.5010	0.4070
P	0.6100	0.4860
Q	0.5090	0.4620
R	0.5970	0.4380
S	0.6380	0.4550
T	0.5980	0.4590
U	0.6930	0.4890
V	0.4970	0.4210
W	0.5290	0.4210
X	0.6220	0.4610
Y	0.6620	0.4880
Z	0.6720	0.4970
a	0.5860	0.4600
b	0.5800	0.4290
c	0.5280	0.4330
d	0.7200	0.5010
e	0.4330	0.3730
f	0.6290	0.4800
g	0.6190	0.4610
h	0.4830	0.4250
i	0.5910	0.4570
j	0.5920	0.4690
k	0.6490	0.4770
l	0.0010	0.1070
m	0.6570	0.4770
n	0.3950	0.3930
o	0.6100	0.4550

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Chain	Atom inclusion	Q-score
p	0.5470	0.4470
q	0.4980	0.3960
r	0.4960	0.4350
s	0.6210	0.4520
t	0.7200	0.5050