



wwPDB EM Validation Summary Report ⓘ

Jan 1, 2023 – 11:22 PM JST

PDB ID : 7CPU
EMDB ID : EMD-30432
Title : Cryo-EM structure of 80S ribosome from mouse kidney
Authors : Huo, Y.G.; He, X.; Jiang, T.; Qin, Y.; Guo, X.J.; Sha, J.H.
Deposited on : 2020-08-08
Resolution : 2.82 Å (reported)
Based on initial model : 6EK0

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

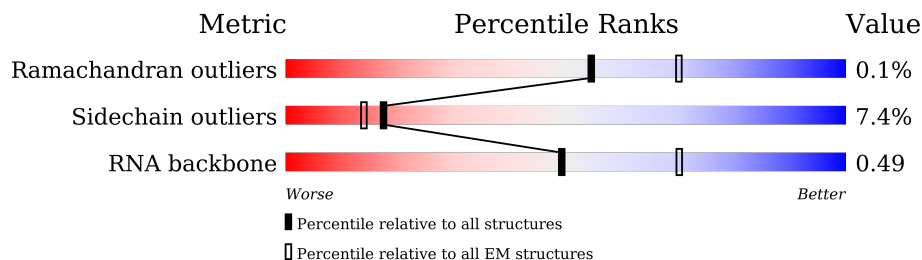
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.82 Å.

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



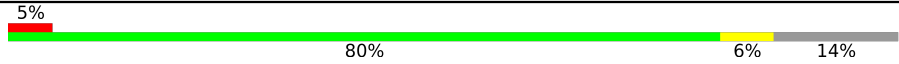
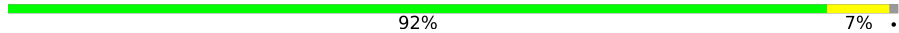




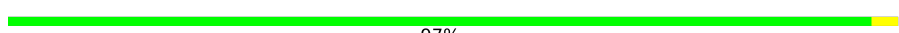








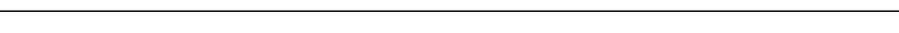
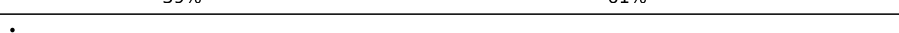


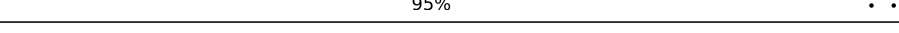
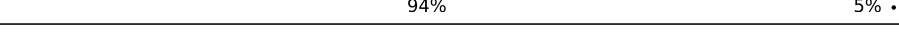



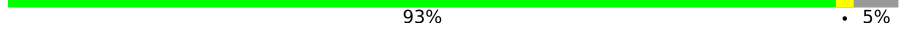
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	LA	257	
2	SA	295	
3	LB	403	
4	SB	264	
5	LC	419	
6	LD	297	
7	LE	296	
8	LF	270	

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Mol	Chain	Length	Quality of chain
9	LG	266	 5% 80% 6% 14%
10	LH	192	 92% 7%
11	LI	214	 90% 6%
12	LJ	178	 89% 7%
13	LL	211	 90% 8%
14	LM	217	 60% 37%
15	LN	204	 97%
16	LO	203	 94% 5%
17	LP	184	 78% 6% 16%
18	LQ	188	 97%
19	LR	196	 84% 5% 11%
20	LS	176	 93% 6%
21	LT	160	 95% 5%
22	LU	128	 73% 5% 22%
23	LV	140	 89% 7%
24	LW	157	 39% 61%
25	LX	156	 72% 24%
26	LY	145	 84% 7% 9%
27	LZ	136	 95%
28	La	148	 94% 5%
29	Lb	160	 57% 5% 38%
30	Lc	115	 78% 18%
31	Ld	125	 5% 84% 14%
32	Le	135	 93% 5%
33	Lf	110	 94% 5%

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Mol	Chain	Length	Quality of chain
34	Lg	117	90% 6%
35	Lh	123	97%
36	Li	105	90% 7%
37	Lj	97	82% 6% 11%
38	Lk	70	96%
39	Lm	128	40% 60%
40	Ln	25	96%
41	Lo	106	92% 6%
42	Lp	92	97%
43	Lr	137	88% 9%
44	L5	4731	56% 18% 25%
45	L7	120	85% 15%
46	L8	158	6% 78% 21%
47	S2	1870	12% 65% 23% 11%
48	SD	243	41% 85% 7% 9%
49	SE	263	18% 88% 10%
50	SF	204	10% 79% 8% 12%
51	SH	194	37% 84% 9% 7%
52	SI	208	15% 79% 9% 12%
53	SK	165	40% 50% 5% 45%
54	SL	158	6% 77% 9% 15%
55	SP	145	10% 79% 19%
56	SQ	146	15% 87% 8% 5%
57	SR	135	36% 84% 13%
58	SS	152	12% 85% 7% 8%

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Mol	Chain	Length	Quality of chain
59	ST	145	
60	SU	119	
61	SV	83	
62	SX	143	
63	Sa	115	
64	Sc	69	
65	Sd	56	
66	Sg	317	
67	SC	293	
68	SG	249	
69	SJ	194	
70	SN	151	
71	SO	151	
72	SW	130	
73	SY	133	
74	SZ	125	
75	Sb	84	
76	Se	133	
77	S6	75	
78	Ll	51	

2 Entry composition [i](#)

There are 81 unique types of molecules in this entry. The entry contains 206288 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 protein called 60S ribosomal protein L8.

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

- Molecule 2 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	SA	207	Total	C	N	O	S	0	0
			1636	1042	288	298	8		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	LB	397	Total	C	N	O	S	0	0
			3202	2039	603	546	14		

- Molecule 4 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	SB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	LC	362	Total	C	N	O	S	0	0
			2891	1819	577	480	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	LD	293	Total	C	N	O	S	0	0
			2385	1506	440	425	14		

- Molecule 7 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	LE	231	1874	1195	358	317	4	0	0

- Molecule 8 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	LF	214	1771	1139	337	287	8	0	0

- Molecule 9 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	LG	229	1848	1179	354	311	4	0	0

- Molecule 10 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	LH	190	1519	956	284	273	6	0	0

- Molecule 11 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	LI	201	1633	1037	316	268	12	0	0

- Molecule 12 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LJ	171	1371	866	255	244	6	0	0

- Molecule 13 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LL	206	1667	1043	343	277	4	0	0

- Molecule 14 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LM	136	Total	C	N	O	S	0	0
			1125	721	218	179	7		

- Molecule 15 is a protein called 60S ribosomal protein L15.

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

- Molecule 16 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LO	201	Total	C	N	O	S	0	0
			1640	1055	320	259	6		

- Molecule 17 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LP	154	Total	C	N	O	S	0	0
			1251	782	243	217	9		

- Molecule 18 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LQ	187	Total	C	N	O	S	0	0
			1515	948	314	249	4		

- Molecule 19 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LR	174	Total	C	N	O	S	0	0
			1457	901	316	231	9		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LS	175	Total	C	N	O	S	0	0
			1451	924	283	234	10		

- Molecule 21 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LT	160	Total	C	N	O	S	0	0
			1307	829	253	218	7		

- Molecule 22 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LU	100	Total	C	N	O	S	0	0
			817	523	143	149	2		

- Molecule 23 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LV	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

- Molecule 24 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LW	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 25 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LX	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 26 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LY	132	Total	C	N	O	S	0	0
			1102	692	223	184	3		

- Molecule 27 is a protein called 60S ribosomal protein L27.

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

- Molecule 28 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	La	147	1164	736	239	185	4	0	0

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	Lb	99	807	505	174	124	4	0	0

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Lc	94	732	465	130	131	6	0	0

- Molecule 31 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	Ld	108	896	566	172	156	2	0	0

- Molecule 32 is a protein called 60S ribosomal protein L32.

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

- Molecule 33 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	Lf	109	876	555	174	143	4	0	0

- Molecule 34 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Lg	110	873	546	180	141	6	0	0

- Molecule 35 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lh	122	Total	C	N	O	S	0	0
			1015	643	204	167	1		

- Molecule 36 is a protein called 60S ribosomal protein L36.

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

- Molecule 37 is a protein called 60S ribosomal protein L37.

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

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lk	69	Total	C	N	O	S	0	0
			568	365	103	99	1		

- Molecule 39 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lm	51	Total	C	N	O	S	0	0
			419	260	88	65	6		

- Molecule 40 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ln	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 41 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lo	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 42 is a protein called 60S ribosomal protein L37a.

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

- Molecule 43 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	Lr	124	994	616	206	167	5	0	0

- Molecule 44 is a RNA chain called Mus musculus 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
44	L5	3539	75867	33789	13863	24677	3538	0	0

- Molecule 45 is a RNA chain called Mus musculus 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
45	L7	120	2558	1141	456	842	119	0	0

- Molecule 46 is a RNA chain called Mus musculus 5.8S ribosomal RNA.

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

- Molecule 47 is a RNA chain called Mus musculus 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
47	S2	1656	35228	15723	6313	11537	1655	0	0

- Molecule 48 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	SD	222	1726	1100	310	309	7	0	0

- Molecule 49 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SE	258	Total	C	N	O	S	0	0
			2050	1311	381	350	8		

- Molecule 50 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SF	179	Total	C	N	O	S	0	0
			1416	888	262	259	7		

- Molecule 51 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SH	180	Total	C	N	O	S	0	0
			1449	924	266	258	1		

- Molecule 52 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SI	183	Total	C	N	O	S	0	0
			1499	943	293	258	5		

- Molecule 53 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SK	90	Total	C	N	O	S	0	0
			760	495	135	124	6		

- Molecule 54 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SL	135	Total	C	N	O	S	0	0
			1110	708	207	189	6		

- Molecule 55 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SP	118	Total	C	N	O	S	0	0
			981	625	183	166	7		

- Molecule 56 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	SQ	139	1109	704	210	192	3	0	0

- Molecule 57 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	SR	131	1064	668	198	194	4	0	0

- Molecule 58 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	SS	140	1157	728	231	197	1	0	0

- Molecule 59 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	ST	140	1090	681	212	195	2	0	0

- Molecule 60 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	SU	95	753	471	142	136	4	0	0

- Molecule 61 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	SV	80	610	373	114	118	5	0	0

- Molecule 62 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	SX	139	1080	682	214	181	3	0	0

- Molecule 63 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Sa	99	Total	C	N	O	S	1	0
			800	497	168	130	5		

- Molecule 64 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Sc	54	Total	C	N	O	S	0	0
			416	257	80	77	2		

- Molecule 65 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Sd	54	Total	C	N	O	S	0	0
			455	284	93	73	5		

- Molecule 66 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sg	276	Total	C	N	O	S	0	0
			2148	1357	378	401	12		

- Molecule 67 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SC	215	Total	C	N	O	S	1	0
			1673	1085	288	291	9		

- Molecule 68 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SG	204	Total	C	N	O	S	0	0
			1645	1029	330	280	6		

- Molecule 69 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SJ	138	Total	C	N	O	S	0	0
			1162	743	230	187	2		

- Molecule 70 is a protein called 40S ribosomal protein S13.

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

- Molecule 71 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	SO	134	1002	612	197	187	6	0	0

- Molecule 72 is a protein called 40S ribosomal protein S15a.

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

- Molecule 73 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	SY	110	891	565	173	149	4	0	0

- Molecule 74 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	SZ	72	574	368	104	101	1	0	0

- Molecule 75 is a protein called 40S ribosomal protein S27.

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

- Molecule 76 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	Se	48	384	234	86	63	1	0	0

- Molecule 77 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
77	S6	75	1604	717	298	515	74	0	0

- Molecule 78 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	L1	50	444	281	98	64	1	0	0

- Molecule 79 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
79	LN	1	Total 1	Mg 1	0
79	LP	1	Total 1	Mg 1	0
79	LT	1	Total 1	Mg 1	0
79	LV	1	Total 1	Mg 1	0
79	Le	1	Total 1	Mg 1	0
79	Lf	1	Total 1	Mg 1	0
79	L5	173	Total 173	Mg 173	0
79	L7	3	Total 3	Mg 3	0
79	L8	5	Total 5	Mg 5	0
79	S2	82	Total 82	Mg 82	0
79	SF	1	Total 1	Mg 1	0
79	Sd	1	Total 1	Mg 1	0

- Molecule 80 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
80	Lg	1	Total 1	Zn 1	0

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Mol	Chain	Residues	Atoms		AltConf
80	Lj	1	Total 1	Zn 1	0
80	Lm	1	Total 1	Zn 1	0
80	Lo	1	Total 1	Zn 1	0
80	Lp	1	Total 1	Zn 1	0
80	Sa	1	Total 1	Zn 1	0
80	Sd	1	Total 1	Zn 1	0

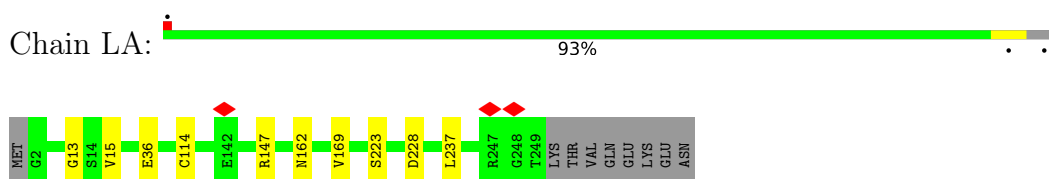
- Molecule 81 is water.

Mol	Chain	Residues	Atoms		AltConf
81	LB	1	Total 1	O 1	0
81	LH	1	Total 1	O 1	0
81	LI	2	Total 2	O 2	0
81	La	2	Total 2	O 2	0
81	L5	9	Total 9	O 9	0
81	S2	3	Total 3	O 3	0
81	SV	1	Total 1	O 1	0

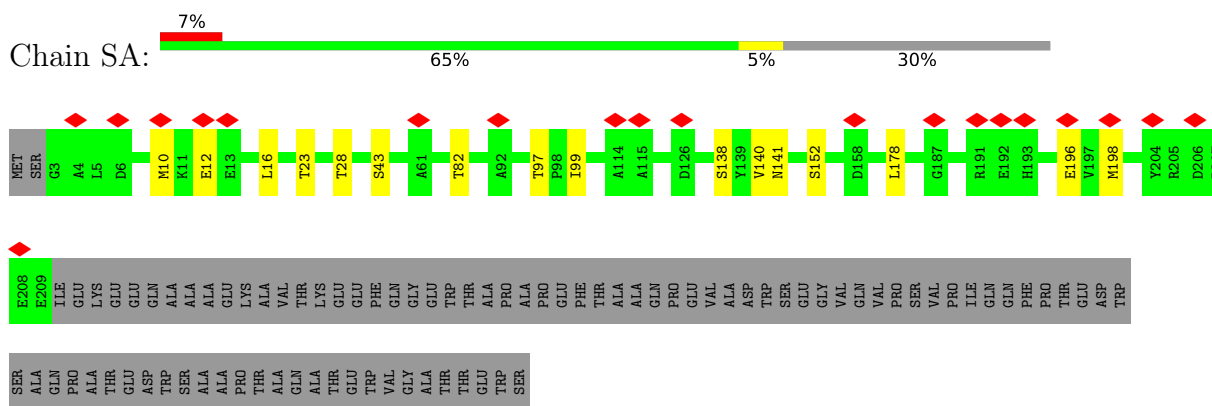
3 Residue-property plots

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.

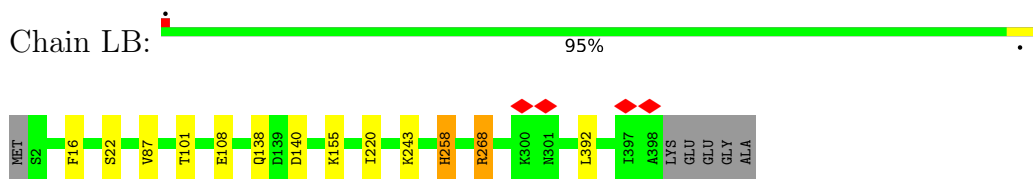
- Molecule 1: 60S ribosomal protein L8



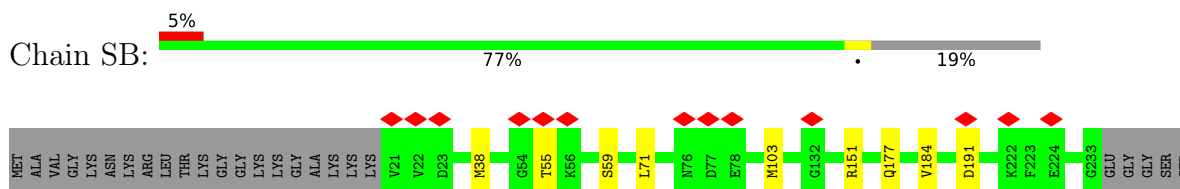
- Molecule 2: 40S ribosomal protein SA

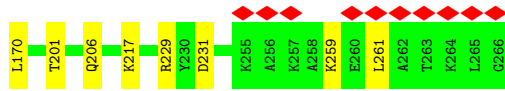


- Molecule 3: 60S ribosomal protein L3



- Molecule 4: 40S ribosomal protein S3a

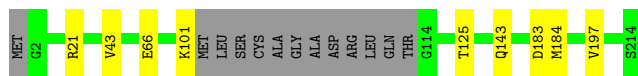
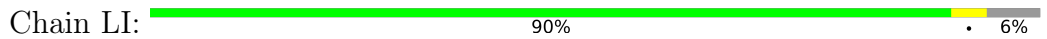




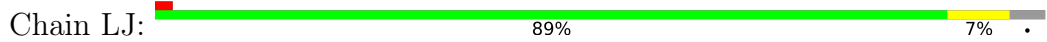
• Molecule 10: 60S ribosomal protein L9



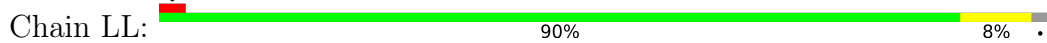
• Molecule 11: 60S ribosomal protein L10



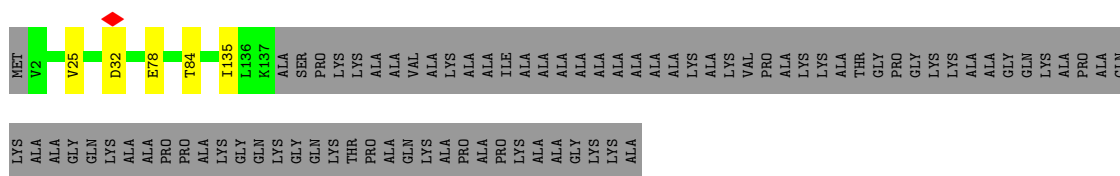
• Molecule 12: 60S ribosomal protein L11



• Molecule 13: 60S ribosomal protein L13



• Molecule 14: 60S ribosomal protein L14

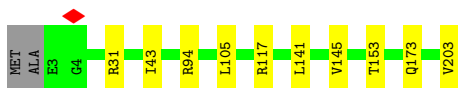


• Molecule 15: 60S ribosomal protein L15




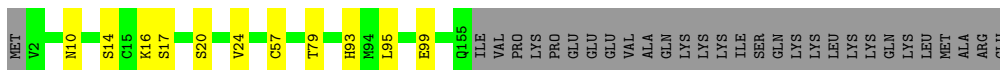
- Molecule 16: 60S ribosomal protein L13a

Chain LO:  94% 5%



- Molecule 17: 60S ribosomal protein L17

Chain LP:  78% 6% 16%




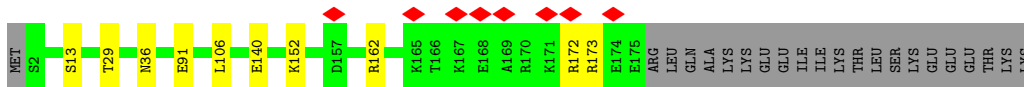
- Molecule 18: 60S ribosomal protein L18

Chain LQ:  97%



- Molecule 19: 60S ribosomal protein L19

Chain LR:  84% 5% 11%



- Molecule 20: 60S ribosomal protein L18a

Chain LS:  93% 6%




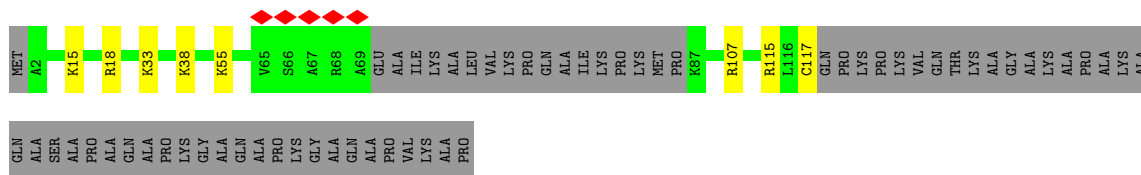
- Molecule 21: 60S ribosomal protein L21

Chain LT:  95% 5%

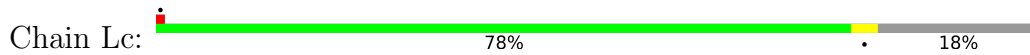


- Molecule 22: 60S ribosomal protein L22

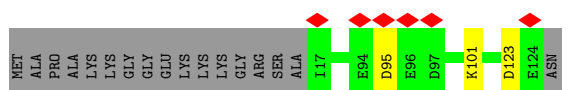
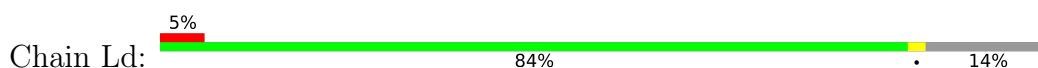
Chain LU:  73% 5% 22%



• Molecule 30: 60S ribosomal protein L30



• Molecule 31: 60S ribosomal protein L31



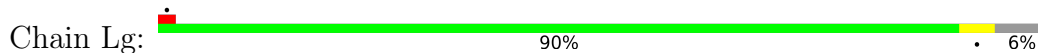
• Molecule 32: 60S ribosomal protein L32



• Molecule 33: 60S ribosomal protein L35a

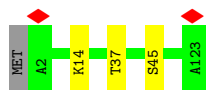


• Molecule 34: 60S ribosomal protein L34

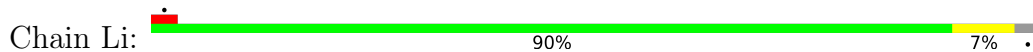


• Molecule 35: 60S ribosomal protein L35

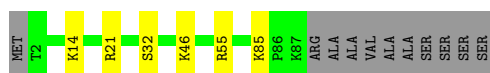
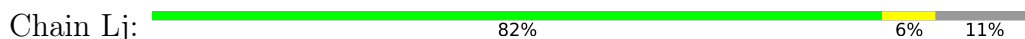




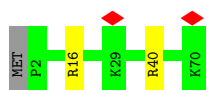
• Molecule 36: 60S ribosomal protein L36



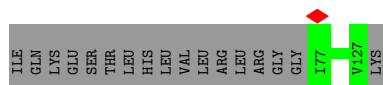
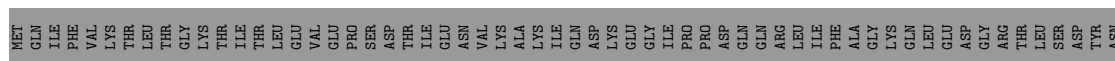
• Molecule 37: 60S ribosomal protein L37



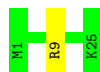
• Molecule 38: 60S ribosomal protein L38



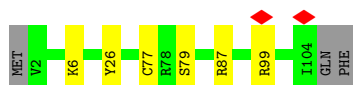
• Molecule 39: Ubiquitin-60S ribosomal protein L40



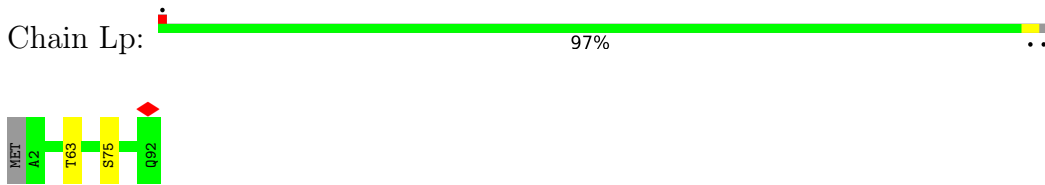
• Molecule 40: 60S ribosomal protein L41



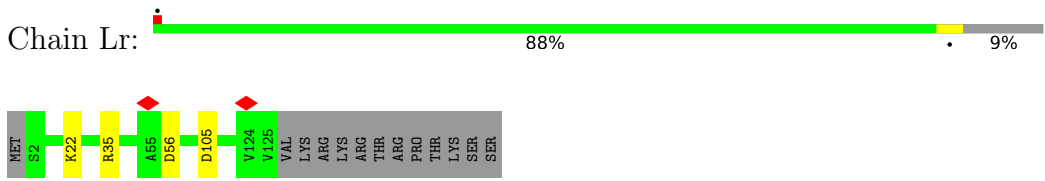
• Molecule 41: 60S ribosomal protein L36a



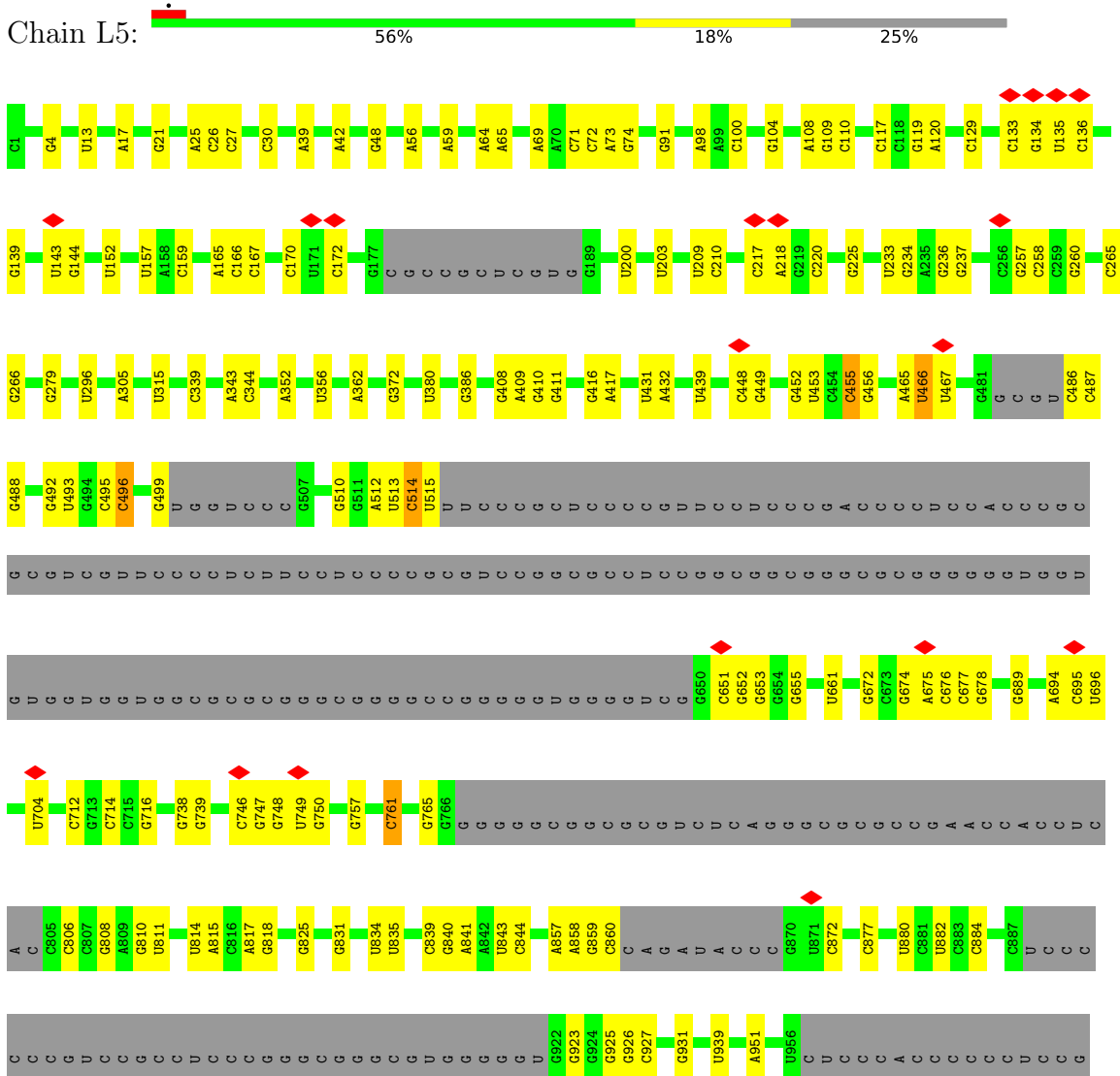
• Molecule 42: 60S ribosomal protein L37a

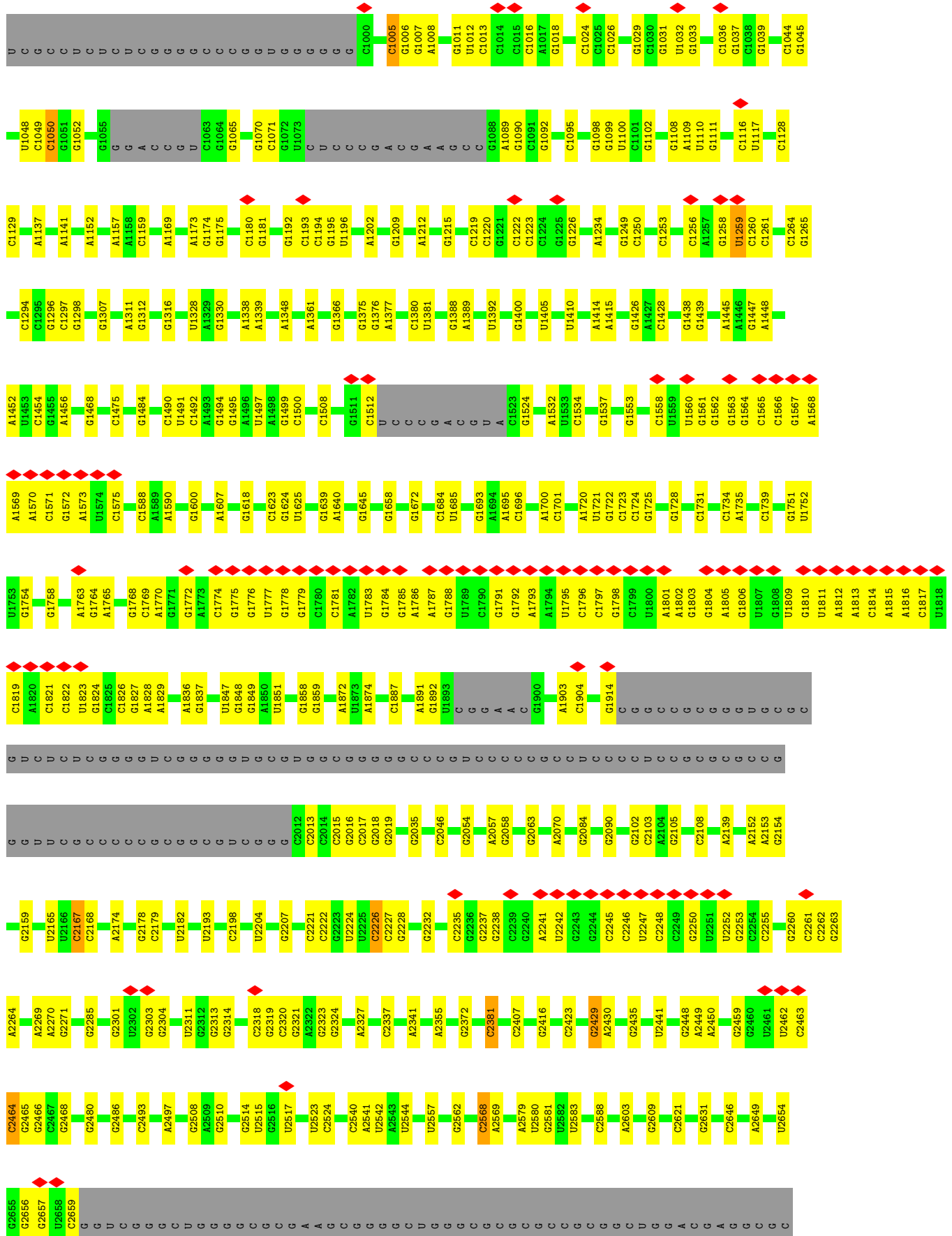


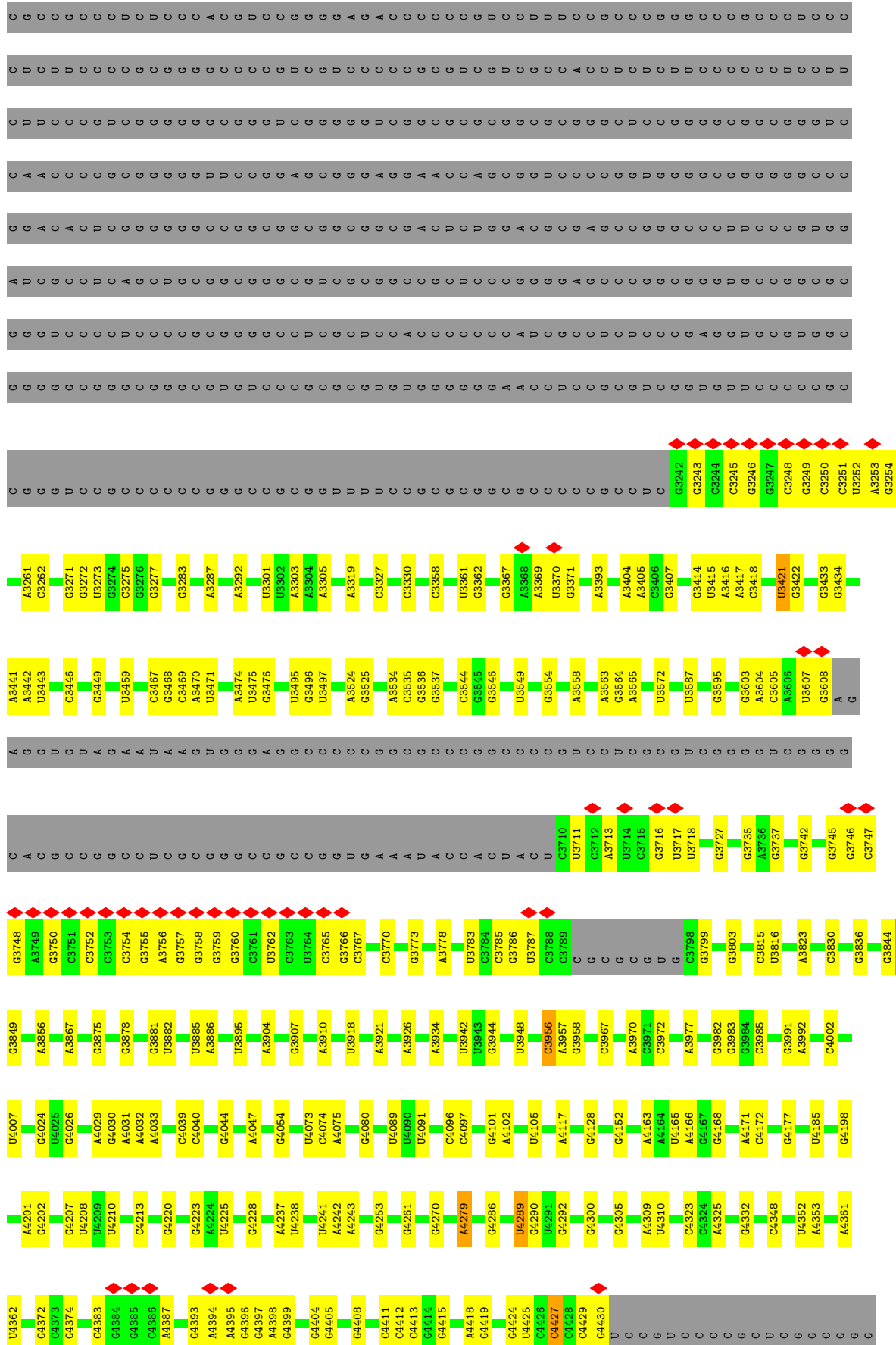
• Molecule 43: 60S ribosomal protein L28

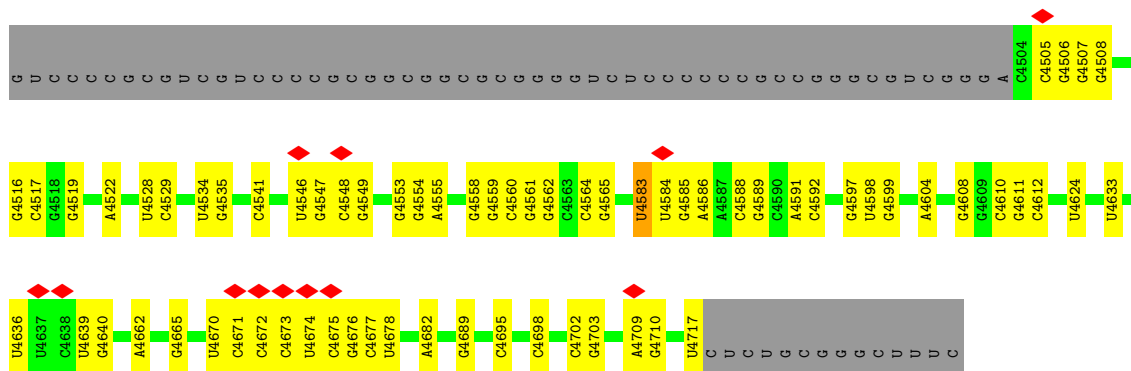


• Molecule 44: Mus musculus 28S ribosomal RNA

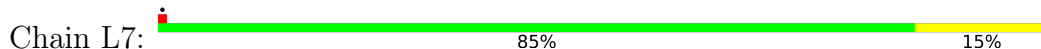




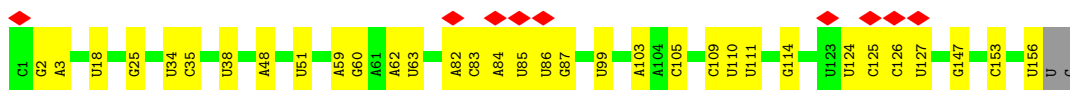
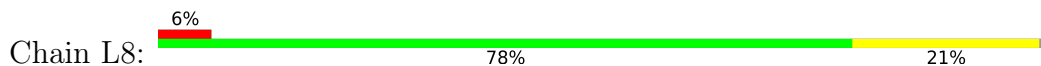




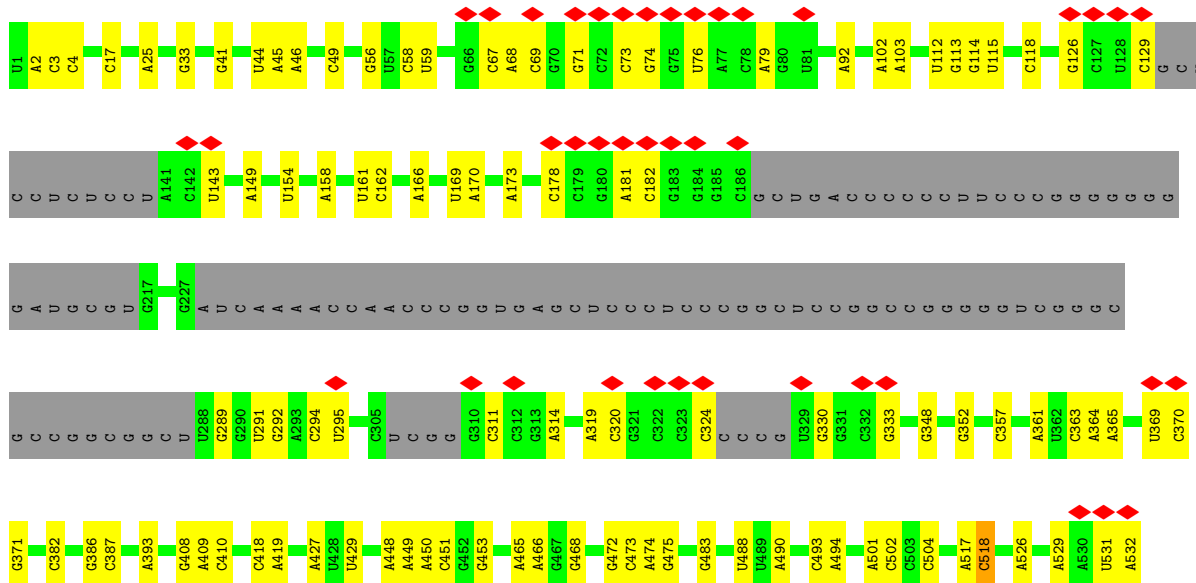
• Molecule 45: Mus musculus 5S ribosomal RNA

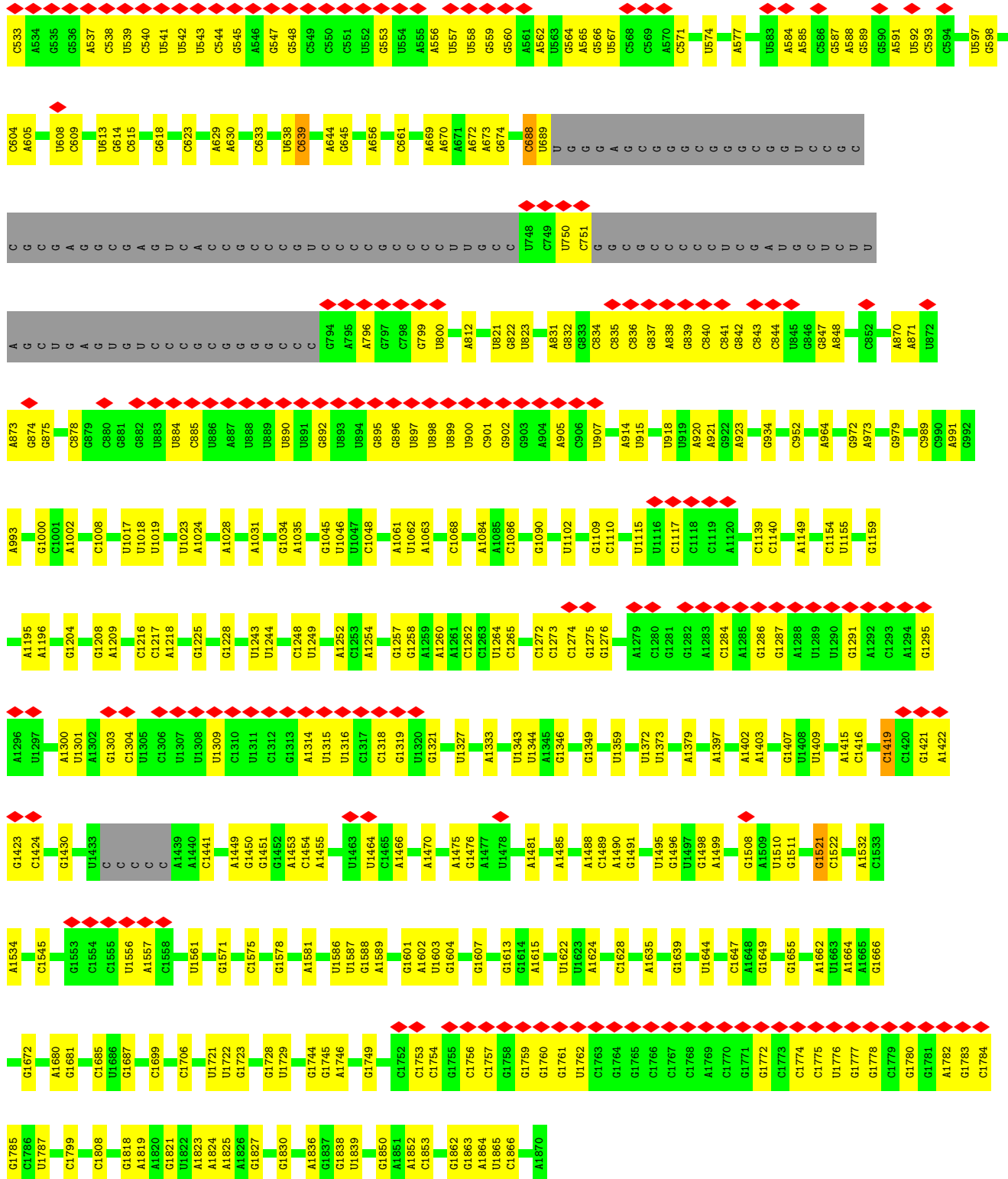


• Molecule 46: Mus musculus 5.8S ribosomal RNA

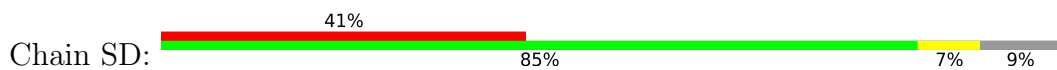


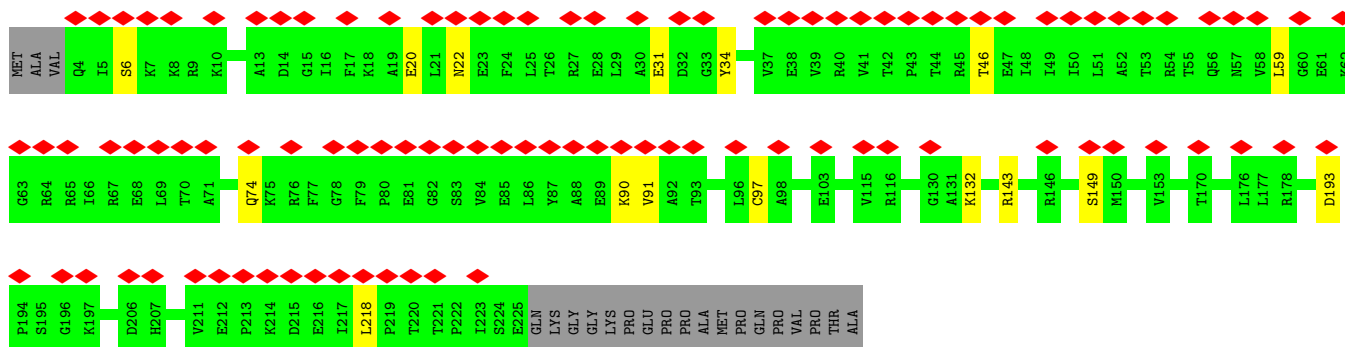
• Molecule 47: Mus musculus 18S ribosomal RNA



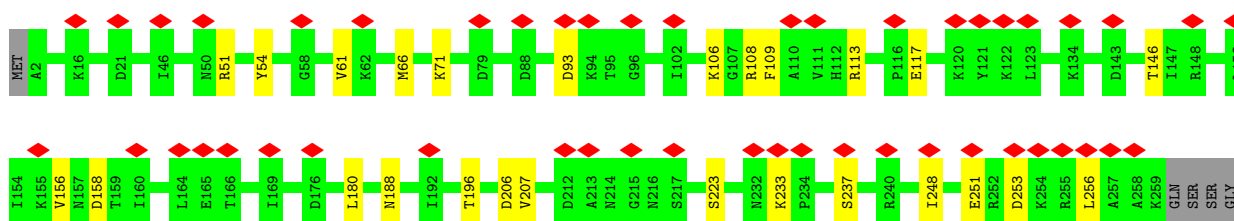


● Molecule 48: 40S ribosomal protein S3

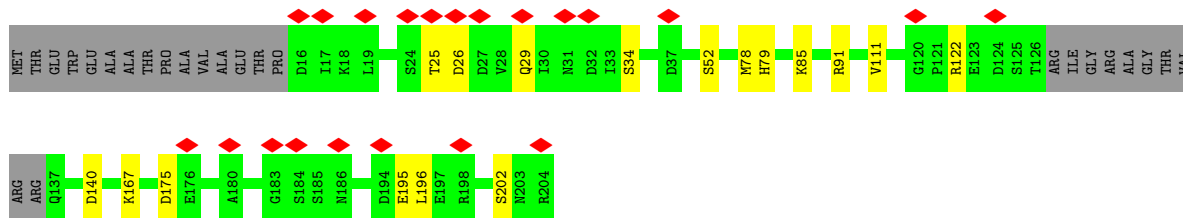
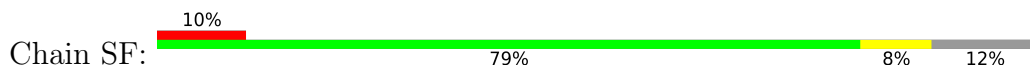




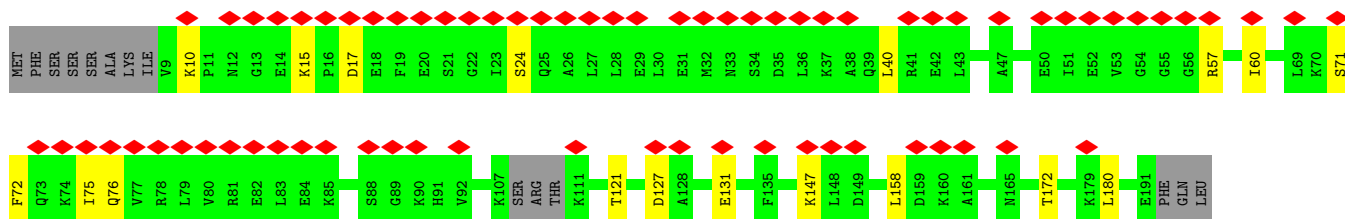
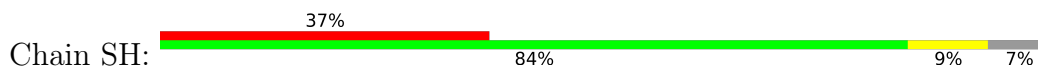
• Molecule 49: 40S ribosomal protein S4, X isoform



• Molecule 50: 40S ribosomal protein S5

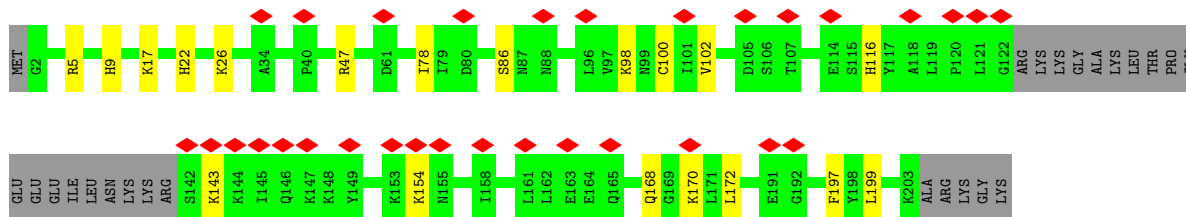


• Molecule 51: 40S ribosomal protein S7

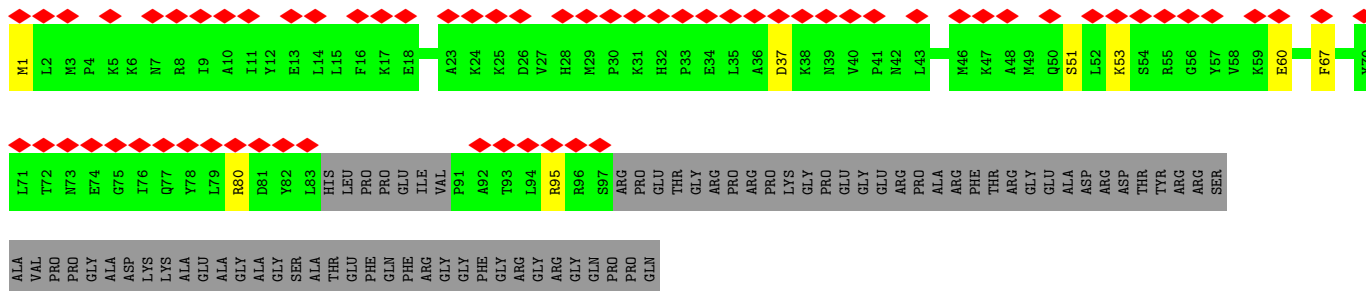
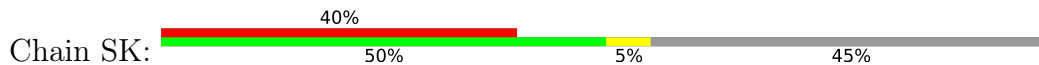


• Molecule 52: 40S ribosomal protein S8

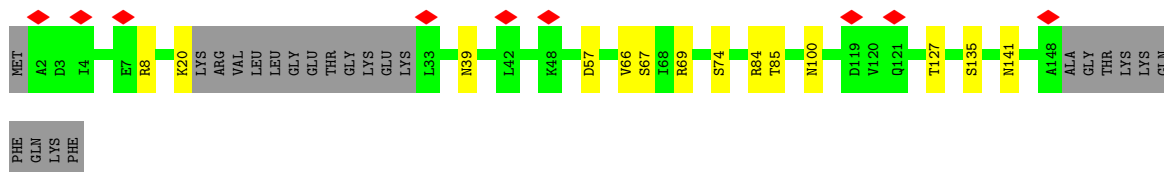
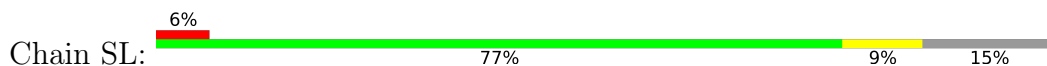




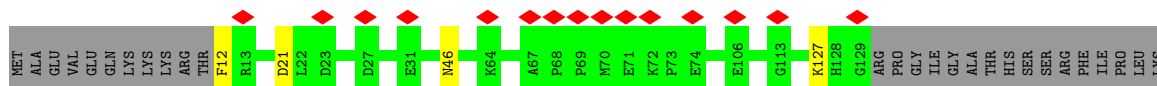
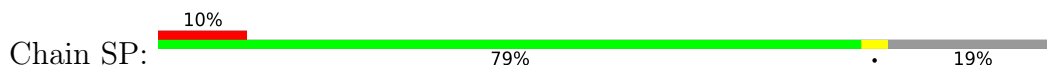
• Molecule 53: 40S ribosomal protein S10



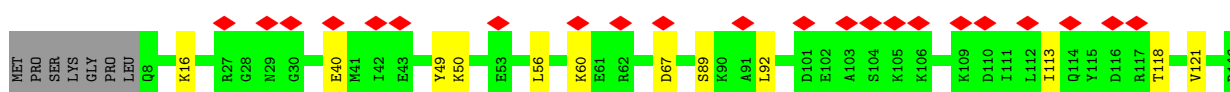
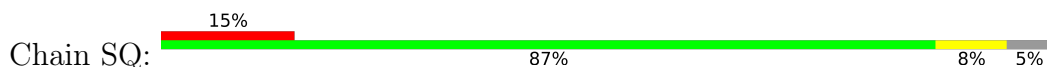
• Molecule 54: 40S ribosomal protein S11



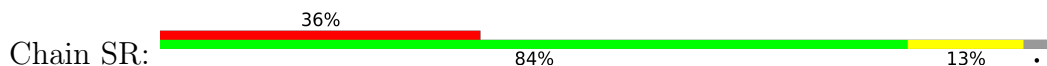
• Molecule 55: 40S ribosomal protein S15

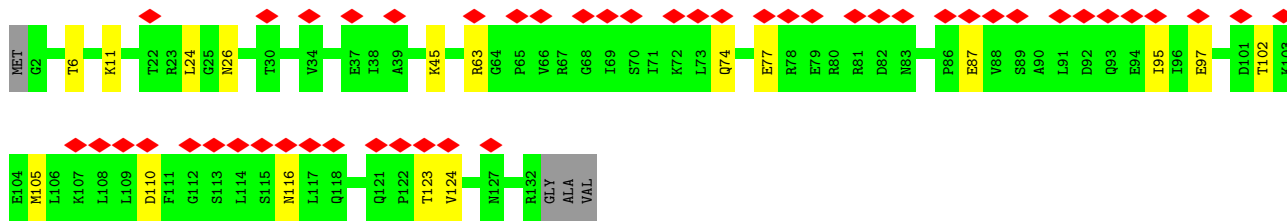


• Molecule 56: 40S ribosomal protein S16

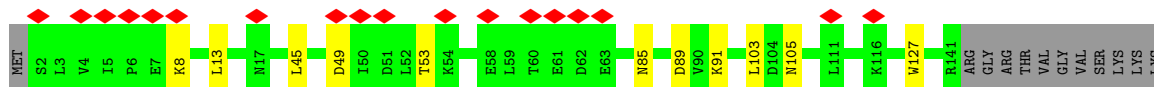
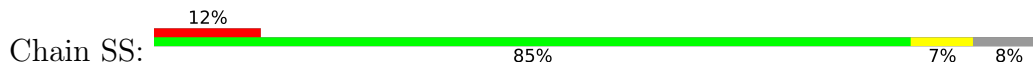


• Molecule 57: 40S ribosomal protein S17

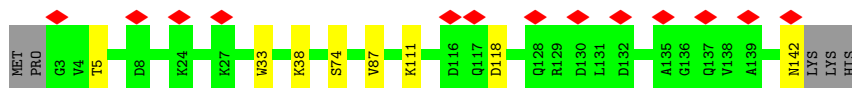




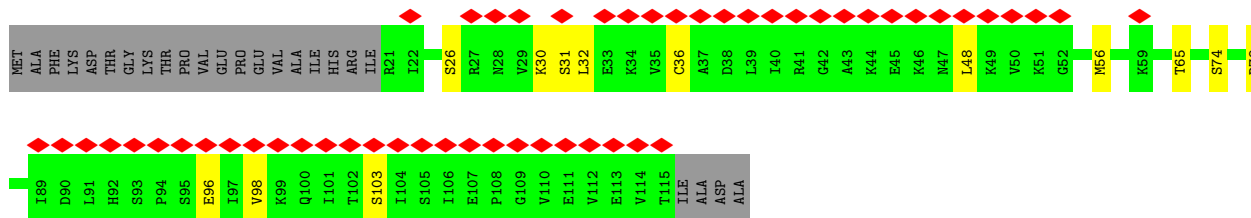
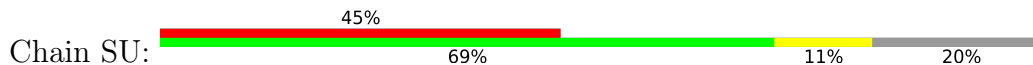
• Molecule 58: 40S ribosomal protein S18



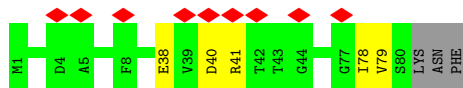
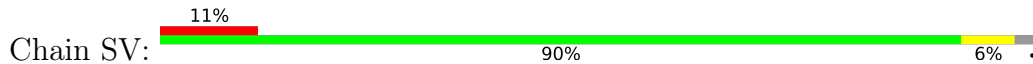
• Molecule 59: 40S ribosomal protein S19



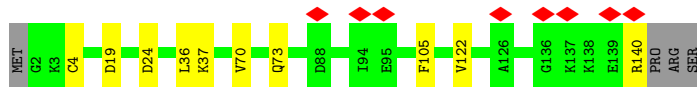
• Molecule 60: 40S ribosomal protein S20



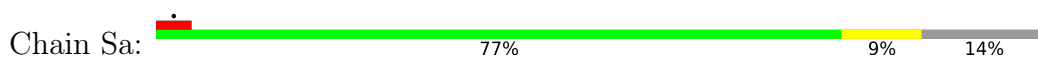
• Molecule 61: 40S ribosomal protein S21



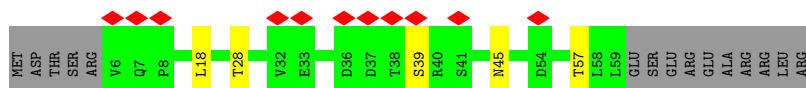
• Molecule 62: 40S ribosomal protein S23



• Molecule 63: 40S ribosomal protein S26



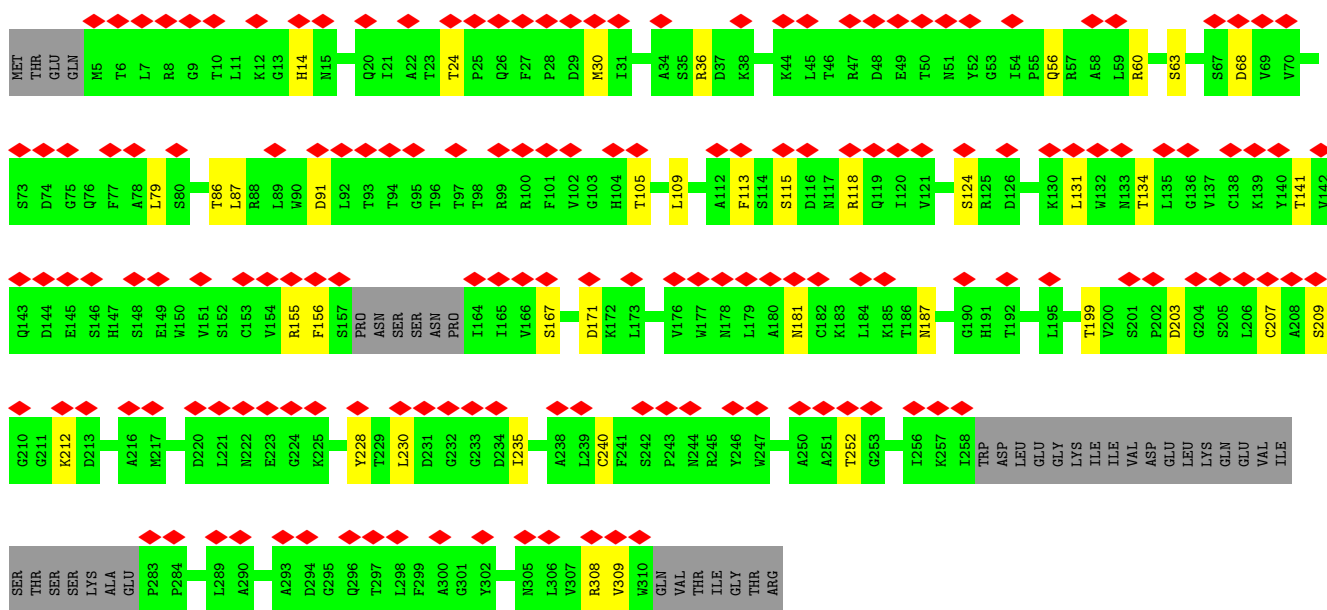
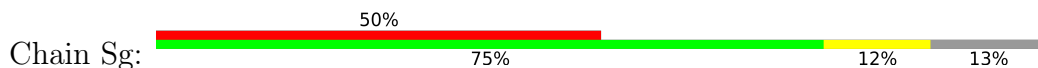
- Molecule 64: 40S ribosomal protein S28



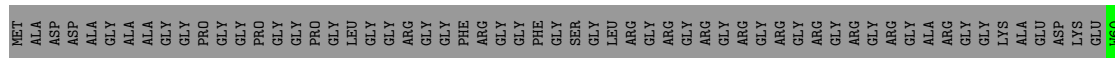
- Molecule 65: 40S ribosomal protein S29

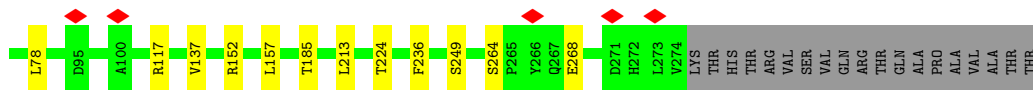


- Molecule 66: Receptor of activated protein C kinase 1

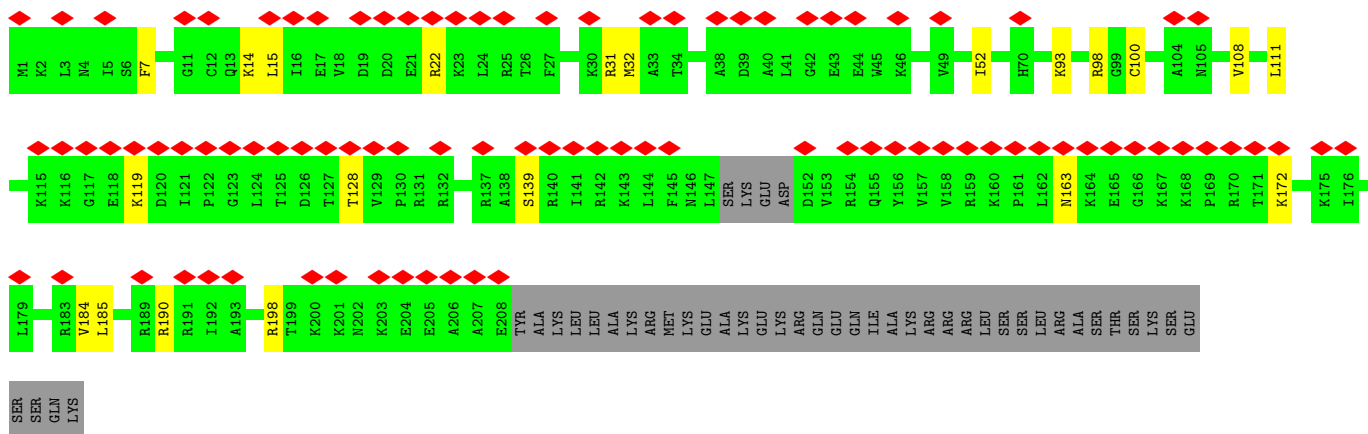
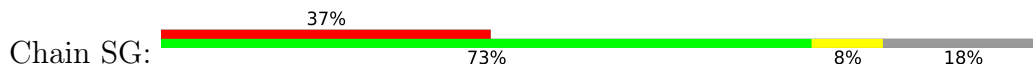


- Molecule 67: 40S ribosomal protein S2

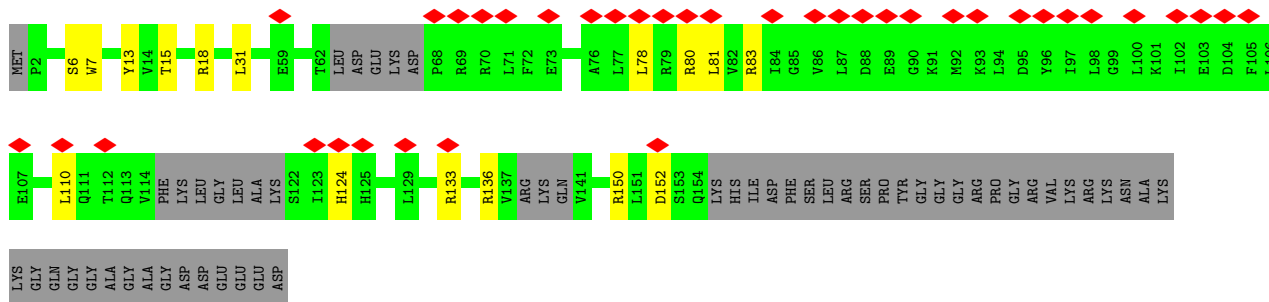




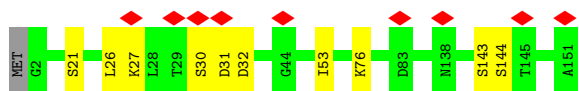
• Molecule 68: 40S ribosomal protein S6



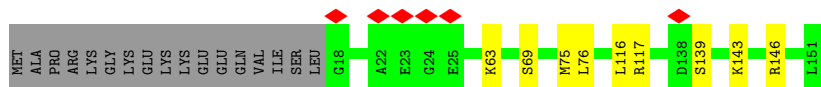
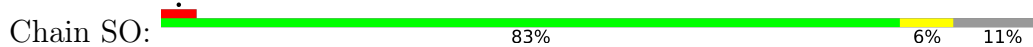
• Molecule 69: 40S ribosomal protein S9



• Molecule 70: 40S ribosomal protein S13



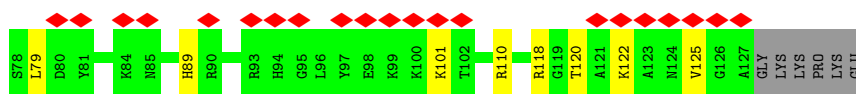
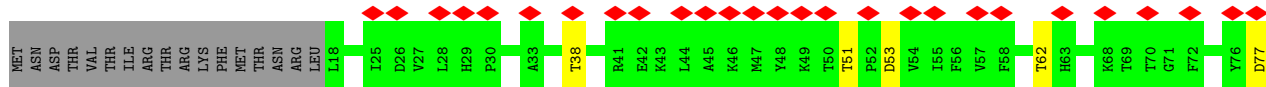
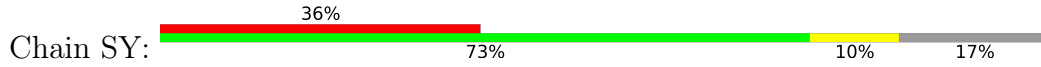
• Molecule 71: 40S ribosomal protein S14



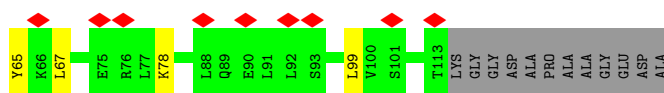
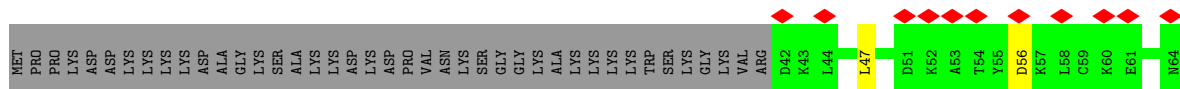
• Molecule 72: 40S ribosomal protein S15a



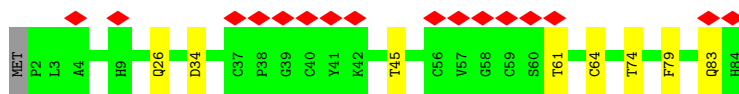
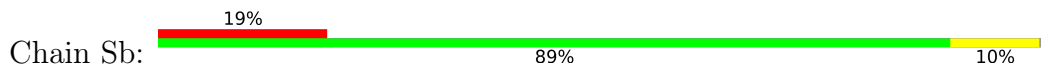
• Molecule 73: 40S ribosomal protein S24



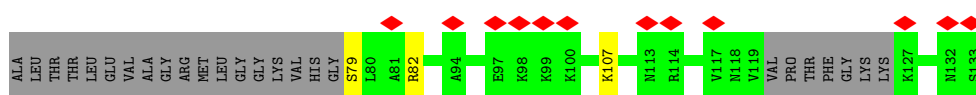
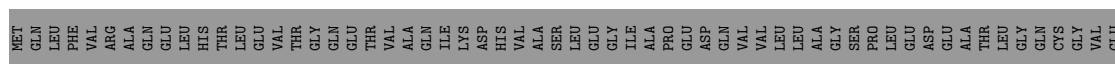
• Molecule 74: 40S ribosomal protein S25



• Molecule 75: 40S ribosomal protein S27

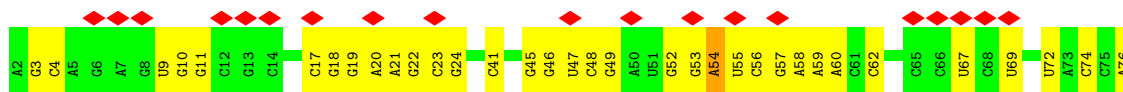


• Molecule 76: 40S ribosomal protein S30



• Molecule 77: tRNA





- Molecule 78: Ribosomal protein L39

Chain Ll: 92% 6%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	280287	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.326	Depositor
Minimum map value	-0.162	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.026	Depositor
Map size (\AA)	416.0, 416.0, 416.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.04, 1.04, 1.04	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	LA	0.42	0/1936	0.54	0/2596
2	SA	0.29	0/1673	0.48	0/2275
3	LB	0.39	0/3269	0.54	2/4375 (0.0%)
4	SB	0.29	0/1756	0.48	0/2350
5	LC	0.37	0/2945	0.52	1/3953 (0.0%)
6	LD	0.38	0/2431	0.48	0/3256
7	LE	0.34	0/1910	0.50	0/2562
8	LF	0.40	0/1805	0.48	0/2408
9	LG	0.34	0/1880	0.46	0/2531
10	LH	0.35	0/1537	0.51	0/2065
11	LI	0.37	0/1671	0.46	0/2230
12	LJ	0.33	0/1394	0.50	0/1864
13	LL	0.36	0/1698	0.48	0/2274
14	LM	0.37	0/1146	0.46	0/1531
15	LN	0.42	0/1746	0.50	0/2338
16	LO	0.39	0/1670	0.48	0/2232
17	LP	0.38	0/1277	0.49	0/1712
18	LQ	0.40	0/1539	0.51	0/2053
19	LR	0.32	0/1473	0.43	0/1947
20	LS	0.41	0/1491	0.50	1/2000 (0.1%)
21	LT	0.39	0/1335	0.47	0/1781
22	LU	0.33	0/831	0.48	0/1115
23	LV	0.38	0/987	0.50	0/1324
24	LW	0.39	0/532	0.46	0/708
25	LX	0.36	0/984	0.45	0/1323
26	LY	0.36	0/1119	0.46	0/1488
27	LZ	0.38	0/1130	0.47	0/1507
28	La	0.41	0/1193	0.48	0/1593
29	Lb	0.32	0/821	0.43	0/1082
30	Lc	0.38	0/742	0.51	0/996
31	Ld	0.37	0/911	0.49	0/1227
32	Le	0.40	0/1071	0.48	0/1429

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lf	0.41	0/895	0.54	0/1198
34	Lg	0.37	0/883	0.51	0/1178
35	Lh	0.33	0/1023	0.44	0/1350
36	Li	0.32	0/843	0.45	0/1115
37	Lj	0.40	0/720	0.50	0/952
38	Lk	0.34	0/574	0.44	0/760
39	Lm	0.35	0/425	0.45	0/564
40	Ln	0.30	0/240	0.44	0/305
41	Lo	0.37	0/855	0.49	0/1128
42	Lp	0.38	0/718	0.49	0/953
43	Lr	0.37	0/1009	0.48	0/1353
44	L5	0.71	1/84865 (0.0%)	0.87	62/132368 (0.0%)
45	L7	0.70	0/2858	0.82	0/4455
46	L8	0.69	0/3701	0.82	2/5766 (0.0%)
47	S2	0.43	0/39386	0.83	36/61368 (0.1%)
48	SD	0.28	0/1754	0.52	0/2362
49	SE	0.27	0/2092	0.50	0/2816
50	SF	0.27	0/1436	0.45	0/1930
51	SH	0.27	0/1470	0.48	0/1968
52	SI	0.28	0/1526	0.48	0/2038
53	SK	0.28	0/780	0.48	0/1046
54	SL	0.31	0/1130	0.49	0/1514
55	SP	0.29	0/1000	0.48	0/1335
56	SQ	0.30	0/1126	0.51	0/1506
57	SR	0.28	0/1078	0.48	0/1447
58	SS	0.28	0/1175	0.45	0/1575
59	ST	0.27	0/1108	0.45	0/1486
60	SU	0.27	0/762	0.50	0/1023
61	SV	0.28	0/616	0.49	0/825
62	SX	0.30	0/1097	0.50	0/1464
63	Sa	0.32	0/816	0.47	0/1093
64	Sc	0.28	0/418	0.57	0/562
65	Sd	0.29	0/466	0.42	0/618
66	Sg	0.26	0/2199	0.55	0/2989
67	SC	0.30	0/1712	0.48	0/2314
68	SG	0.27	0/1666	0.50	0/2222
69	SJ	0.26	0/1178	0.51	0/1574
70	SN	0.29	0/1232	0.43	0/1656
71	SO	0.29	0/1015	0.51	0/1361
72	SW	0.30	0/1051	0.49	0/1406
73	SY	0.27	0/907	0.46	0/1204
74	SZ	0.29	0/580	0.49	0/780
75	Sb	0.27	0/665	0.46	0/891

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Se	0.26	0/386	0.50	0/504
77	S6	0.38	0/1795	0.96	4/2798 (0.1%)
78	L1	0.65	0/454	0.60	0/599
All	All	0.54	1/221588 (0.0%)	0.74	108/325844 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	LA	0	1
3	LB	0	2
10	LH	0	1
12	LJ	0	1
14	LM	0	1
50	SF	0	1
59	ST	0	1
61	SV	0	1
68	SG	0	1
All	All	0	10

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	L5	1338	A	N9-C4	-5.93	1.34	1.37

The worst 5 of 108 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	L5	486	C	C2-N1-C1'	9.59	129.35	118.80
47	S2	1454	C	N1-C2-O2	8.86	124.22	118.90
47	S2	1419	C	N1-C2-O2	8.82	124.19	118.90
47	S2	1454	C	C2-N1-C1'	8.63	128.30	118.80
44	L5	2464	C	N1-C2-O2	8.56	124.04	118.90

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	LA	13	GLY	Peptide

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Mol	Chain	Res	Type	Group
3	LB	16	PHE	Peptide
3	LB	258	HIS	Peptide
10	LH	173	ARG	Peptide
12	LJ	173	ILE	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	
1	LA	246/257 (96%)	220 (89%)	26 (11%)	0	100	100
2	SA	205/295 (70%)	183 (89%)	22 (11%)	0	100	100
3	LB	395/403 (98%)	374 (95%)	21 (5%)	0	100	100
4	SB	211/264 (80%)	194 (92%)	17 (8%)	0	100	100
5	LC	360/419 (86%)	323 (90%)	36 (10%)	1 (0%)	41	70
6	LD	291/297 (98%)	271 (93%)	20 (7%)	0	100	100
7	LE	227/296 (77%)	201 (88%)	26 (12%)	0	100	100
8	LF	212/270 (78%)	200 (94%)	12 (6%)	0	100	100
9	LG	225/266 (85%)	207 (92%)	18 (8%)	0	100	100
10	LH	188/192 (98%)	172 (92%)	16 (8%)	0	100	100
11	LI	197/214 (92%)	193 (98%)	4 (2%)	0	100	100
12	LJ	169/178 (95%)	153 (90%)	16 (10%)	0	100	100
13	LL	204/211 (97%)	187 (92%)	17 (8%)	0	100	100
14	LM	134/217 (62%)	125 (93%)	9 (7%)	0	100	100
15	LN	201/204 (98%)	190 (94%)	10 (5%)	1 (0%)	29	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	LO	199/203 (98%)	192 (96%)	7 (4%)	0	100	100
17	LP	152/184 (83%)	142 (93%)	10 (7%)	0	100	100
18	LQ	185/188 (98%)	174 (94%)	11 (6%)	0	100	100
19	LR	172/196 (88%)	166 (96%)	6 (4%)	0	100	100
20	LS	173/176 (98%)	164 (95%)	9 (5%)	0	100	100
21	LT	158/160 (99%)	153 (97%)	5 (3%)	0	100	100
22	LU	98/128 (77%)	86 (88%)	12 (12%)	0	100	100
23	LV	128/140 (91%)	118 (92%)	10 (8%)	0	100	100
24	LW	60/157 (38%)	56 (93%)	4 (7%)	0	100	100
25	LX	116/156 (74%)	110 (95%)	6 (5%)	0	100	100
26	LY	130/145 (90%)	124 (95%)	6 (5%)	0	100	100
27	LZ	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
28	La	145/148 (98%)	132 (91%)	13 (9%)	0	100	100
29	Lb	95/160 (59%)	88 (93%)	7 (7%)	0	100	100
30	Lc	92/115 (80%)	85 (92%)	7 (8%)	0	100	100
31	Ld	106/125 (85%)	98 (92%)	8 (8%)	0	100	100
32	Le	126/135 (93%)	115 (91%)	11 (9%)	0	100	100
33	Lf	107/110 (97%)	102 (95%)	5 (5%)	0	100	100
34	Lg	108/117 (92%)	107 (99%)	1 (1%)	0	100	100
35	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
36	Li	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
37	Lj	84/97 (87%)	78 (93%)	5 (6%)	1 (1%)	13	37
38	Lk	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
39	Lm	49/128 (38%)	49 (100%)	0	0	100	100
40	Ln	23/25 (92%)	23 (100%)	0	0	100	100
41	Lo	101/106 (95%)	94 (93%)	7 (7%)	0	100	100
42	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
43	Lr	122/137 (89%)	116 (95%)	6 (5%)	0	100	100
48	SD	220/243 (90%)	192 (87%)	28 (13%)	0	100	100
49	SE	256/263 (97%)	222 (87%)	33 (13%)	1 (0%)	34	64
50	SF	175/204 (86%)	158 (90%)	17 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	SH	176/194 (91%)	148 (84%)	28 (16%)	0	100	100
52	SI	179/208 (86%)	167 (93%)	12 (7%)	0	100	100
53	SK	86/165 (52%)	75 (87%)	11 (13%)	0	100	100
54	SL	131/158 (83%)	118 (90%)	13 (10%)	0	100	100
55	SP	116/145 (80%)	106 (91%)	10 (9%)	0	100	100
56	SQ	137/146 (94%)	117 (85%)	20 (15%)	0	100	100
57	SR	129/135 (96%)	117 (91%)	12 (9%)	0	100	100
58	SS	138/152 (91%)	120 (87%)	18 (13%)	0	100	100
59	ST	138/145 (95%)	126 (91%)	12 (9%)	0	100	100
60	SU	93/119 (78%)	84 (90%)	9 (10%)	0	100	100
61	SV	78/83 (94%)	71 (91%)	6 (8%)	1 (1%)	12	34
62	SX	137/143 (96%)	125 (91%)	12 (9%)	0	100	100
63	Sa	98/115 (85%)	90 (92%)	8 (8%)	0	100	100
64	Sc	52/69 (75%)	41 (79%)	11 (21%)	0	100	100
65	Sd	52/56 (93%)	47 (90%)	5 (10%)	0	100	100
66	Sg	270/317 (85%)	213 (79%)	57 (21%)	0	100	100
67	SC	214/293 (73%)	199 (93%)	14 (6%)	1 (0%)	29	59
68	SG	200/249 (80%)	180 (90%)	20 (10%)	0	100	100
69	SJ	130/194 (67%)	115 (88%)	15 (12%)	0	100	100
70	SN	148/151 (98%)	142 (96%)	6 (4%)	0	100	100
71	SO	132/151 (87%)	116 (88%)	16 (12%)	0	100	100
72	SW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
73	SY	108/133 (81%)	93 (86%)	15 (14%)	0	100	100
74	SZ	70/125 (56%)	59 (84%)	11 (16%)	0	100	100
75	Sb	81/84 (96%)	74 (91%)	7 (9%)	0	100	100
76	Se	44/133 (33%)	38 (86%)	6 (14%)	0	100	100
78	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
All	All	10666/12499 (85%)	9765 (92%)	895 (8%)	6 (0%)	54	80

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
61	SV	79	VAL

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Mol	Chain	Res	Type
37	Lj	21	ARG
49	SE	248	ILE
67	SC	78	LEU
15	LN	84	PRO

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
1	LA	190/199 (96%)	181 (95%)	9 (5%)	26 57
2	SA	173/242 (72%)	157 (91%)	16 (9%)	9 26
3	LB	344/348 (99%)	332 (96%)	12 (4%)	36 68
4	SB	194/229 (85%)	185 (95%)	9 (5%)	27 58
5	LC	304/348 (87%)	279 (92%)	25 (8%)	11 31
6	LD	245/249 (98%)	231 (94%)	14 (6%)	20 49
7	LE	208/256 (81%)	193 (93%)	15 (7%)	14 37
8	LF	185/234 (79%)	180 (97%)	5 (3%)	44 77
9	LG	197/223 (88%)	180 (91%)	17 (9%)	10 29
10	LH	169/171 (99%)	156 (92%)	13 (8%)	13 34
11	LI	171/181 (94%)	162 (95%)	9 (5%)	22 52
12	LJ	144/149 (97%)	132 (92%)	12 (8%)	11 31
13	LL	173/178 (97%)	156 (90%)	17 (10%)	8 23
14	LM	116/157 (74%)	112 (97%)	4 (3%)	37 69
15	LN	171/172 (99%)	166 (97%)	5 (3%)	42 74
16	LO	172/173 (99%)	162 (94%)	10 (6%)	20 48
17	LP	135/163 (83%)	124 (92%)	11 (8%)	11 32
18	LQ	164/165 (99%)	160 (98%)	4 (2%)	49 80
19	LR	154/175 (88%)	144 (94%)	10 (6%)	17 43
20	LS	155/156 (99%)	145 (94%)	10 (6%)	17 43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	LT	140/140 (100%)	132 (94%)	8 (6%)	20	49
22	LU	90/114 (79%)	83 (92%)	7 (8%)	12	33
23	LV	100/107 (94%)	95 (95%)	5 (5%)	24	55
24	LW	54/126 (43%)	54 (100%)	0	100	100
25	LX	106/133 (80%)	100 (94%)	6 (6%)	20	49
26	LY	123/135 (91%)	113 (92%)	10 (8%)	11	32
27	LZ	117/118 (99%)	111 (95%)	6 (5%)	24	54
28	La	120/121 (99%)	112 (93%)	8 (7%)	16	41
29	Lb	83/124 (67%)	75 (90%)	8 (10%)	8	24
30	Lc	79/97 (81%)	75 (95%)	4 (5%)	24	54
31	Ld	99/110 (90%)	96 (97%)	3 (3%)	41	73
32	Le	114/121 (94%)	111 (97%)	3 (3%)	46	78
33	Lf	88/89 (99%)	82 (93%)	6 (7%)	16	40
34	Lg	94/100 (94%)	89 (95%)	5 (5%)	22	52
35	Lh	109/110 (99%)	106 (97%)	3 (3%)	43	76
36	Li	86/89 (97%)	79 (92%)	7 (8%)	11	32
37	Lj	73/80 (91%)	68 (93%)	5 (7%)	16	40
38	Lk	64/65 (98%)	62 (97%)	2 (3%)	40	72
39	Lm	47/116 (40%)	47 (100%)	0	100	100
40	Ln	24/24 (100%)	23 (96%)	1 (4%)	30	62
41	Lo	91/94 (97%)	85 (93%)	6 (7%)	16	42
42	Lp	74/75 (99%)	72 (97%)	2 (3%)	44	77
43	Lr	108/121 (89%)	104 (96%)	4 (4%)	34	66
48	SD	186/202 (92%)	170 (91%)	16 (9%)	10	29
49	SE	221/225 (98%)	196 (89%)	25 (11%)	6	17
50	SF	152/170 (89%)	136 (90%)	16 (10%)	7	20
51	SH	161/174 (92%)	143 (89%)	18 (11%)	6	18
52	SI	159/180 (88%)	140 (88%)	19 (12%)	5	15
53	SK	81/136 (60%)	73 (90%)	8 (10%)	8	22
54	SL	123/142 (87%)	109 (89%)	14 (11%)	5	17
55	SP	107/130 (82%)	103 (96%)	4 (4%)	34	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	SQ	115/121 (95%)	103 (90%)	12 (10%)	7	20
57	SR	119/121 (98%)	102 (86%)	17 (14%)	3	9
58	SS	122/132 (92%)	111 (91%)	11 (9%)	9	27
59	ST	110/115 (96%)	103 (94%)	7 (6%)	17	44
60	SU	88/107 (82%)	75 (85%)	13 (15%)	3	9
61	SV	64/67 (96%)	61 (95%)	3 (5%)	26	57
62	SX	111/115 (96%)	101 (91%)	10 (9%)	9	27
63	Sa	87/98 (89%)	77 (88%)	10 (12%)	5	17
64	Sc	48/62 (77%)	43 (90%)	5 (10%)	7	20
65	Sd	48/49 (98%)	45 (94%)	3 (6%)	18	44
66	Sg	237/275 (86%)	198 (84%)	39 (16%)	2	6
67	SC	182/224 (81%)	171 (94%)	11 (6%)	19	47
68	SG	178/218 (82%)	158 (89%)	20 (11%)	6	18
69	SJ	126/168 (75%)	110 (87%)	16 (13%)	4	13
70	SN	130/131 (99%)	120 (92%)	10 (8%)	13	34
71	SO	104/119 (87%)	95 (91%)	9 (9%)	10	28
72	SW	112/113 (99%)	103 (92%)	9 (8%)	12	32
73	SY	93/115 (81%)	80 (86%)	13 (14%)	3	10
74	SZ	64/103 (62%)	58 (91%)	6 (9%)	8	25
75	Sb	75/76 (99%)	67 (89%)	8 (11%)	6	19
76	Se	39/106 (37%)	36 (92%)	3 (8%)	13	34
78	Ll	47/48 (98%)	44 (94%)	3 (6%)	17	44
All	All	9336/10619 (88%)	8642 (93%)	694 (7%)	17	36

5 of 694 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	SQ	89	SER
66	Sg	187	ASN
57	SR	87	GLU
56	SQ	67	ASP
62	SX	19	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 156 such sidechains are listed below:

Mol	Chain	Res	Type
55	SP	41	GLN
68	SG	197	GLN
56	SQ	77	HIS
62	SX	61	GLN
73	SY	85	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	L5	3521/4731 (74%)	853 (24%)	19 (0%)
45	L7	119/120 (99%)	18 (15%)	0
46	L8	155/158 (98%)	32 (20%)	0
47	S2	1638/1870 (87%)	425 (25%)	9 (0%)
77	S6	74/75 (98%)	32 (43%)	4 (5%)
All	All	5507/6954 (79%)	1360 (24%)	32 (0%)

5 of 1360 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	L5	4	G
44	L5	13	U
44	L5	17	A
44	L5	21	G
44	L5	25	A

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
77	S6	19	G
77	S6	53	G
44	L5	3271	G
44	L5	2540	C
77	S6	54	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 278 ligands modelled in this entry, 278 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

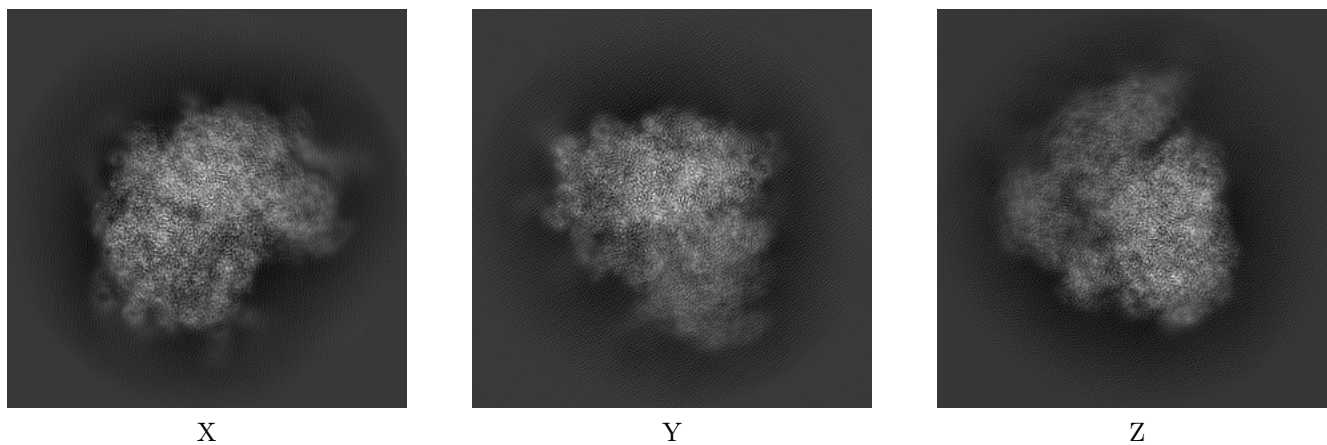
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30432. 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](#)

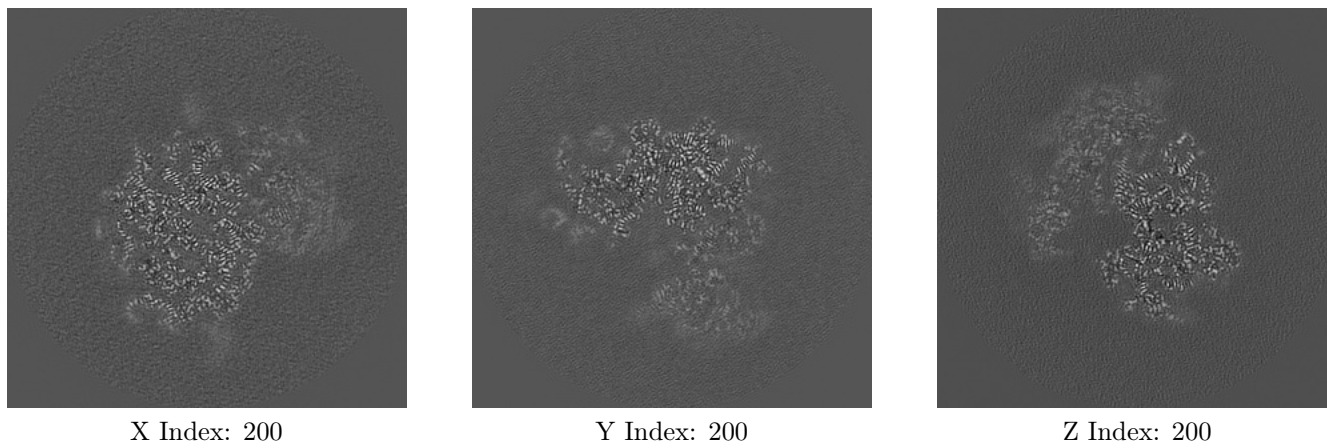
6.1.1 Primary map



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

6.2 Central slices [i](#)

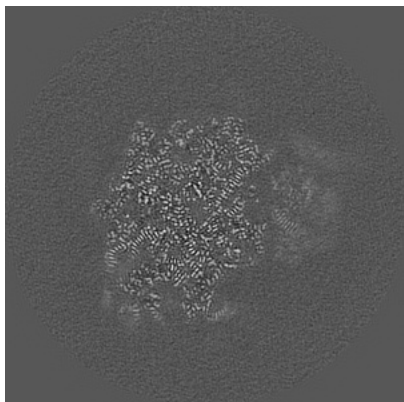
6.2.1 Primary map



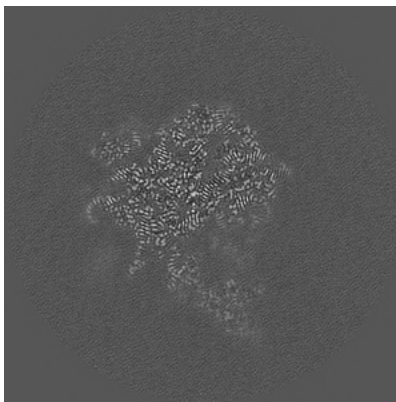
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

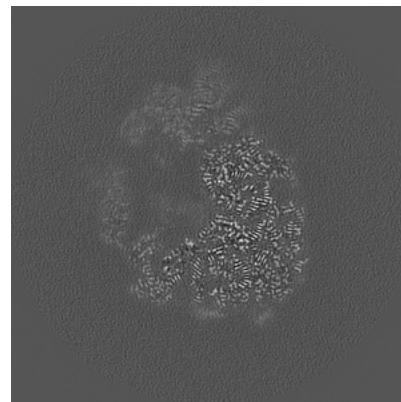
6.3.1 Primary map



X Index: 219



Y Index: 159

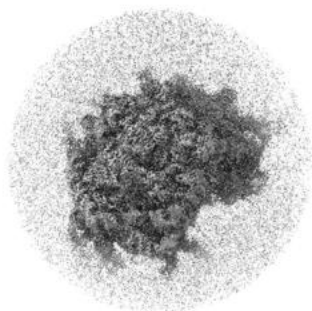


Z Index: 181

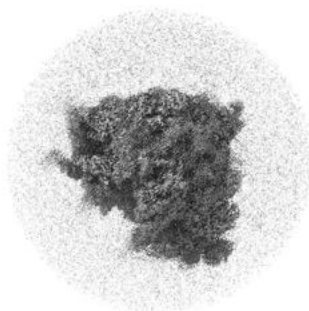
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

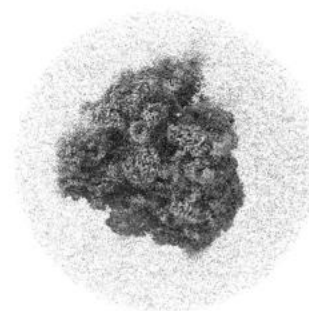
6.4.1 Primary map



X



Y



Z

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

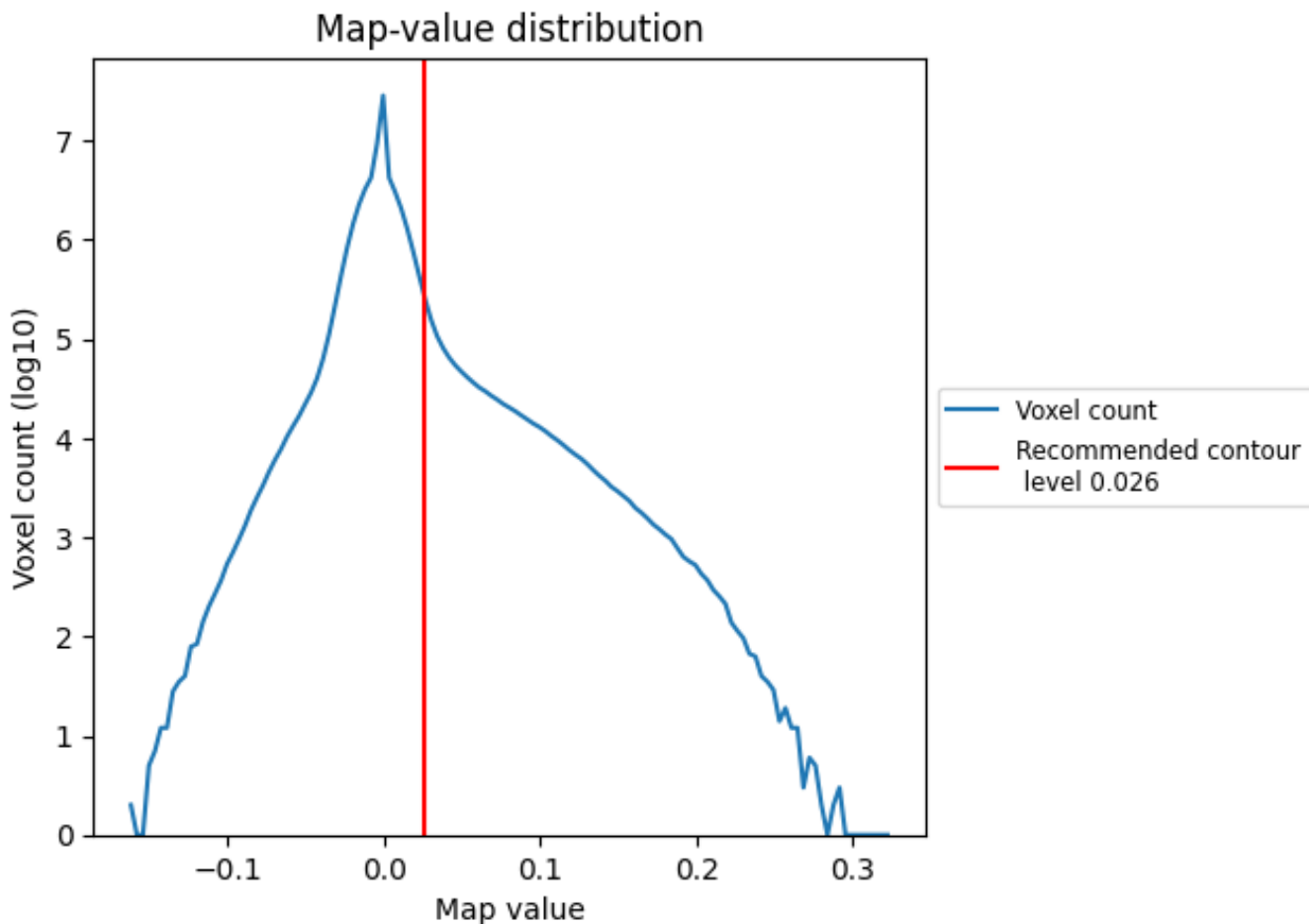
6.5 Mask visualisation

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

7 Map analysis [i](#)

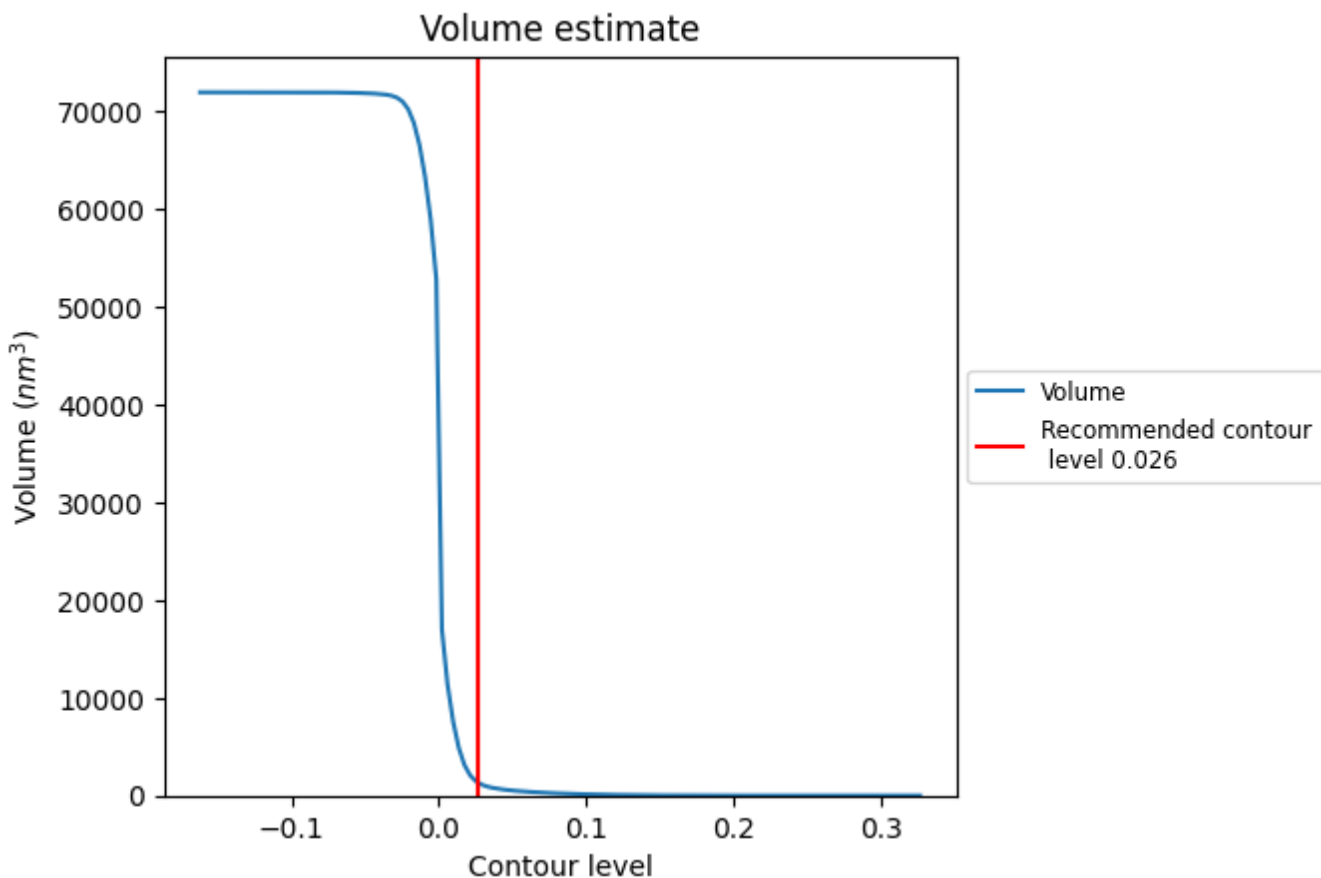
This section contains the results of statistical analysis of the map.

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.

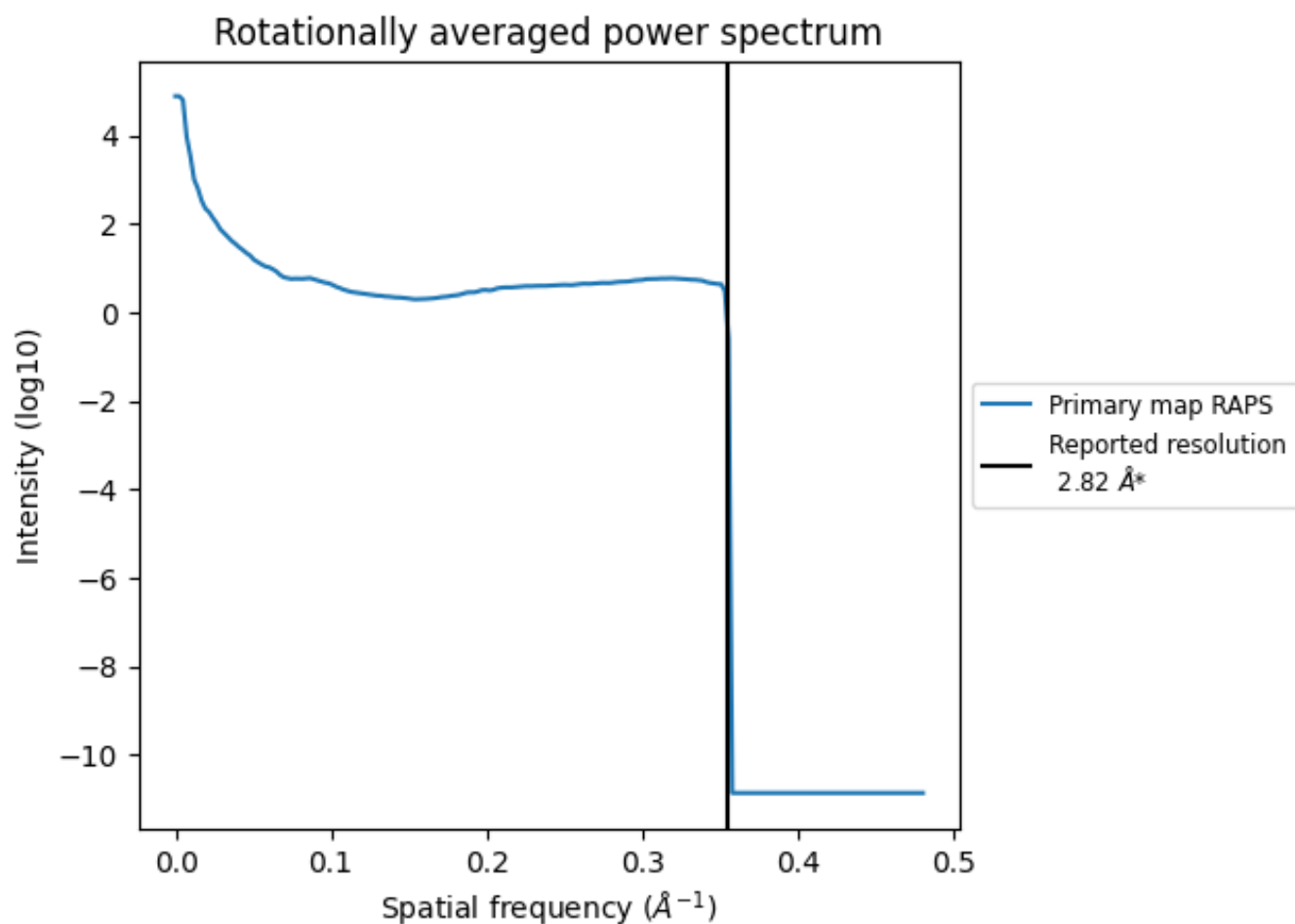
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1382 nm³; this corresponds to an approximate mass of 1248 kDa.

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

7.3 Rotationally averaged power spectrum [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.355 Å⁻¹

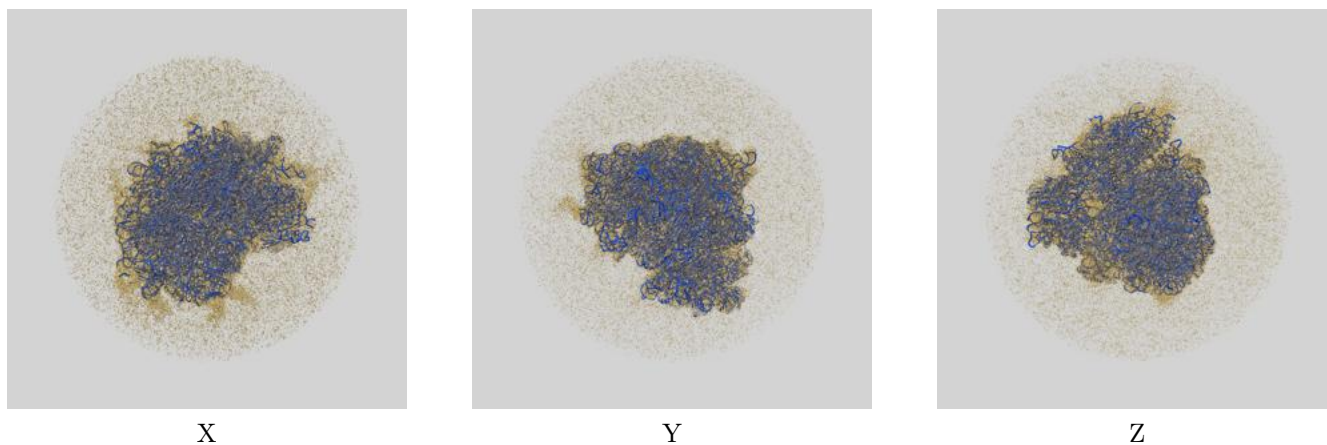
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

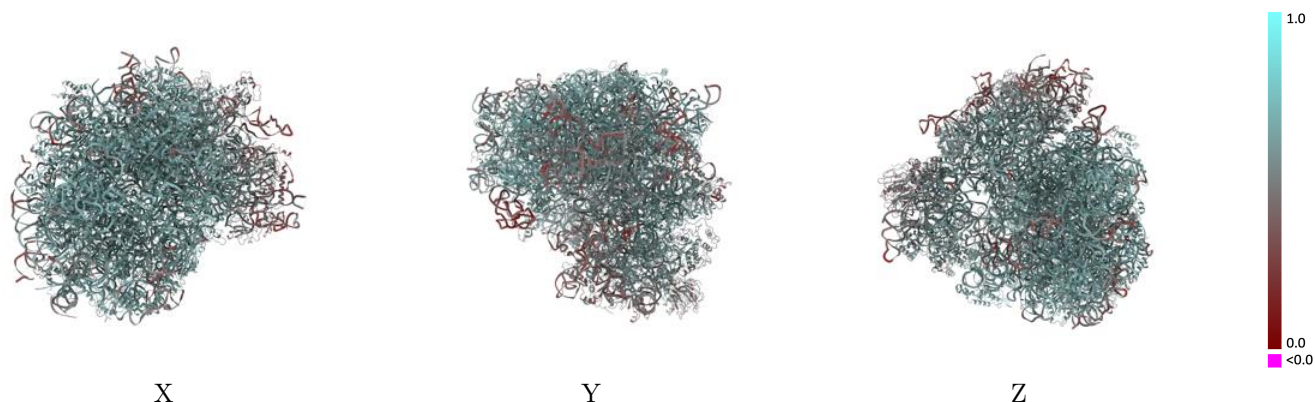
This section contains information regarding the fit between EMDB map EMD-30432 and PDB model 7CPU. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



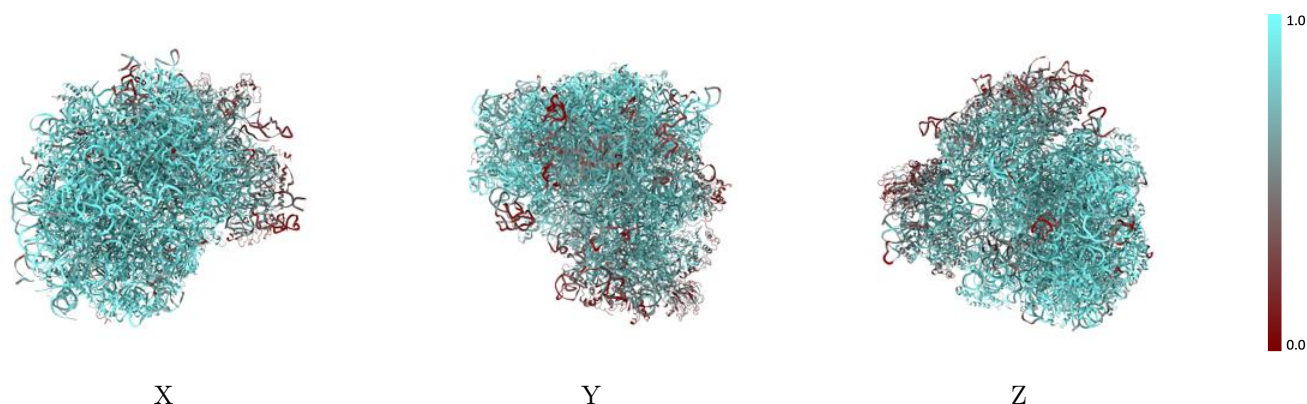
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



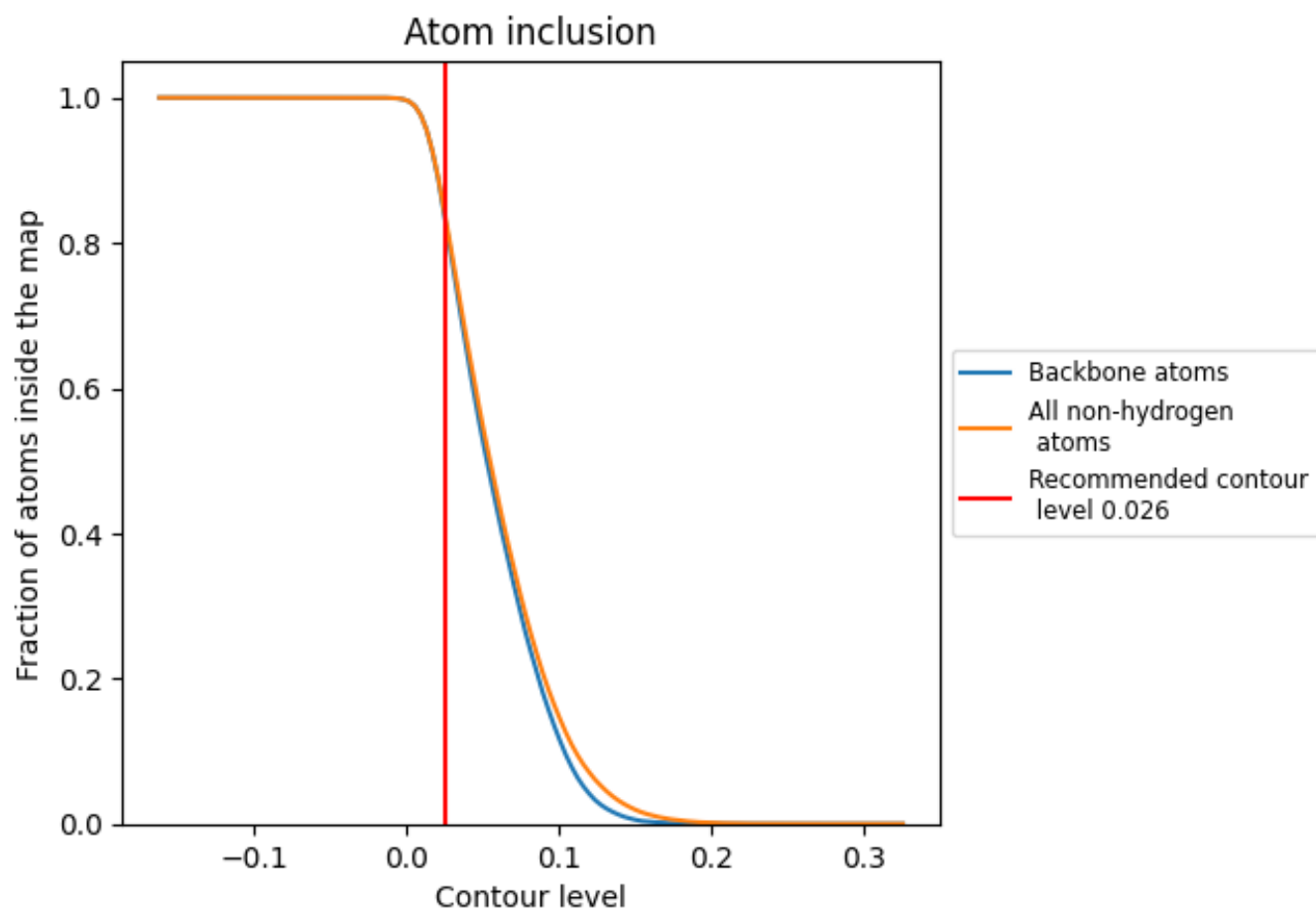
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.026).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8337	 0.5800
L5	 0.9054	 0.5950
L7	 0.9805	 0.6350
L8	 0.9241	 0.6160
LA	 0.9411	 0.6470
LB	 0.9261	 0.6370
LC	 0.9170	 0.6310
LD	 0.9018	 0.6180
LE	 0.8351	 0.5930
LF	 0.9463	 0.6470
LG	 0.8502	 0.6060
LH	 0.9082	 0.6220
LI	 0.9242	 0.6350
LJ	 0.8414	 0.5920
LL	 0.8976	 0.6180
LM	 0.9374	 0.6330
LN	 0.9692	 0.6540
LO	 0.9370	 0.6420
LP	 0.9243	 0.6410
LQ	 0.9414	 0.6510
LR	 0.8491	 0.6110
LS	 0.9500	 0.6510
LT	 0.9034	 0.6240
LU	 0.8010	 0.5750
LV	 0.9223	 0.6380
LW	 0.9220	 0.6360
LX	 0.9021	 0.6350
LY	 0.9061	 0.6300
LZ	 0.8816	 0.6120
La	 0.9575	 0.6520
Lb	 0.8683	 0.6130
Lc	 0.8895	 0.6130
Ld	 0.8775	 0.6240
Le	 0.9450	 0.6480
Lf	 0.9597	 0.6560






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Chain	Atom inclusion	Q-score
Lg	 0.9200	 0.6350
Lh	 0.8930	 0.6290
Li	 0.8684	 0.6110
Lj	 0.9554	 0.6430
Lk	 0.7914	 0.6040
Ll	 0.9314	 0.6430
Lm	 0.9286	 0.6360
Ln	 0.8165	 0.6030
Lo	 0.9009	 0.6360
Lp	 0.8940	 0.6370
Lr	 0.9361	 0.6330
S2	 0.7821	 0.5320
S6	 0.5954	 0.4350
SA	 0.6803	 0.5450
SB	 0.7616	 0.5770
SC	 0.7795	 0.5800
SD	 0.4545	 0.4910
SE	 0.5973	 0.4910
SF	 0.6647	 0.5500
SG	 0.4534	 0.4760
SH	 0.4944	 0.4990
SI	 0.6349	 0.5060
SJ	 0.5544	 0.4460
SK	 0.3162	 0.4500
SL	 0.7614	 0.5690
SN	 0.7534	 0.5840
SO	 0.7903	 0.5810
SP	 0.7024	 0.5480
SQ	 0.6524	 0.5310
SR	 0.5193	 0.5050
SS	 0.6935	 0.5600
ST	 0.6975	 0.5500
SU	 0.4128	 0.4550
SV	 0.6818	 0.5480
SW	 0.8426	 0.6000
SX	 0.7498	 0.5810
SY	 0.4429	 0.4160
SZ	 0.5722	 0.5180
Sa	 0.8150	 0.5910
Sb	 0.6541	 0.5470
Sc	 0.6015	 0.5180
Sd	 0.7517	 0.5660

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Chain	Atom inclusion	Q-score
Se	 0.5176	 0.4890
Sg	 0.3745	 0.4500