



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 10:40 AM UTC

PDB ID : 8BSJ / pdb_00008bsj
EMDB ID : EMD-16226
Title : Giardia Ribosome in PRE-T Classical State (C)
Authors : Majumdar, S.; Emmerich, A.G.; Sanyal, S.
Deposited on : 2022-11-25
Resolution : 6.49 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

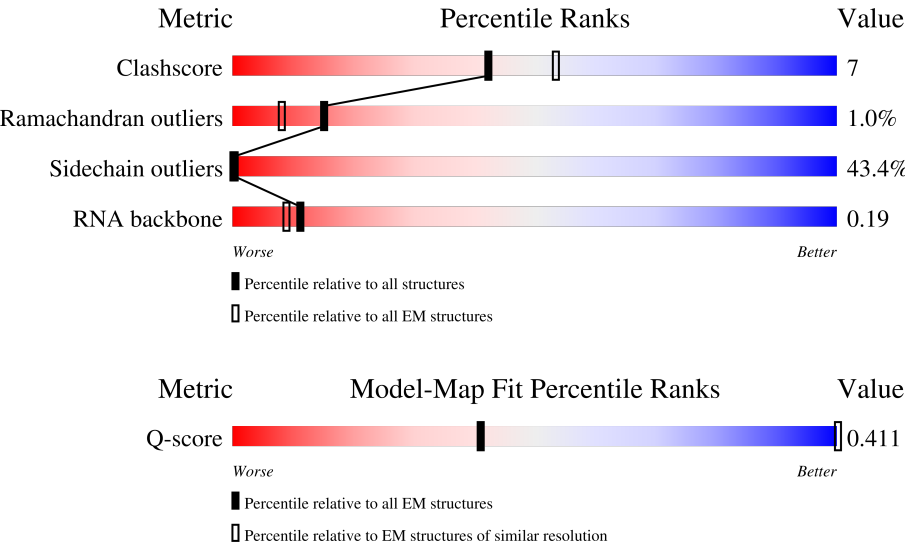
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 6.49 Å.

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



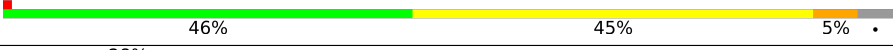
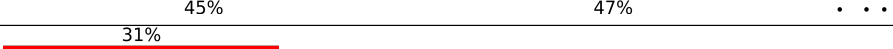
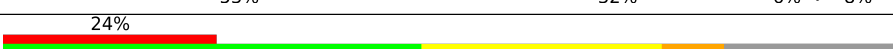
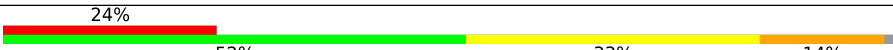
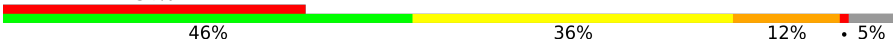
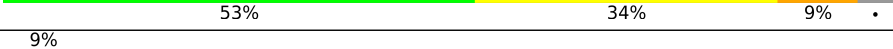
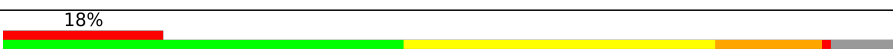
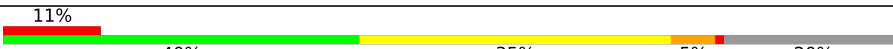
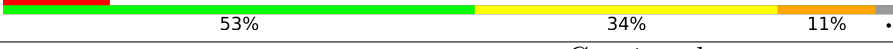
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	496 (6.00 - 6.99)

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	251	14% 58% 31% 8% .
2	LB	379	16% 50% 34% 14% ..
3	LC	316	19% 56% 34% 8% .

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Mol	Chain	Length	Quality of chain
4	LD	142	
5	LE	121	
6	LF	297	
7	LG	51	
8	LH	235	
9	LI	225	
10	LJ	185	
11	LK	210	
12	LL	173	
13	LM	234	
14	LN	131	
15	LO	204	
16	LP	197	
17	LQ	164	
18	LR	179	
19	LS	196	
20	LT	173	
21	LU	159	
22	LV	124	
23	LW	142	
24	LX	189	
25	LY	141	
26	LZ	135	
27	La	135	
28	Lb	149	

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Mol	Chain	Length	Quality of chain
29	Lc	62	
30	Ld	109	
31	Le	106	
32	Lf	136	
33	Lg	123	
34	Lh	120	
35	Li	124	
36	Lj	90	
37	Lk	89	
38	Ll	77	
39	Ln	217	
40	Lo	25	
41	Lp	106	
42	Lq	94	
43	Ls	127	
44	Lt	2697	
45	SA	245	
46	SB	242	
47	SC	217	
48	SD	248	
49	SE	268	
50	SF	190	
51	SG	248	
52	SH	190	
53	SI	174	

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Mol	Chain	Length	Quality of chain
54	SJ	130	
55	SK	189	
56	SL	134	
57	SM	154	
58	SO	143	
59	SP	154	
60	SQ	145	
61	SR	145	
62	ST	158	
63	SU	137	
64	SV	154	
65	SW	139	
66	SX	126	
67	SY	89	
68	Sb	132	
69	Sc	88	
70	Sd	109	
71	Se	81	
72	Sg	64	
73	Sh	51	
74	Sj	69	
75	St	1454	
76	u	75	
76	v	75	
77	x	74	

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Mol	Chain	Length	Quality of chain
78	y	11	27% 18% 55% 27%

2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 178791 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 Ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	243	Total	C	N	O	S	0	0
			1823	1125	371	315	12		

- Molecule 2 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LB	374	Total	C	N	O	S	0	0
			2960	1871	560	508	21		

- Molecule 3 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LC	309	Total	C	N	O	S	0	0
			2412	1516	469	419	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LD	140	Total	C	N	O	P	0	0
			2995	1331	555	969	140		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LE	116	Total	C	N	O	P	0	0
			2480	1106	452	806	116		

- Molecule 6 is a protein called Ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LF	289	Total	C	N	O	S	0	0
			2325	1471	433	413	8		

- Molecule 7 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	LG	50	Total	C	N	O	0	0
			439	281	94	64		

- Molecule 8 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LH	217	Total	C	N	O	S	0	0
			1753	1112	321	315	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LI	183	Total	C	N	O	S	0	0
			1468	935	268	260	5		

- Molecule 10 is a protein called Ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LJ	184	Total	C	N	O	S	0	0
			1452	917	264	261	10		

- Molecule 11 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LK	197	Total	C	N	O	S	0	0
			1609	1011	317	273	8		

- Molecule 12 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LL	165	Total	C	N	O	S	0	0
			1325	837	247	236	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LM	195	Total	C	N	O	S	0	0
			1560	971	316	267	6		

- Molecule 14 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LN	126	Total	C	N	O	S	0	0
			993	630	181	176	6		

- Molecule 15 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LO	201	Total	C	N	O	S	0	0
			1699	1075	355	263	6		

- Molecule 16 is a protein called Ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LP	189	Total	C	N	O	S	0	0
			1539	970	300	257	12		

- Molecule 17 is a protein called Ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LQ	153	Total	C	N	O	S	0	0
			1231	778	239	210	4		

- Molecule 18 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LR	178	Total	C	N	O	S	0	0
			1402	871	279	243	9		

- Molecule 19 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LS	187	Total	C	N	O	S	0	0
			1548	953	328	262	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LT	170	Total	C	N	O	S	0	0
			1423	899	272	243	9		

- Molecule 21 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LU	150	Total	C	N	O	S	0	0
			1216	757	252	201	6		

- Molecule 22 is a protein called Ribosomal L22e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LV	105	Total	C	N	O	S	0	0
			861	550	147	162	2		

- Molecule 23 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LW	132	Total	C	N	O	S	0	0
			1015	641	193	176	5		

- Molecule 24 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LX	60	Total	C	N	O	S	0	0
			512	323	103	79	7		

- Molecule 25 is a protein called Ribosomal protein L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LY	113	Total	C	N	O	S	0	0
			913	588	163	159	3		

- Molecule 26 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LZ	133	Total	C	N	O	S	0	0
			1076	665	219	184	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	La	121	Total	C	N	O	S	0	0
			968	614	183	166	5		

- Molecule 28 is a protein called Ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lb	145	Total	C	N	O	S	0	0
			1179	746	234	196	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lc	55	Total	C	N	O	S	0	0
			456	275	103	76	2		

- Molecule 30 is a protein called Ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ld	98	Total	C	N	O	S	0	0
			737	463	129	141	4		

- Molecule 31 is a protein called Ribosomal protein L31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Le	97	Total	C	N	O		0	0
			791	503	153	135			

- Molecule 32 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lf	125	Total	C	N	O	S	0	0
			1031	655	206	164	6		

- Molecule 33 is a protein called Ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lg	98	Total	C	N	O	S	0	0
			778	498	147	130	3		

- Molecule 34 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lh	104	Total	C	N	O	S	0	0
			834	515	173	142	4		

- Molecule 35 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Li	118	Total	C	N	O	S	0	0
			958	606	188	159	5		

- Molecule 36 is a protein called Ribosomal protein L36-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lj	84	Total	C	N	O	S	0	0
			684	434	136	110	4		

- Molecule 37 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lk	85	Total	C	N	O	S	0	0
			689	420	148	114	7		

- Molecule 38 is a protein called Ribosomal L38e.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ll	72	Total	C	N	O	S	0	0
			558	353	99	102	4		

- Molecule 39 is a protein called Ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ln	200	Total	C	N	O	S	0	0
			1592	1025	278	284	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lo	25	Total	C	N	O	S	0	0
			227	140	57	27	3		

- Molecule 41 is a protein called Ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lp	91	Total	C	N	O	S	0	0
			748	466	154	123	5		

- Molecule 42 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lq	91	Total	C	N	O	S	0	0
			708	437	144	120	7		

- Molecule 43 is a protein called Ubiquitin/Ribosomal protein L40e.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ls	47	Total	C	N	O	S	0	0
			388	234	83	64	7		

- Molecule 44 is a RNA chain called Large Subunit rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lt	2593	Total	C	N	O	P	0	0
			55643	24727	10311	18012	2593		

- Molecule 45 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SA	194	Total	C	N	O	S	0	0
			1553	1001	272	272	8		

- Molecule 46 is a protein called Ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SB	213	Total	C	N	O	S	0	0
			1640	1041	298	296	5		

- Molecule 47 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SC	206	Total	C	N	O	S	0	0
			1636	1030	302	288	16		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SD	228	Total	C	N	O	S	0	0
			1847	1168	344	322	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SE	260	Total	C	N	O	S	0	0
			2085	1333	384	356	12		

- Molecule 50 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SF	179	Total	C	N	O	S	0	0
			1387	864	260	254	9		

- Molecule 51 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SG	224	Total	C	N	O	S	0	0
			1768	1112	332	314	10		

- Molecule 52 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SH	184	Total	C	N	O	S	0	0
			1481	948	258	268	7		

- Molecule 53 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SI	167	Total	C	N	O	S	0	0
			1311	822	251	235	3		

- Molecule 54 is a protein called Ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SJ	129	Total	C	N	O	S	0	0
			1031	659	192	177	3		

- Molecule 55 is a protein called Ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SK	172	Total	C	N	O	S	0	0
			1395	871	276	242	6		

- Molecule 56 is a protein called Ribosomal protein S10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SL	109	Total	C	N	O	S	0	0
			890	578	149	160	3		

- Molecule 57 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SM	147	Total	C	N	O	S	0	0
			1217	773	237	201	6		

- Molecule 58 is a protein called SSU ribosomal protein S12P.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SO	140	Total	C	N	O	S	0	0
			1088	688	214	182	4		

- Molecule 59 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SP	150	Total	C	N	O	S	0	0
			1192	758	228	201	5		

- Molecule 60 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SQ	124	Total	C	N	O	S	0	0
			911	561	188	159	3		

- Molecule 61 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SR	113	Total	C	N	O	S	0	0
			918	584	179	147	8		

- Molecule 62 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	ST	151	Total	C	N	O	S	0	0
			1180	736	229	212	3		

- Molecule 63 is a protein called Ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SU	121	Total	C	N	O	S	0	0
			963	597	184	177	5		

- Molecule 64 is a protein called Ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SV	142	Total	C	N	O	S	0	0
			1124	692	228	198	6		

- Molecule 65 is a protein called Ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SW	138	Total	C	N	O	S	0	0
			1080	686	204	187	3		

- Molecule 66 is a protein called Ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SX	107	Total	C	N	O	S	0	0
			853	539	153	156	5		

- Molecule 67 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SY	85	Total	C	N	O	S	0	0
			642	397	119	120	6		

- Molecule 68 is a protein called Ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sb	120	Total	C	N	O	S	0	0
			952	604	179	163	6		

- Molecule 69 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sc	75	Total	C	N	O	S	0	0
			597	377	107	107	6		

- Molecule 70 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sd	97	Total	C	N	O	S	0	0
			787	485	162	133	7		

- Molecule 71 is a protein called Ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Se	80	Total	C	N	O	S	0	0
			629	397	110	116	6		

- Molecule 72 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Sg	61	Total	C	N	O	S	0	0
			486	300	95	89	2		

- Molecule 73 is a protein called Ribosomal protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sh	48	Total	C	N	O	S	0	0
			401	253	78	65	5		

- Molecule 74 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sj	67	Total	C	N	O	S	0	0
			543	341	114	87	1		

- Molecule 75 is a RNA chain called Small Subunit rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	St	1454	Total	C	N	O	P	0	0
			31176	13861	5772	10090	1453		

- Molecule 76 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	u	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		
76	v	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 77 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	x	74	Total	C	N	O	P	0	0
			1582	708	291	509	74		

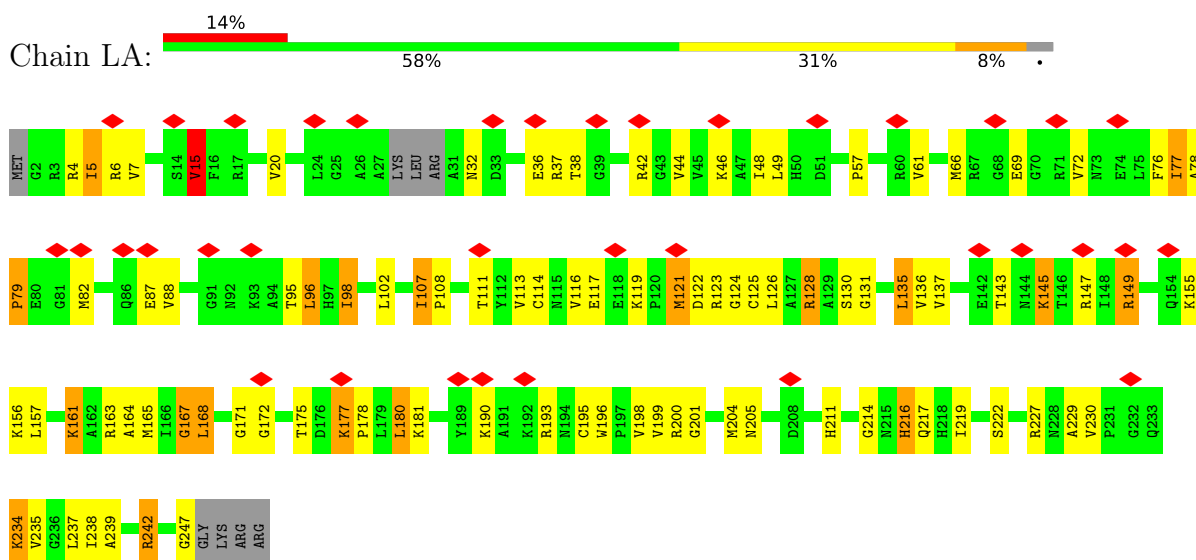
- Molecule 78 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	y	11	Total	C	N	O	P	0	0
			240	108	49	72	11		

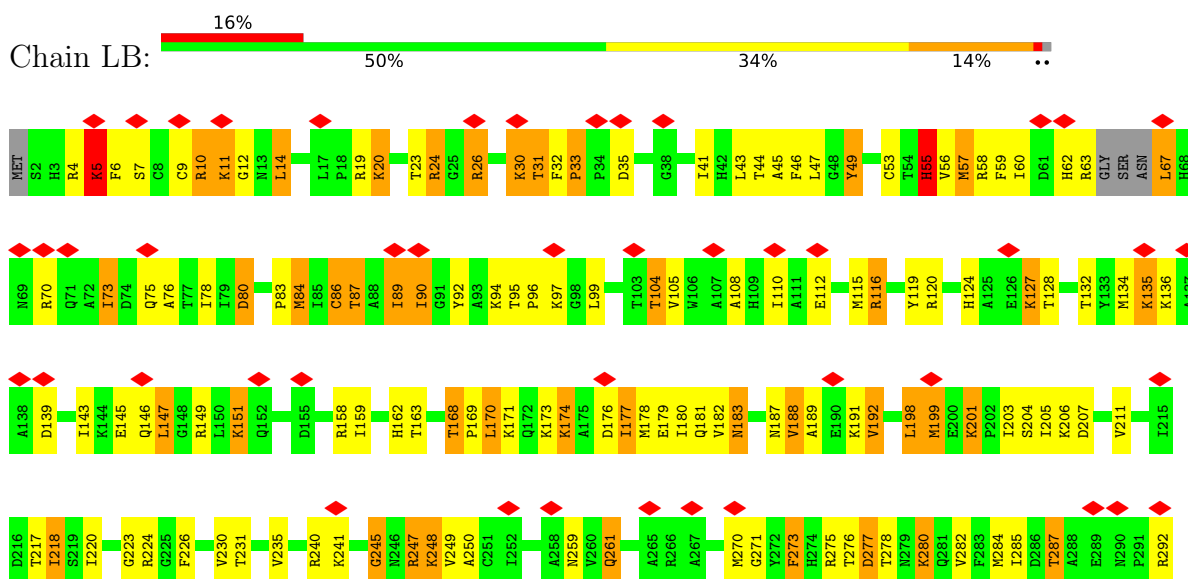
3 Residue-property plots

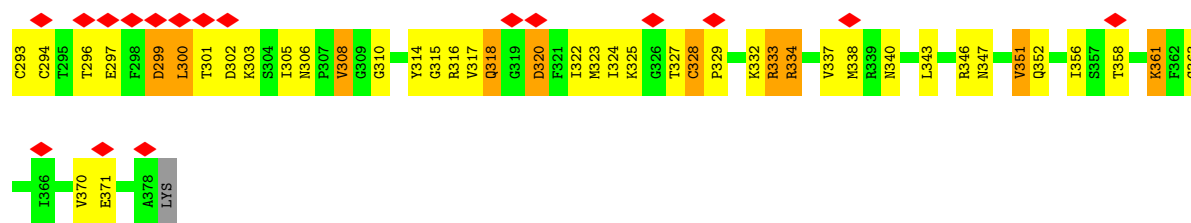
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Ribosomal protein L2

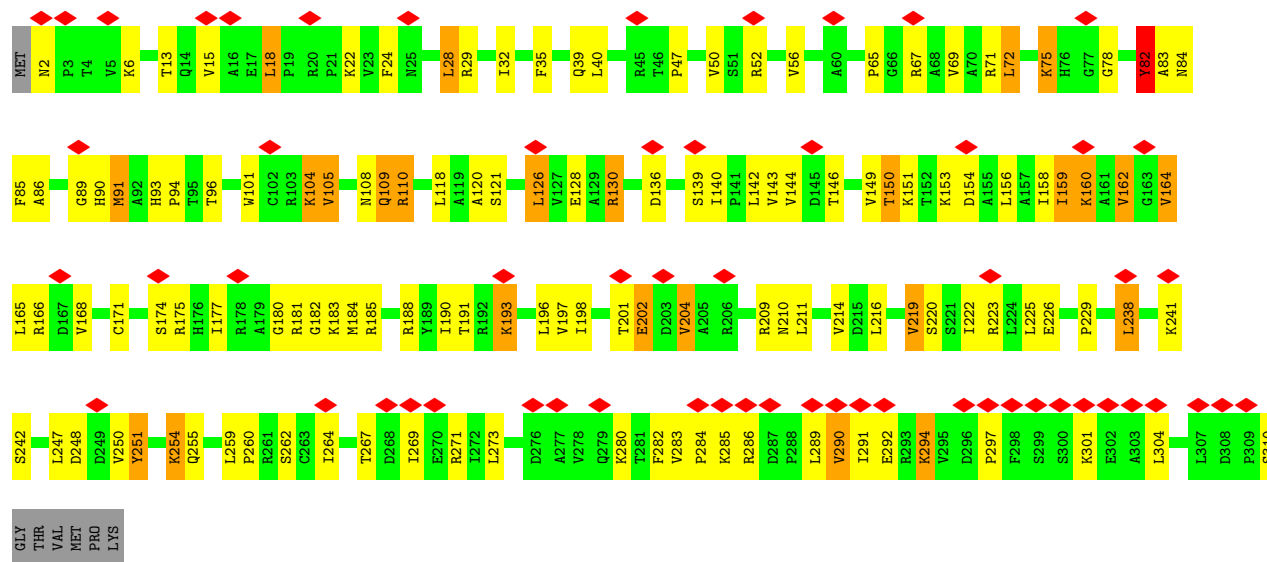


• Molecule 2: Ribosomal protein L3

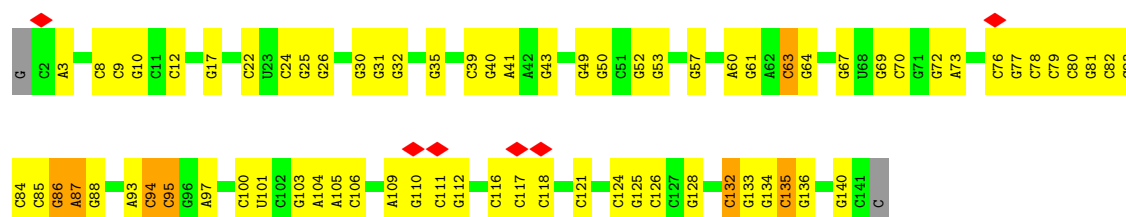




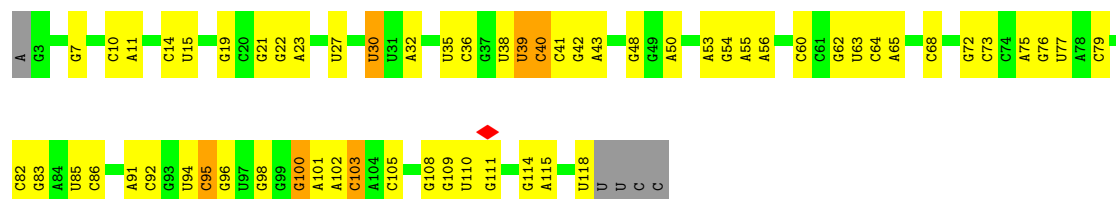
• Molecule 3: Ribosomal protein L4



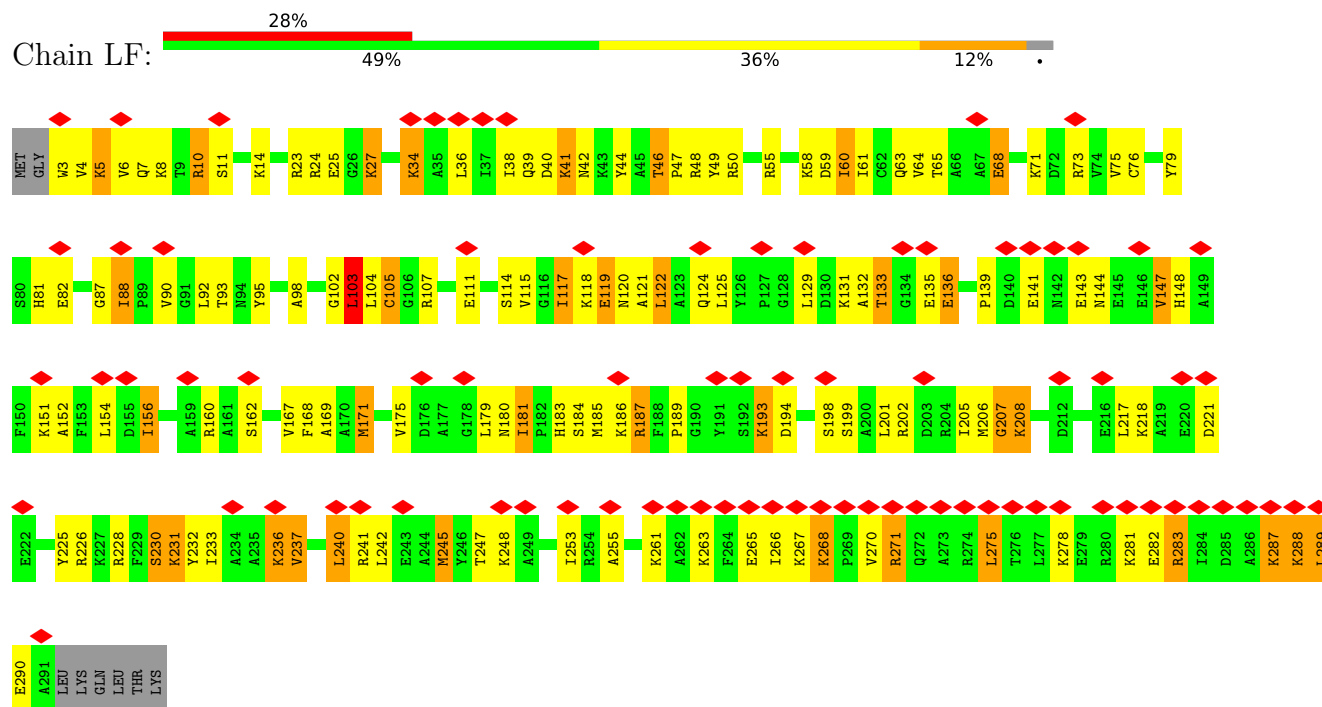
• Molecule 4: 5.8S rRNA



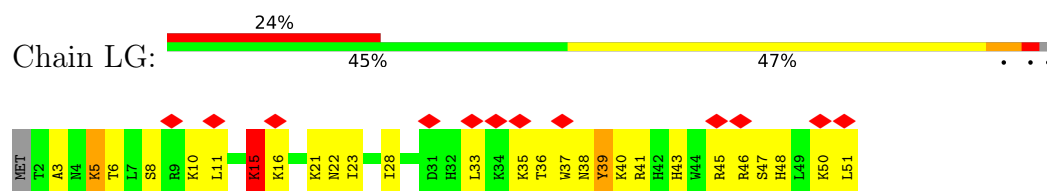
• Molecule 5: 5S rRNA



- Molecule 6: Ribosomal protein L5



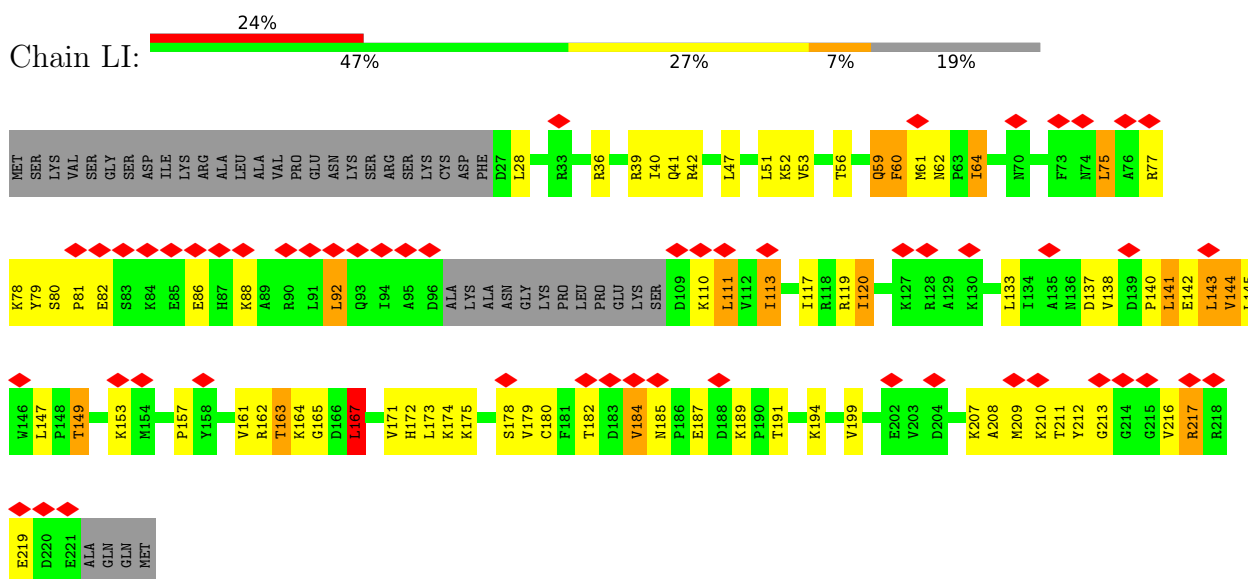
- Molecule 7: Ribosomal protein L39



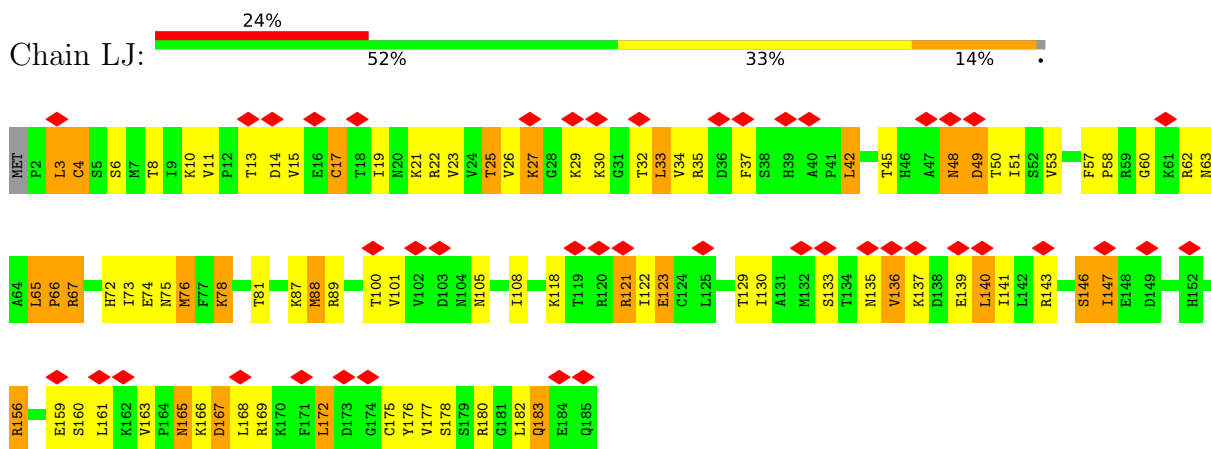
- Molecule 8: Ribosomal protein L7



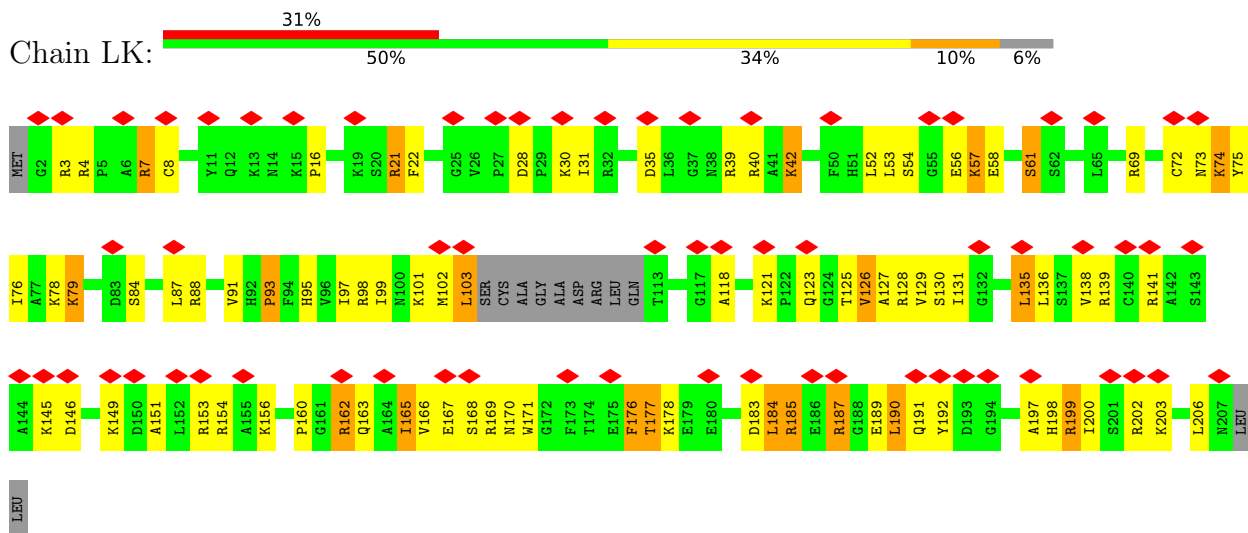
- Molecule 9: 60S ribosomal protein L7a



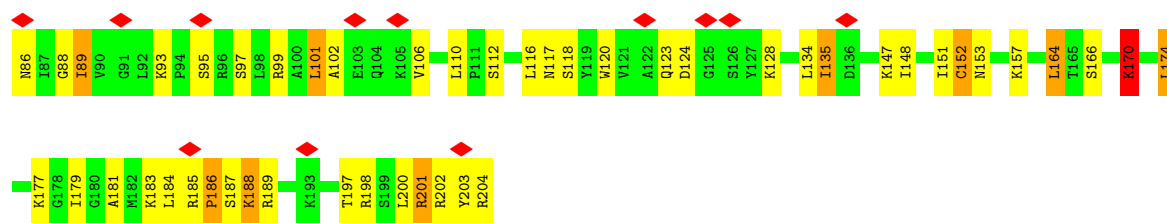
• Molecule 10: Ribosomal protein L6



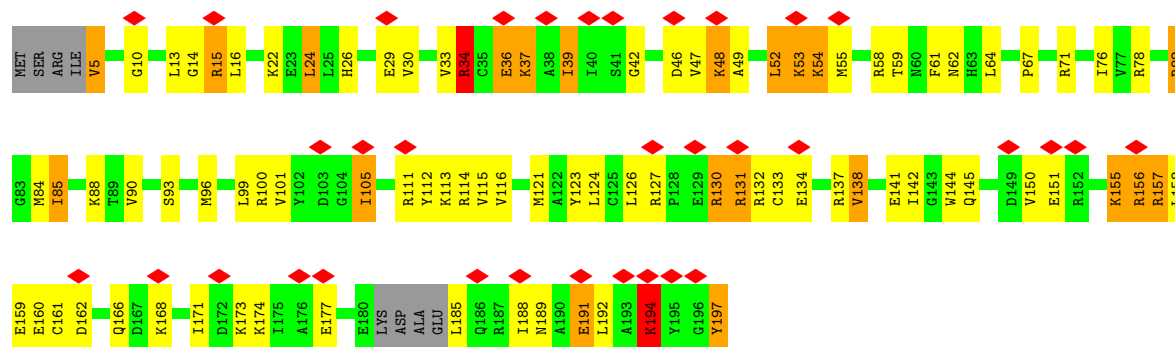
• Molecule 11: Ribosomal protein L10



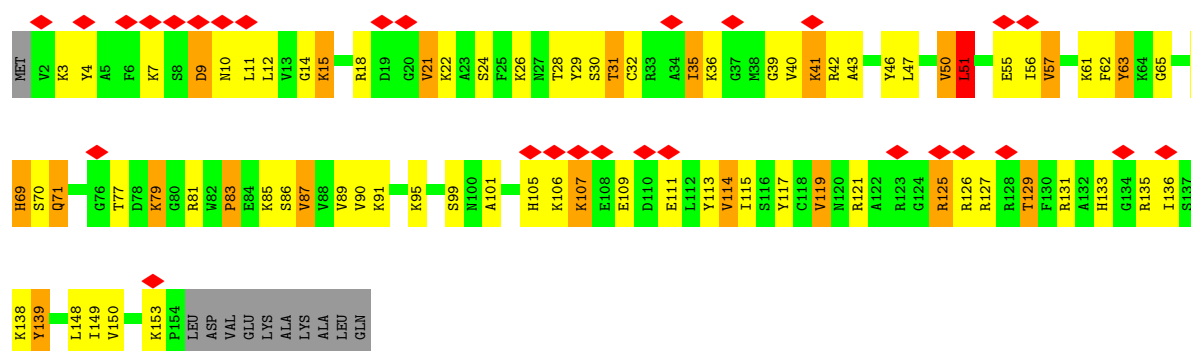
• Molecule 12: Ribosomal protein L11



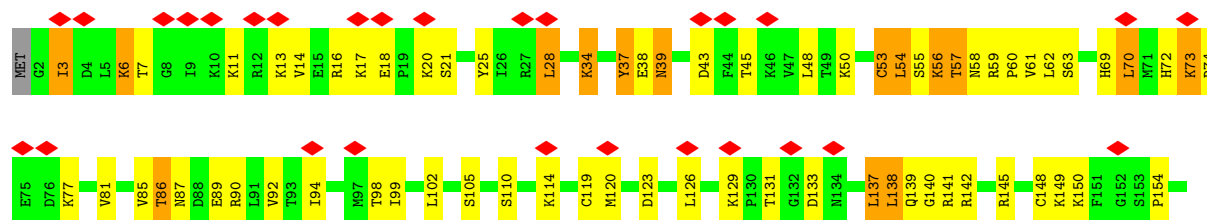
• Molecule 16: Ribosomal protein L13a

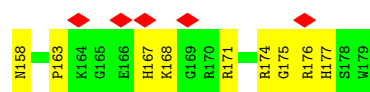


• Molecule 17: Ribosomal protein L17

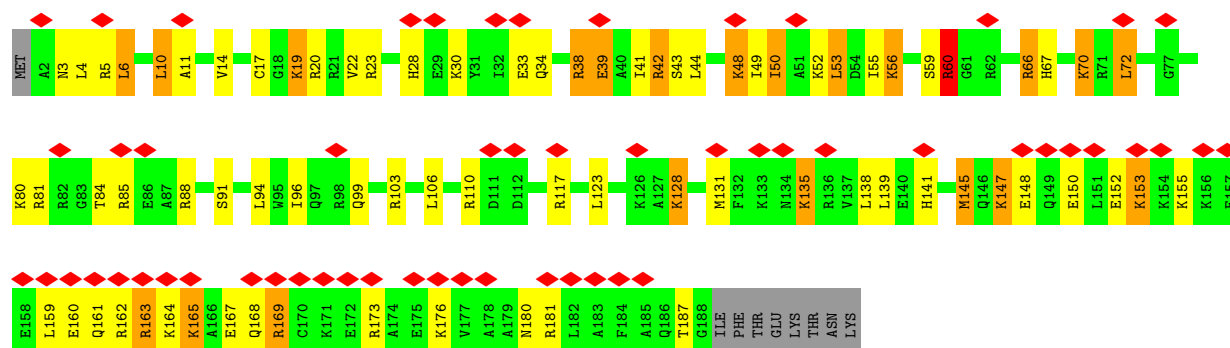


• Molecule 18: Ribosomal protein L18

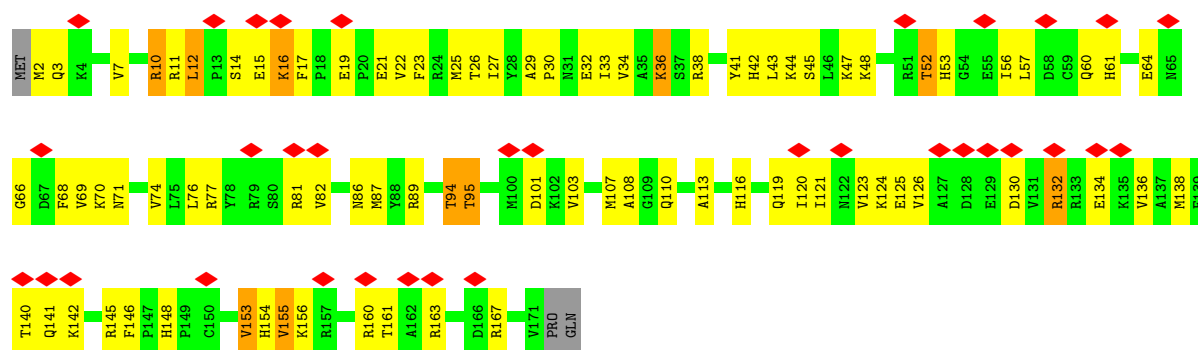




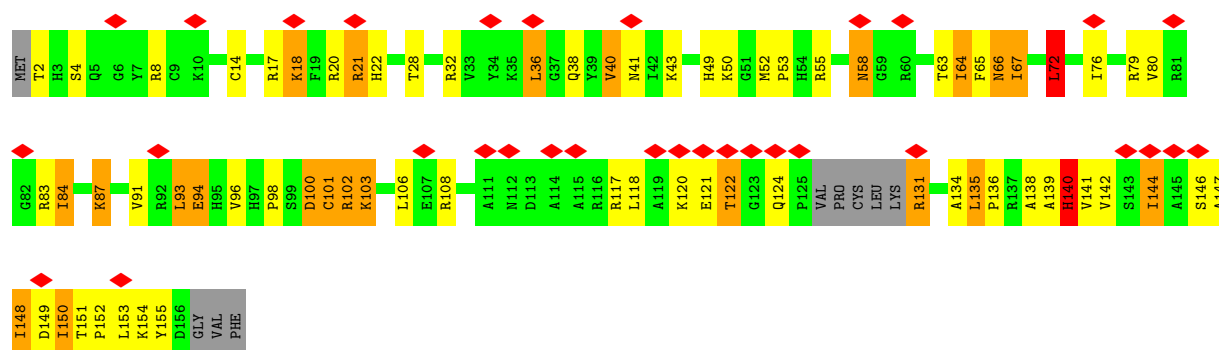
• Molecule 19: Ribosomal protein L19



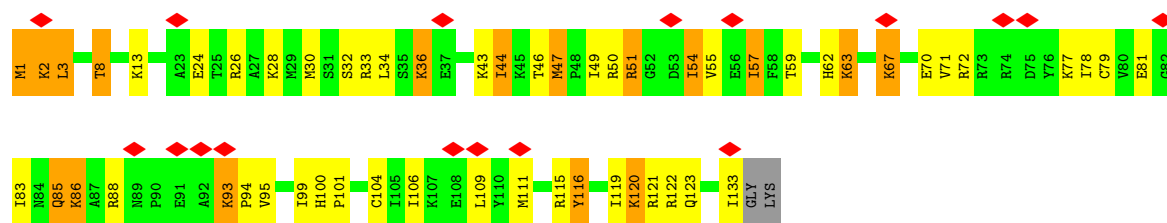
• Molecule 20: 60S ribosomal protein L18a



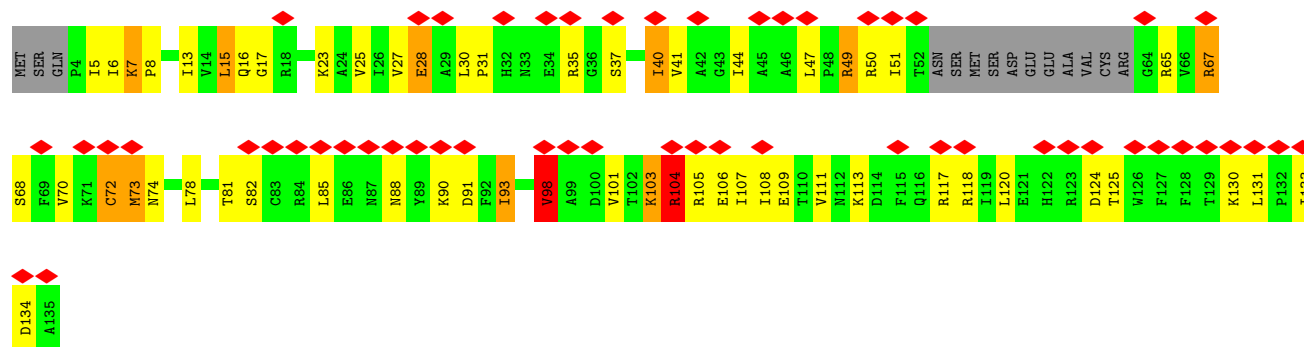
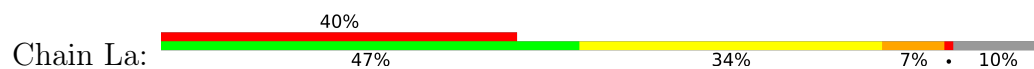
• Molecule 21: Ribosomal protein L21



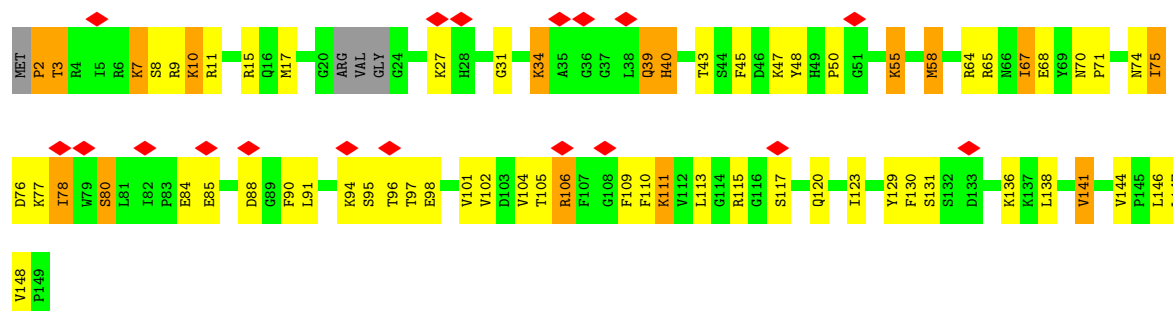
• Molecule 22: Ribosomal L22e



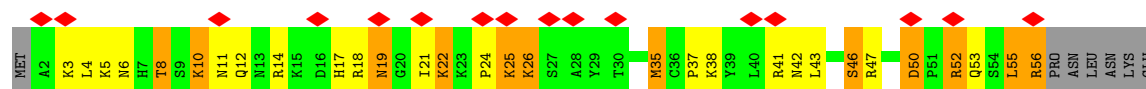
• Molecule 27: 60S ribosomal protein L27



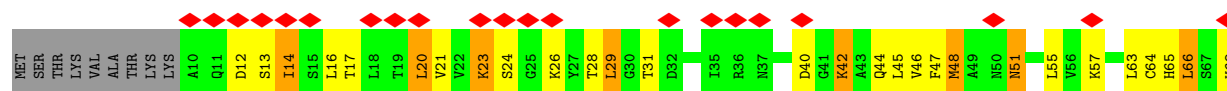
• Molecule 28: Ribosomal protein L27a

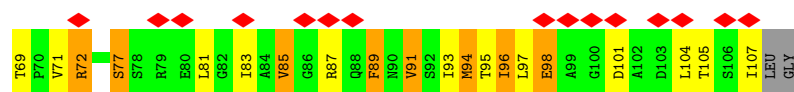


• Molecule 29: 60S ribosomal protein L29

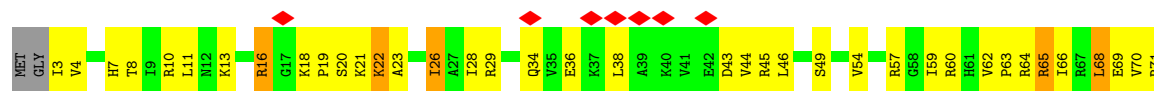
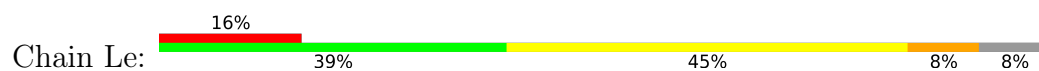


• Molecule 30: Ribosomal protein L30

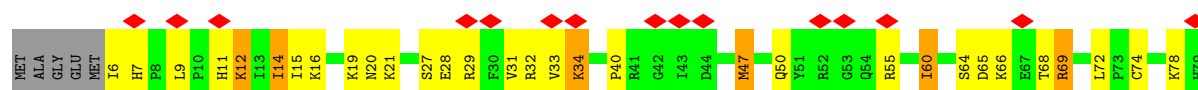




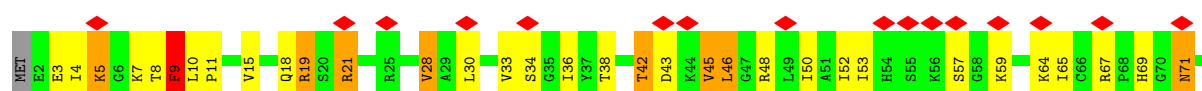
- Molecule 31: Ribosomal protein L31B



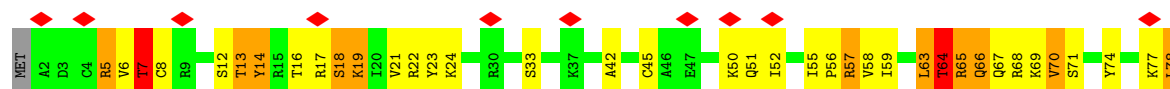
- Molecule 32: Ribosomal protein L32



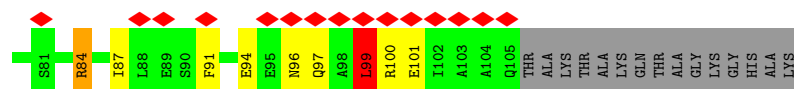
- Molecule 33: Ribosomal protein L35a



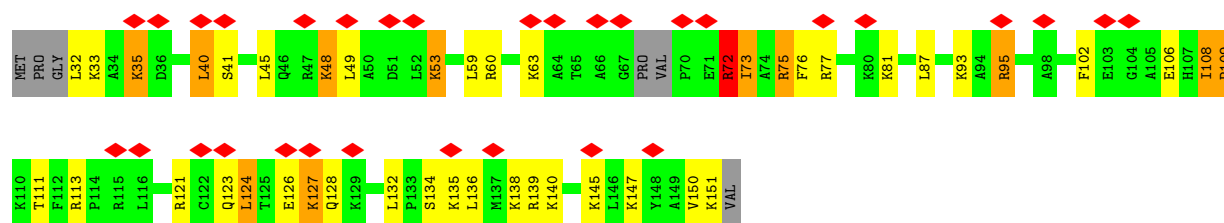
- Molecule 34: Ribosomal protein L34



- Molecule 35: Ribosomal protein L29

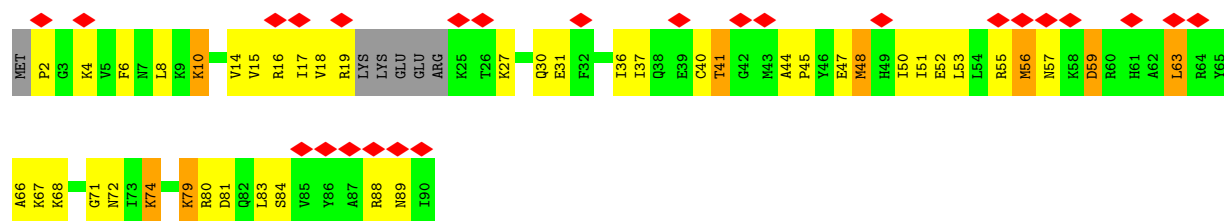


Chain Li: 



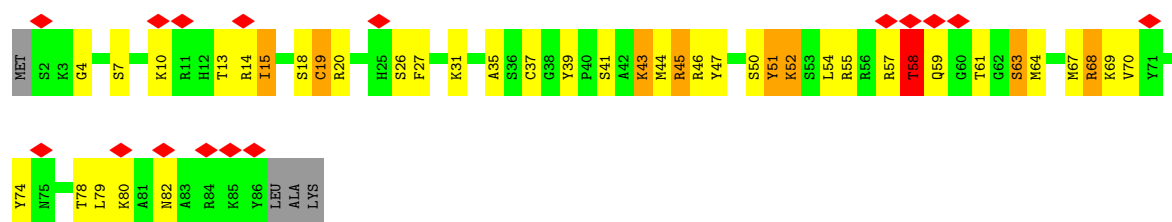
• Molecule 36: Ribosomal protein L36-1

Chain Lj: 



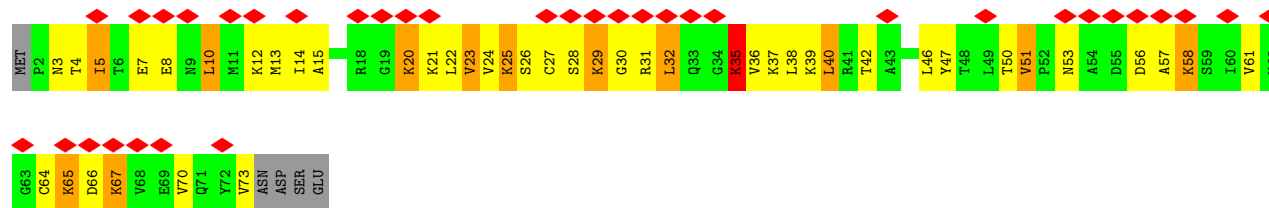
• Molecule 37: Ribosomal protein L37

Chain Lk: 

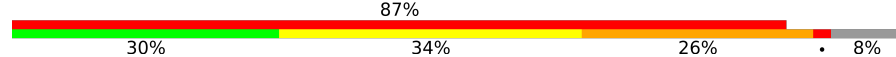


• Molecule 38: Ribosomal L38e

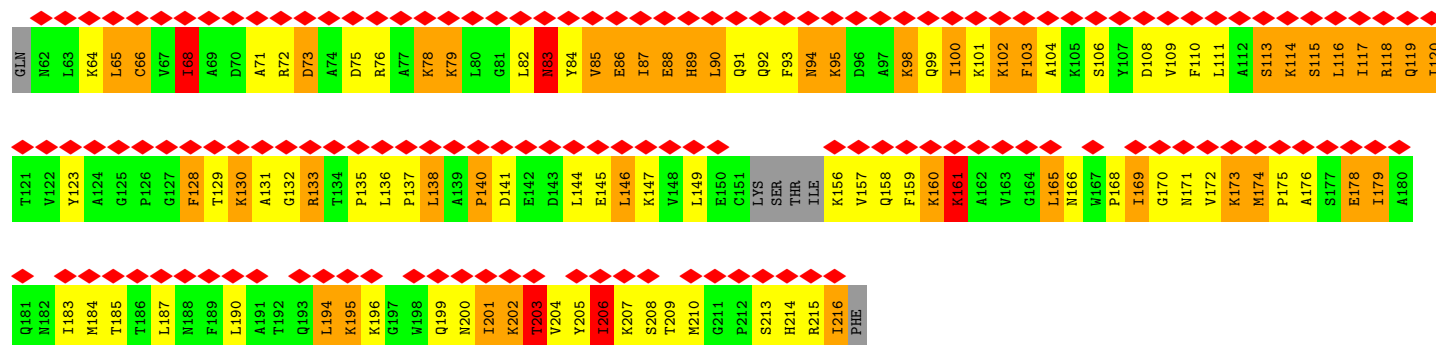
Chain Ll: 



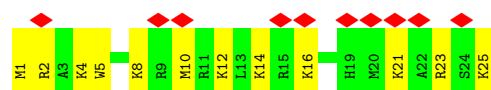
• Molecule 39: Ribosomal protein L10a

Chain Ln: 

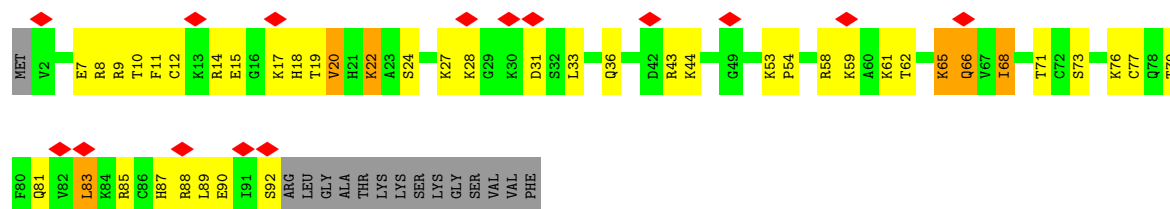




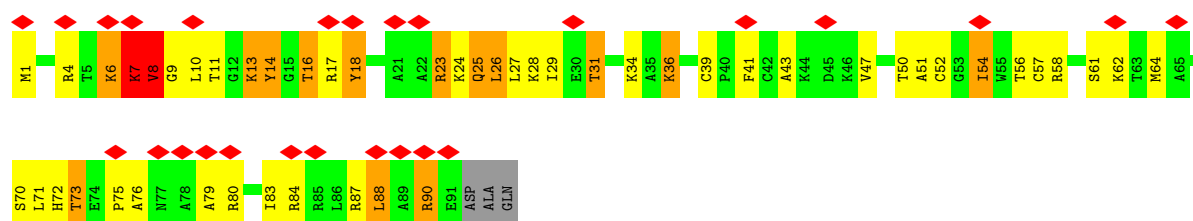
• Molecule 40: 60S ribosomal protein L41



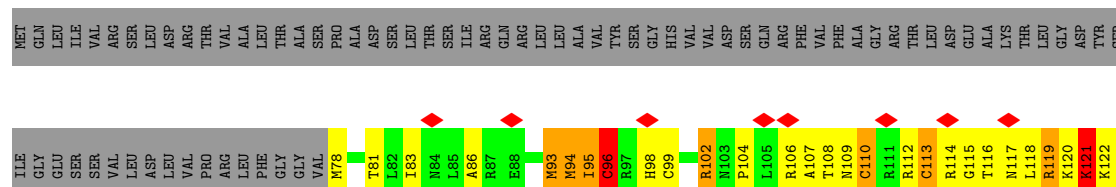
• Molecule 41: Ribosomal protein L44



• Molecule 42: Ribosomal protein L37a

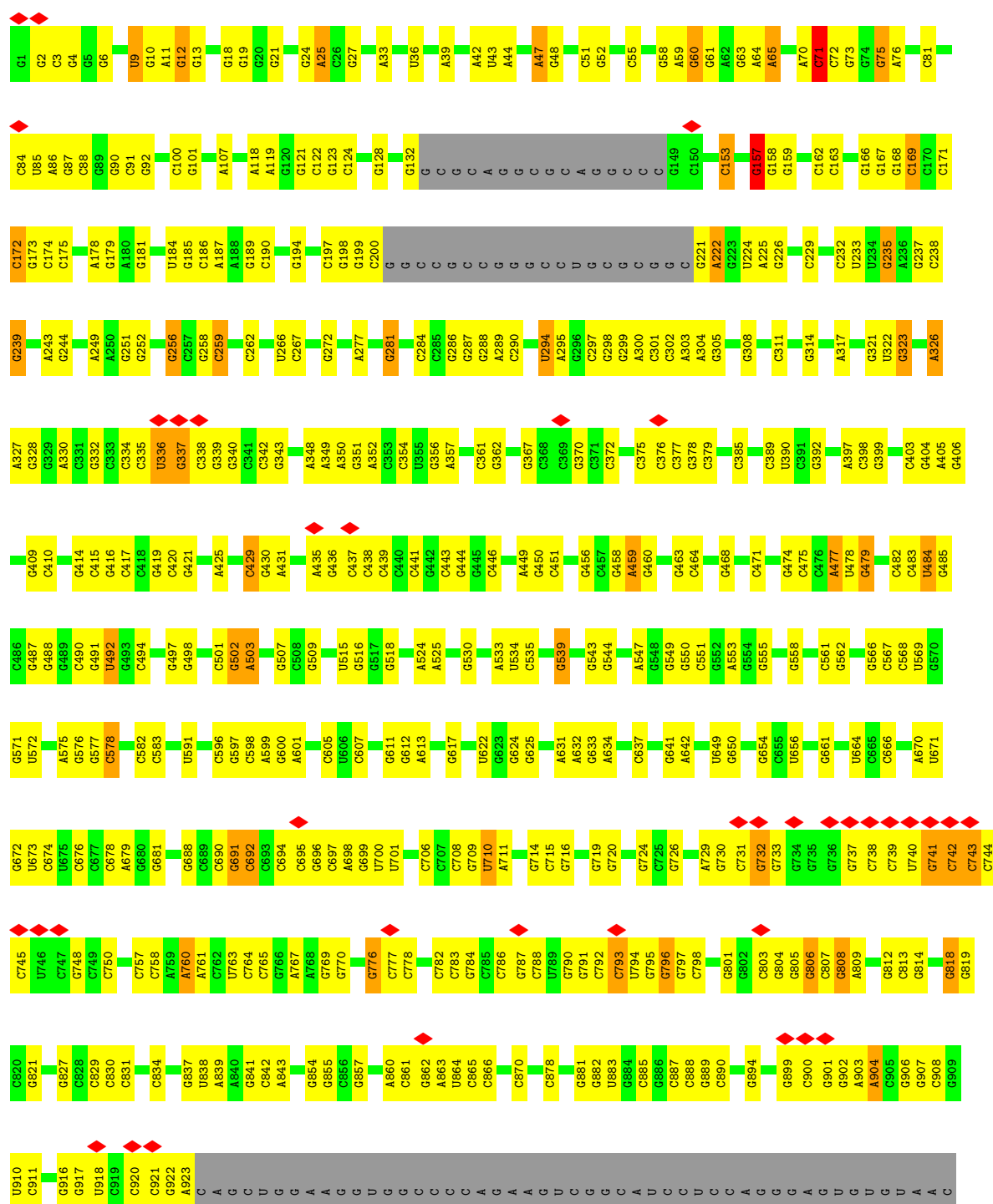


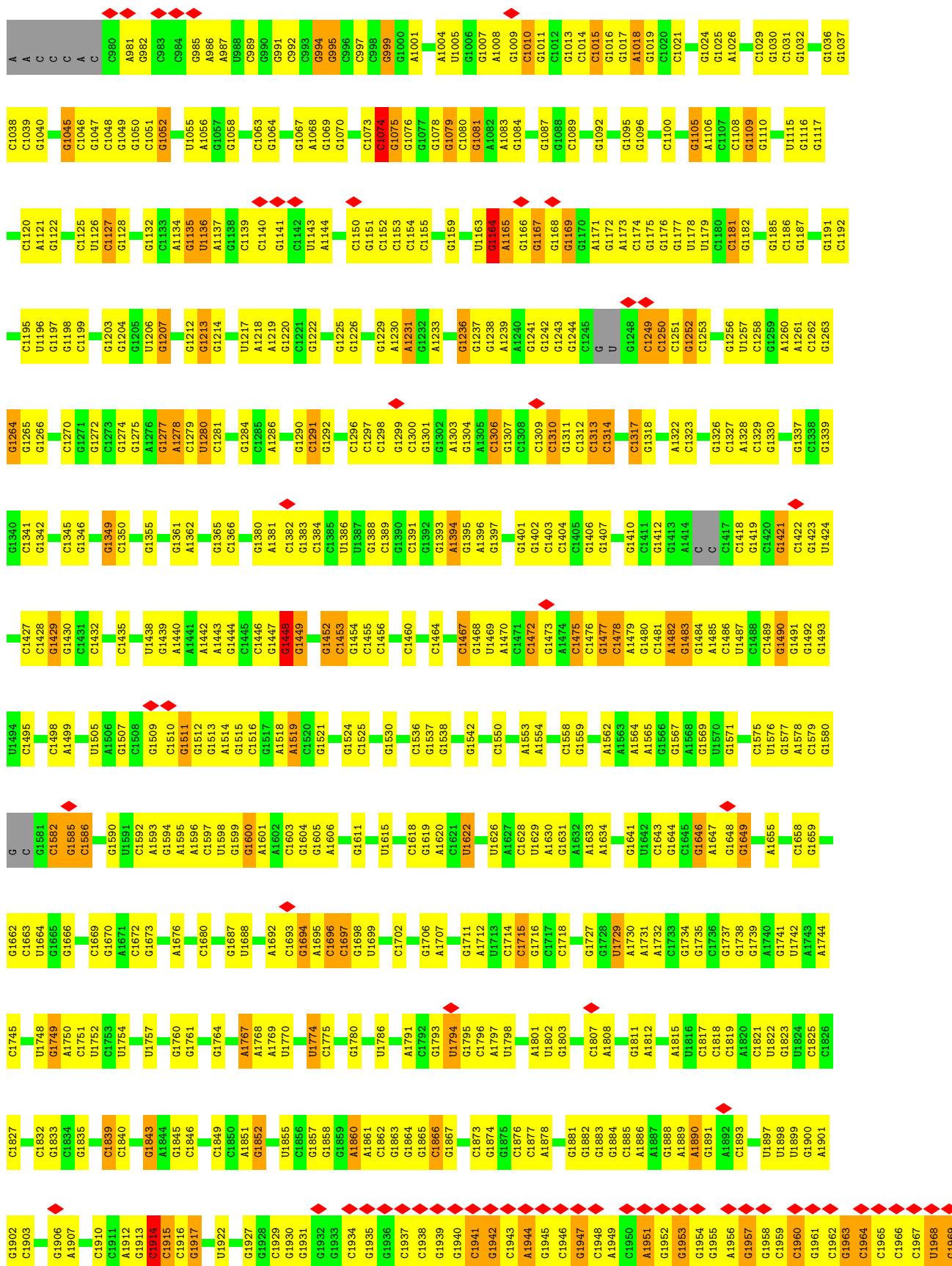
• Molecule 43: Ubiquitin/Ribosomal protein L40e

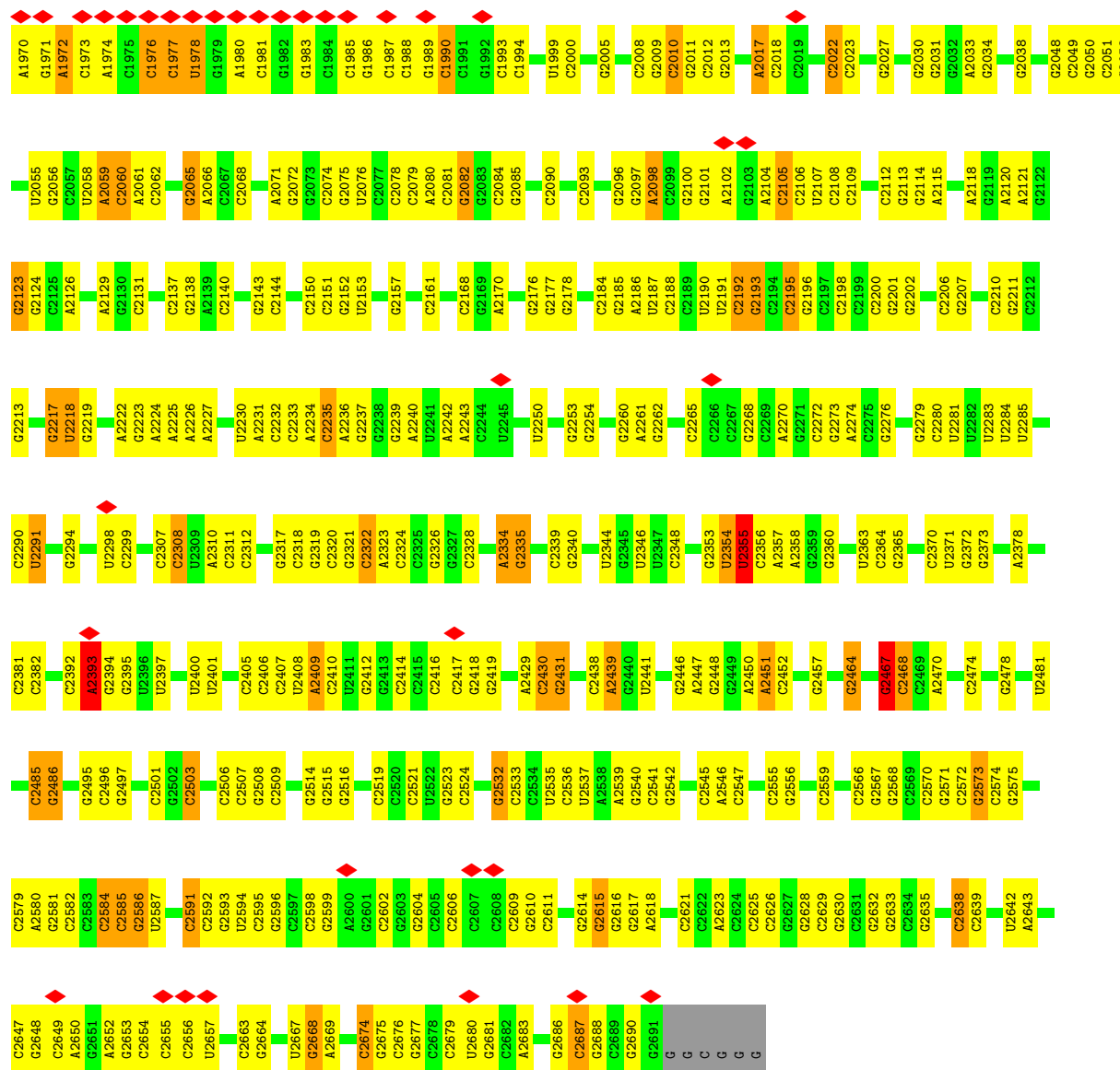


TYR
ALA

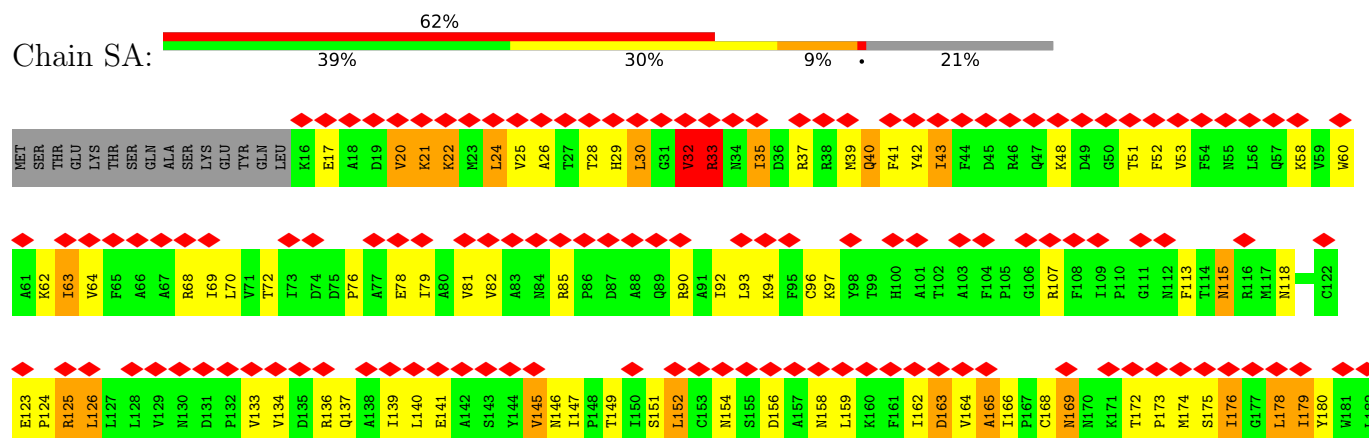
● Molecule 44: Large Subunit rRNA

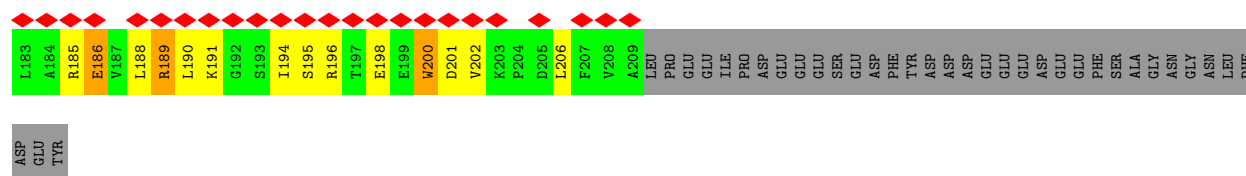
Chain Lt:  5% 46% 43% 7%



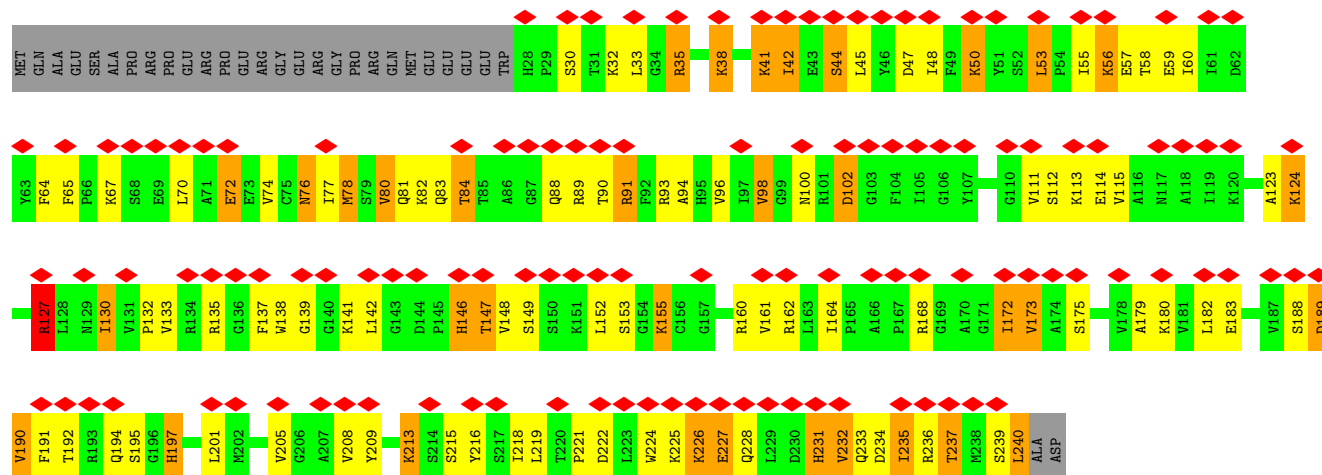


• Molecule 45: 40S ribosomal protein SA

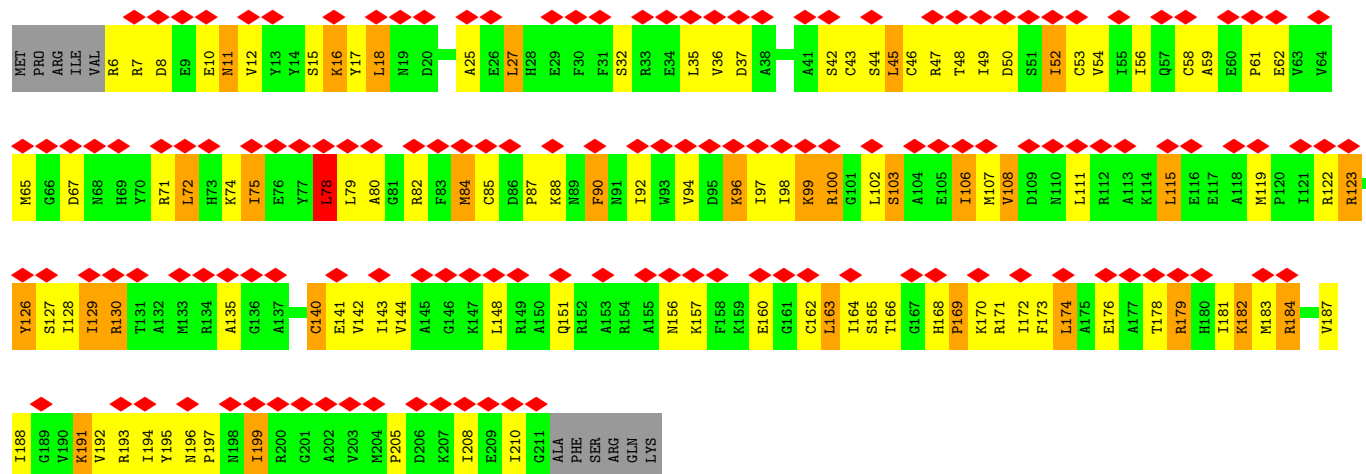




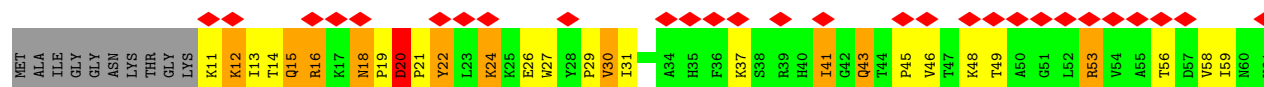
• Molecule 46: Ribosomal protein S2

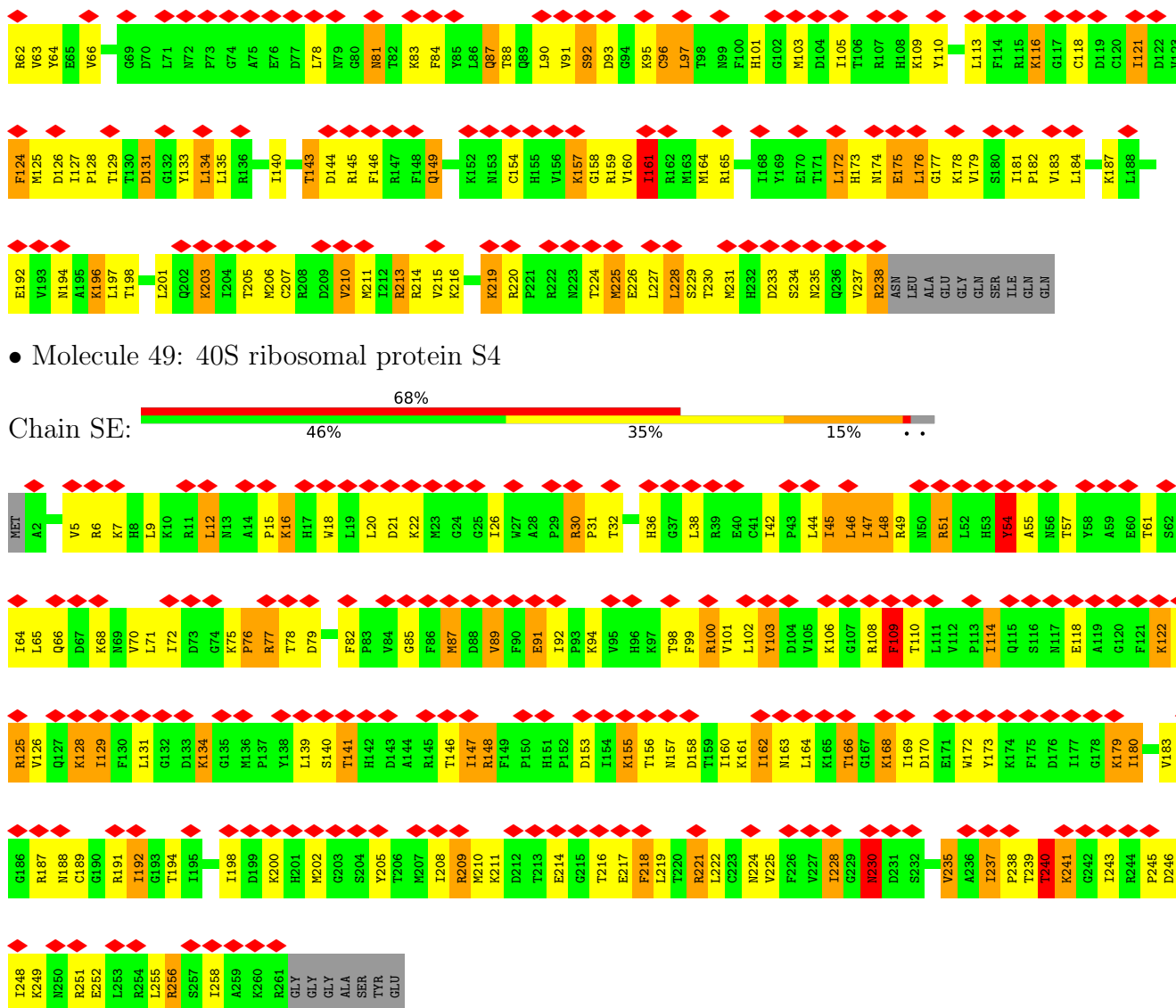


• Molecule 47: Ribosomal protein S3

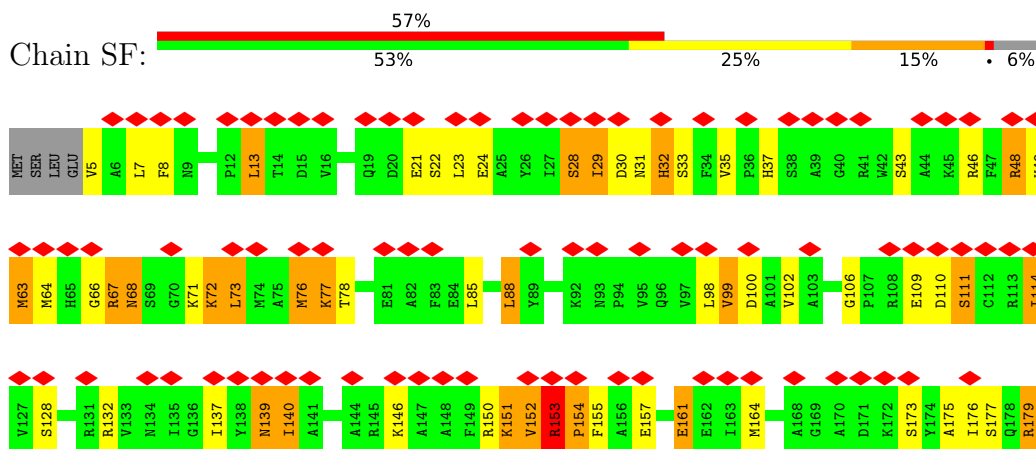


• Molecule 48: 40S ribosomal protein S3a

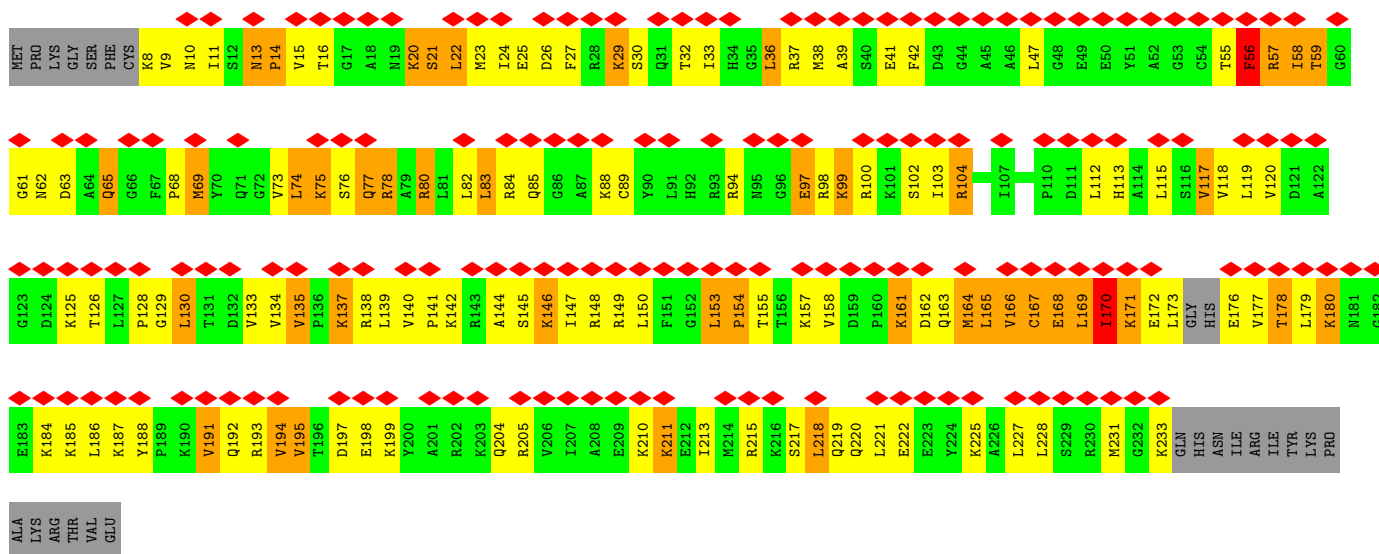




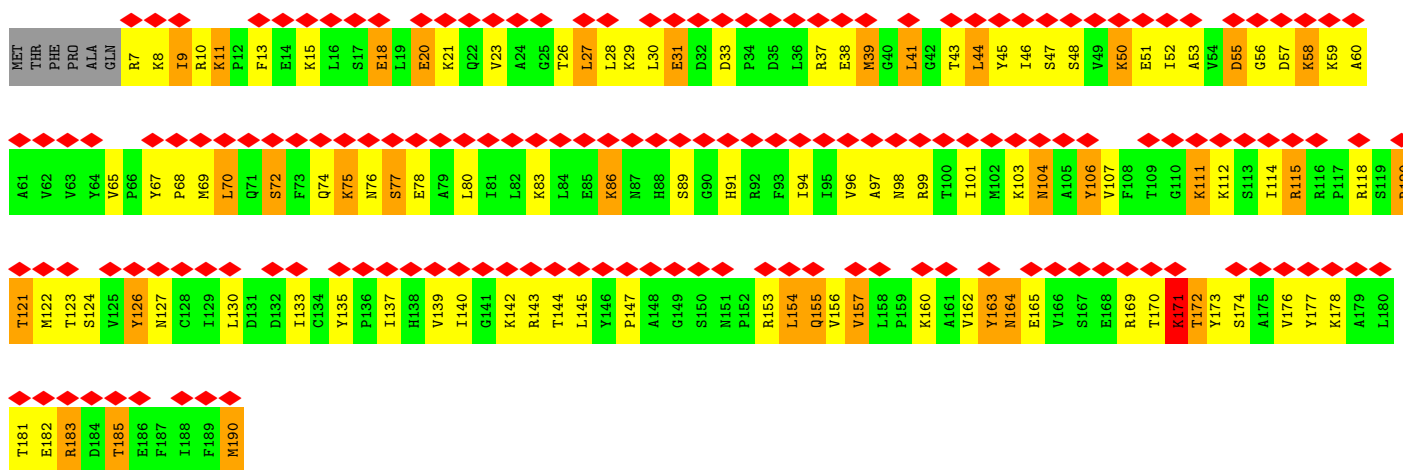
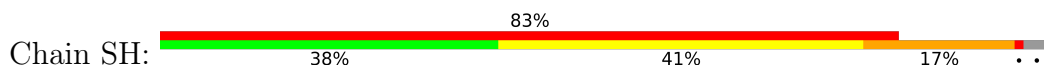
• Molecule 50: Ribosomal protein S5



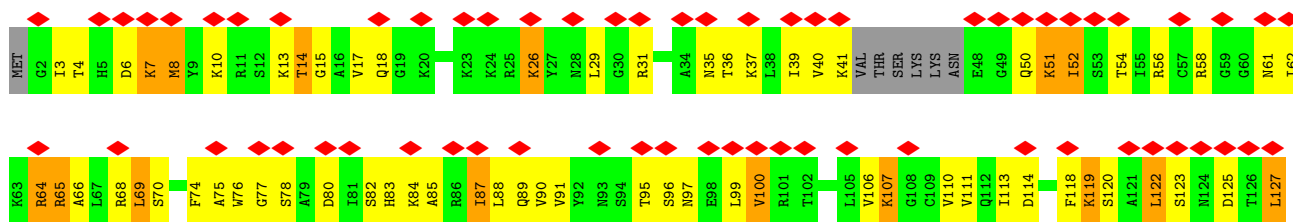
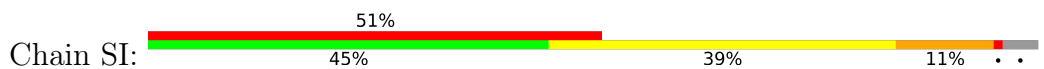
• Molecule 51: 40S ribosomal protein S6

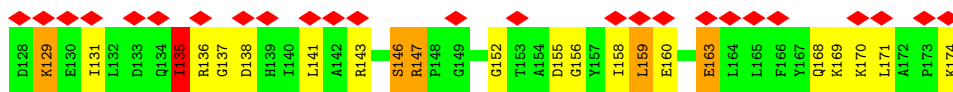


• Molecule 52: 40S ribosomal protein S7

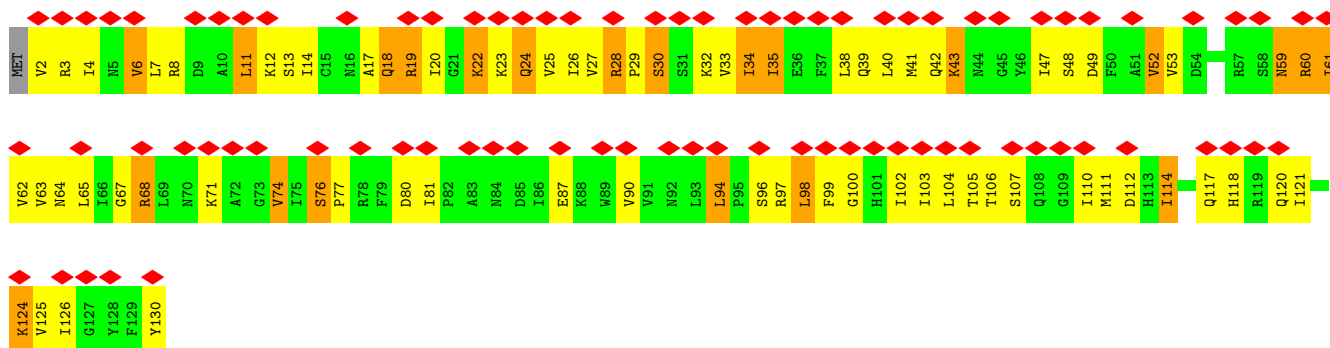
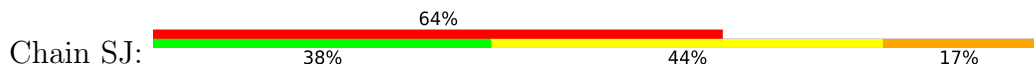


• Molecule 53: 40S ribosomal protein S8

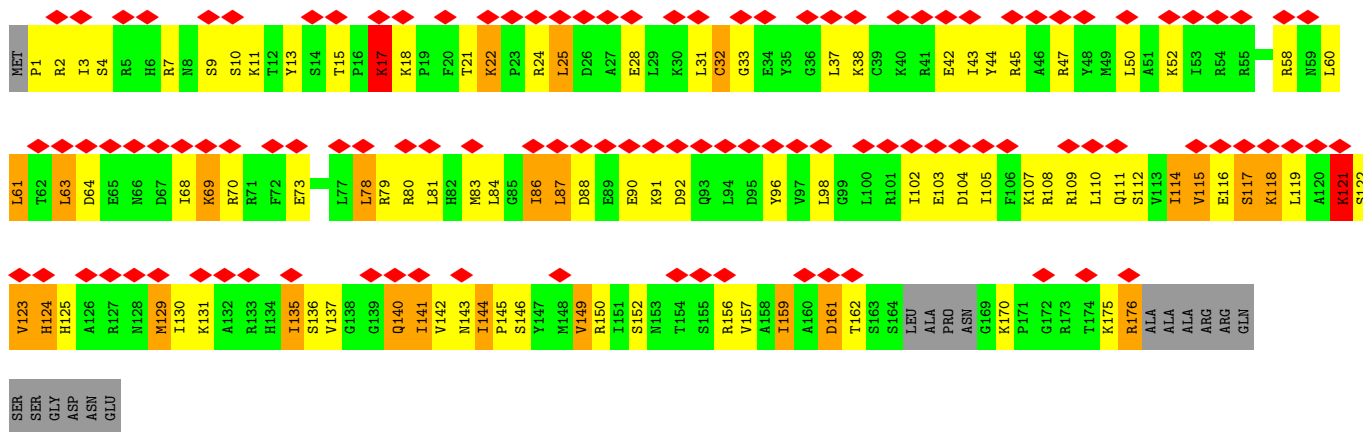
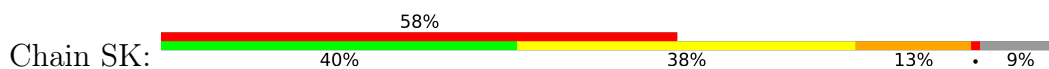


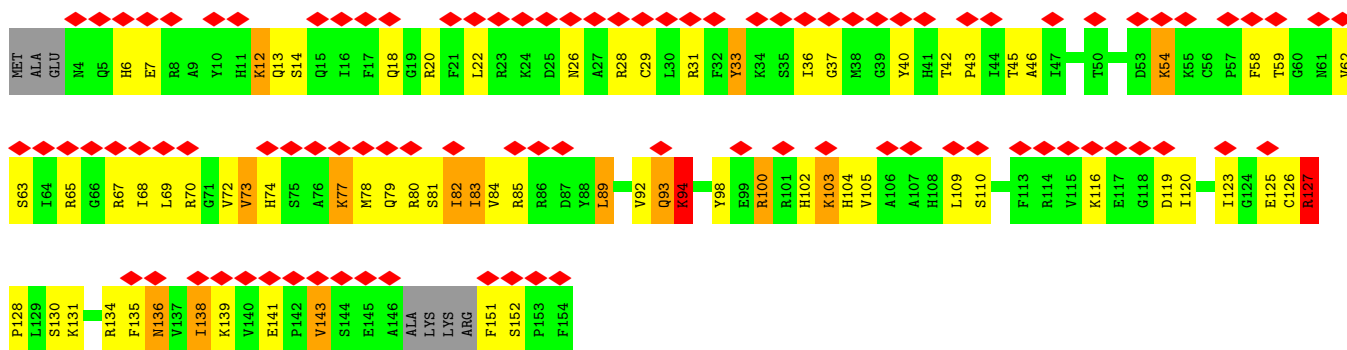


• Molecule 54: Ribosomal protein S15A

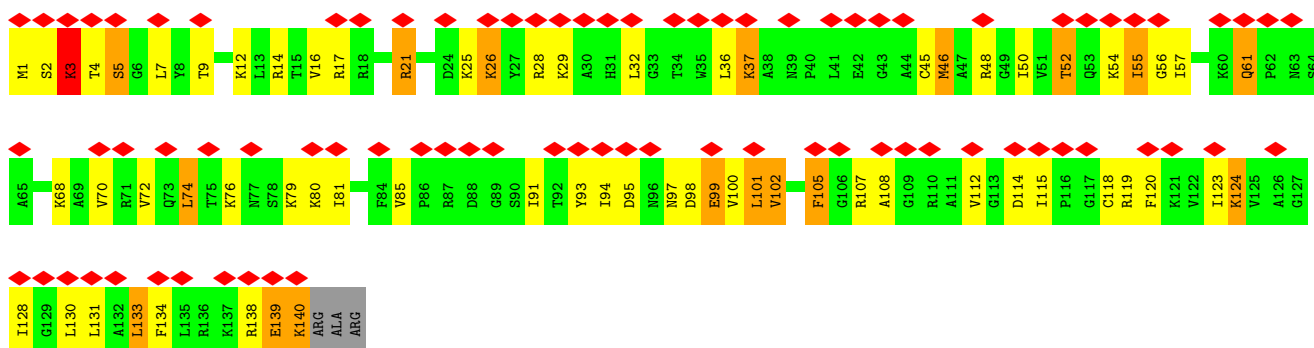


• Molecule 55: Ribosomal protein S9

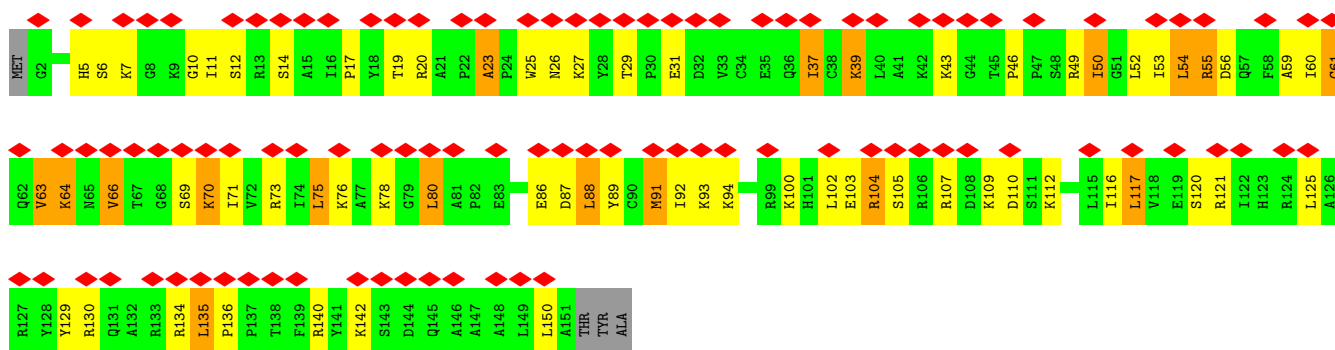




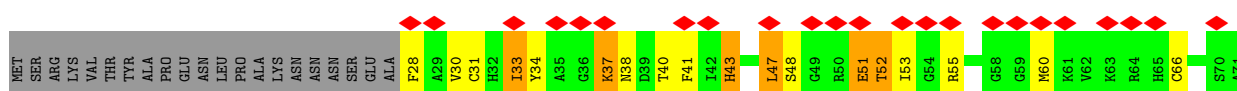
• Molecule 58: SSU ribosomal protein S12P

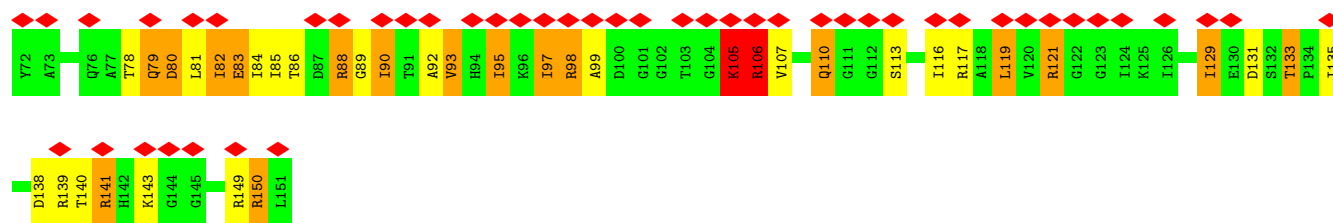


• Molecule 59: Ribosomal protein S13

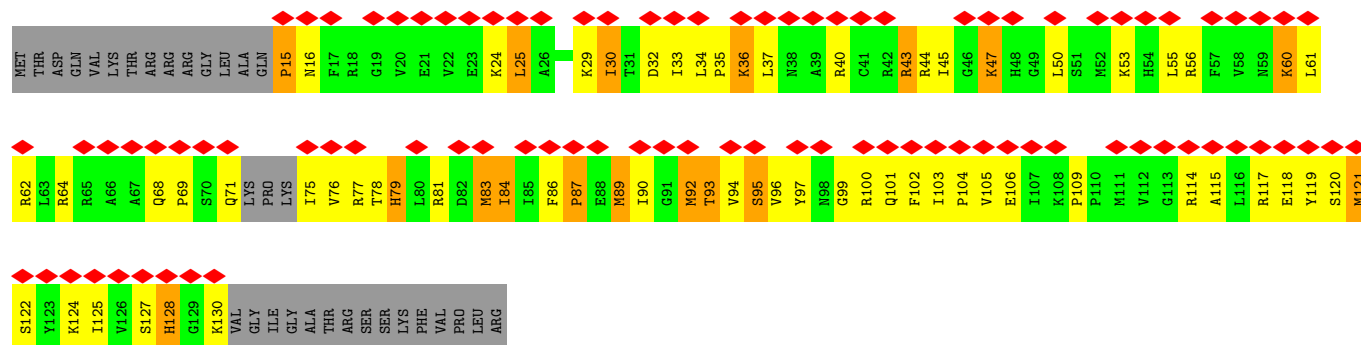


• Molecule 60: Ribosomal protein S14

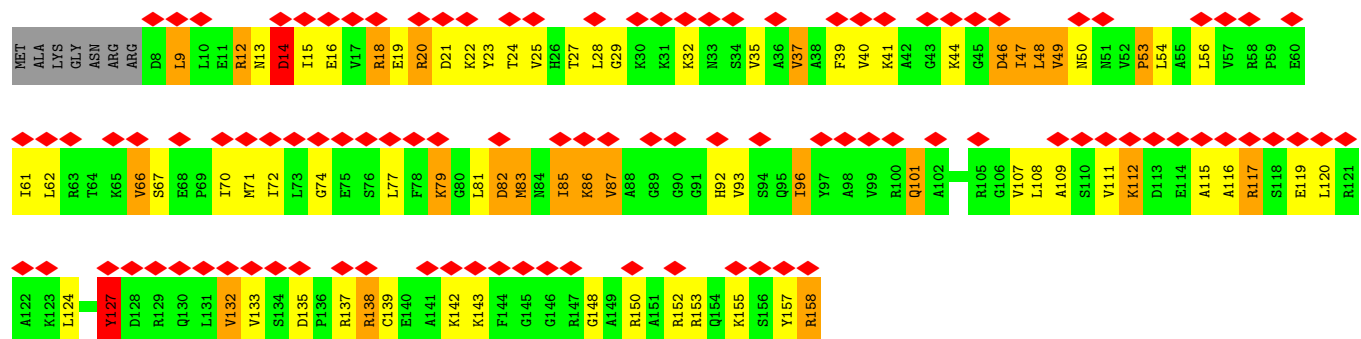




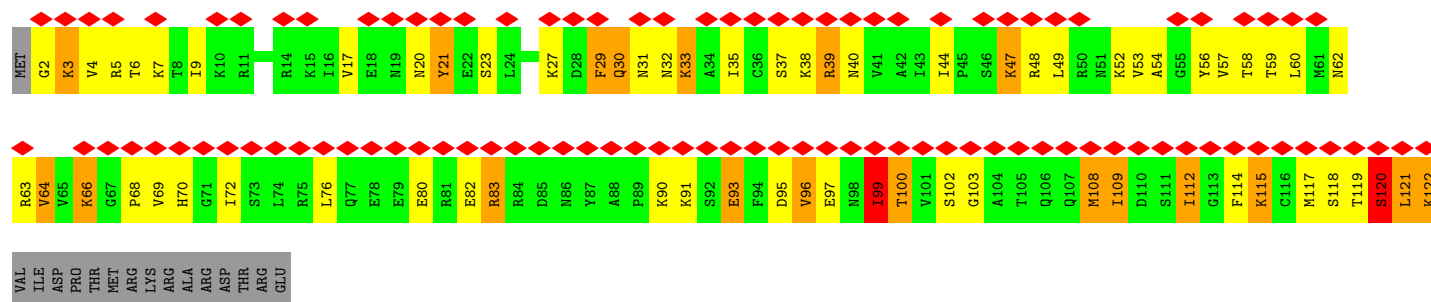
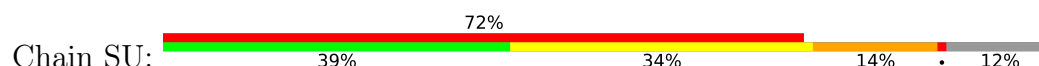
• Molecule 61: Ribosomal protein S15



• Molecule 62: Ribosomal protein S16

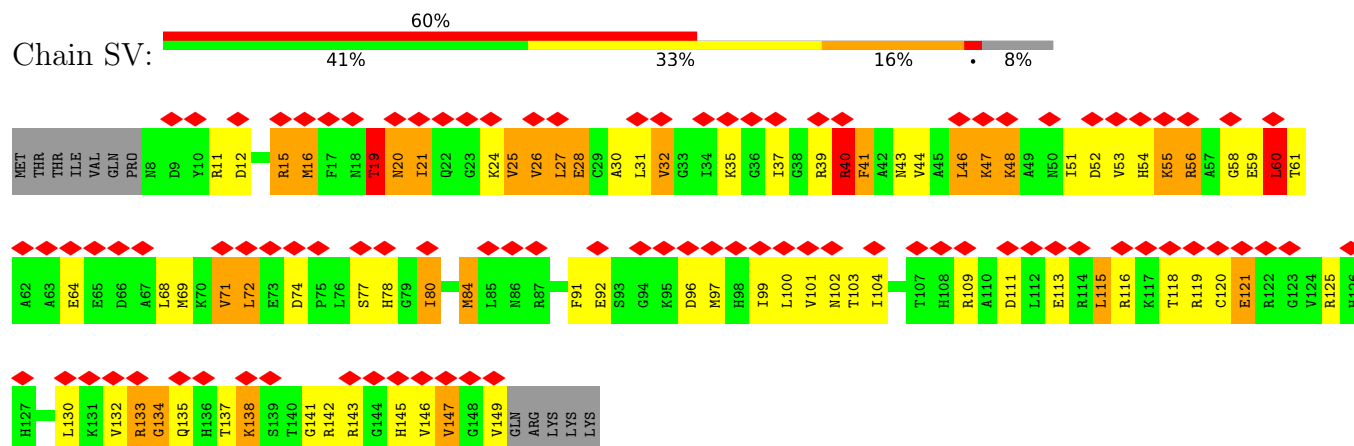


• Molecule 63: Ribosomal protein S17



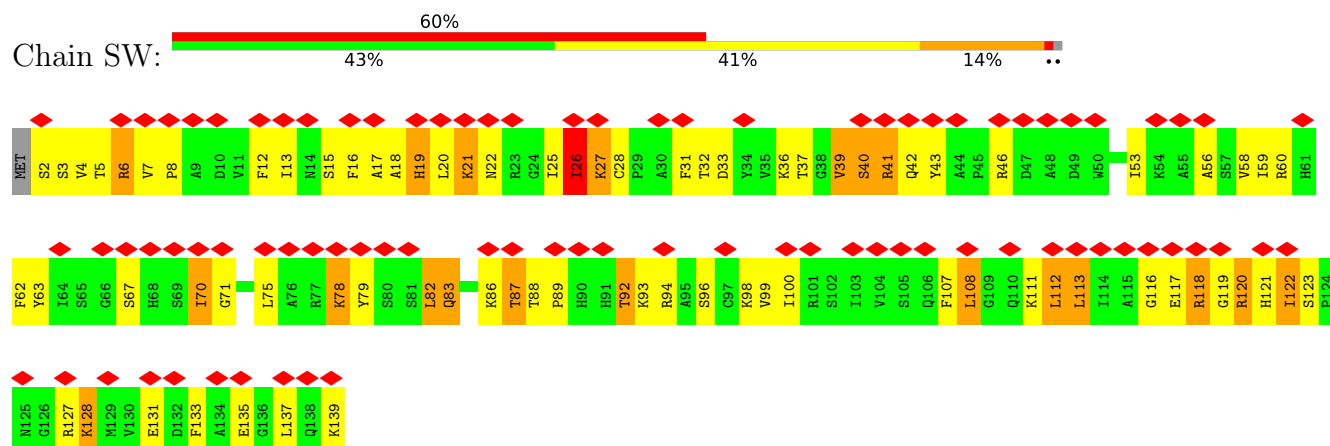
- Molecule 64: Ribosomal protein S18

Chain SV:



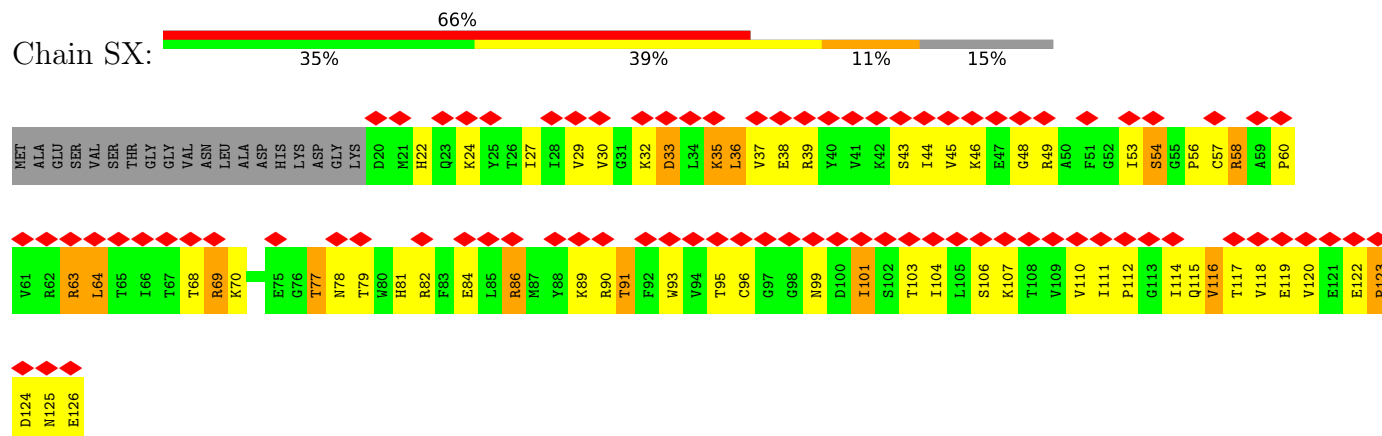
- Molecule 65: Ribosomal protein S19e

Chain SW:



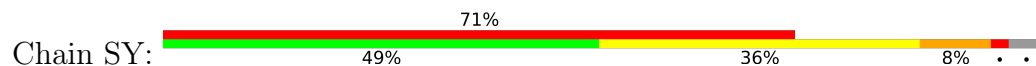
- Molecule 66: Ribosomal protein S20

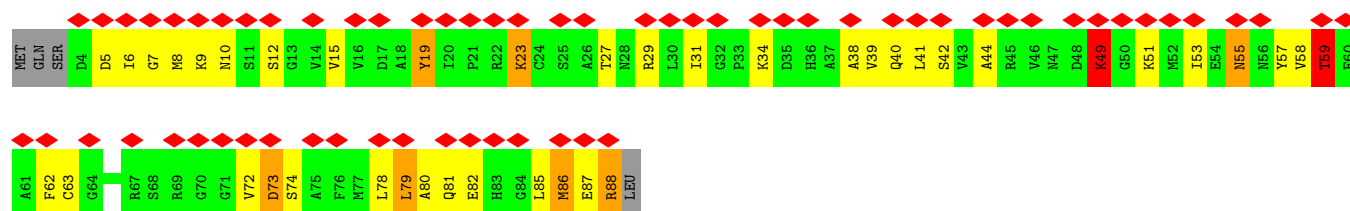
Chain SX:



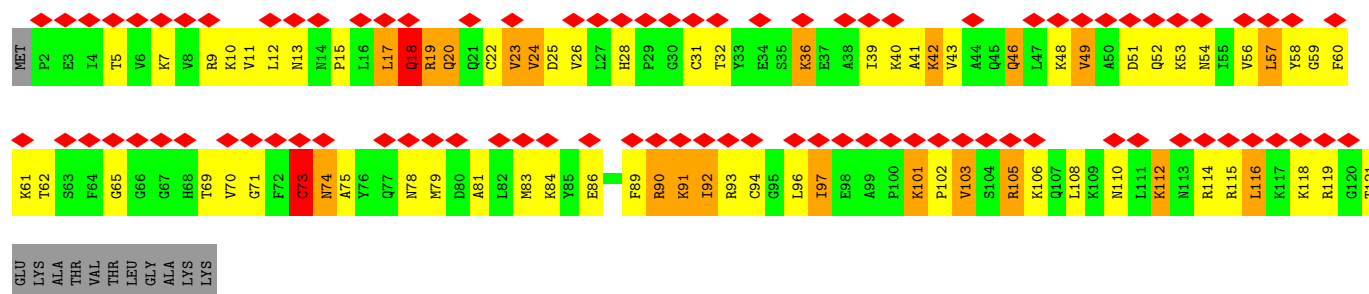
- Molecule 67: 40S ribosomal protein S21

Chain SY:

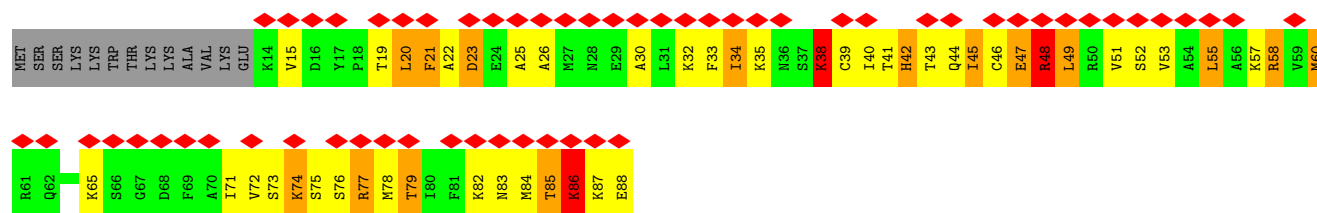




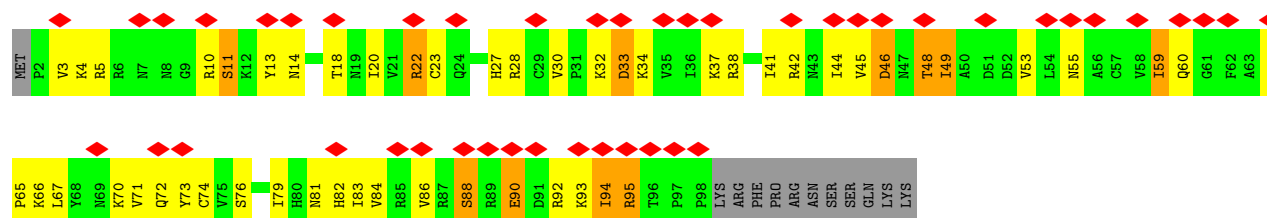
• Molecule 68: Ribosomal protein S24



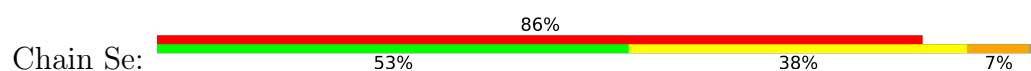
• Molecule 69: 40S ribosomal protein S25

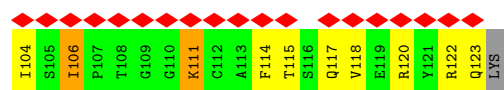


• Molecule 70: 40S ribosomal protein S26

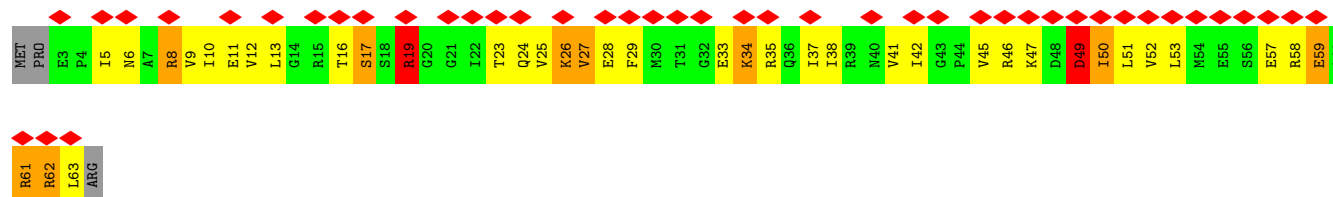


• Molecule 71: Ribosomal protein S27

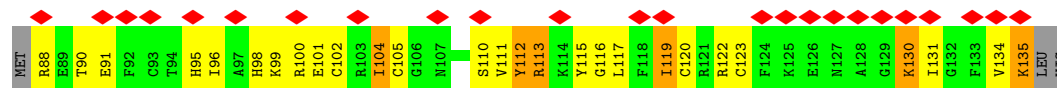




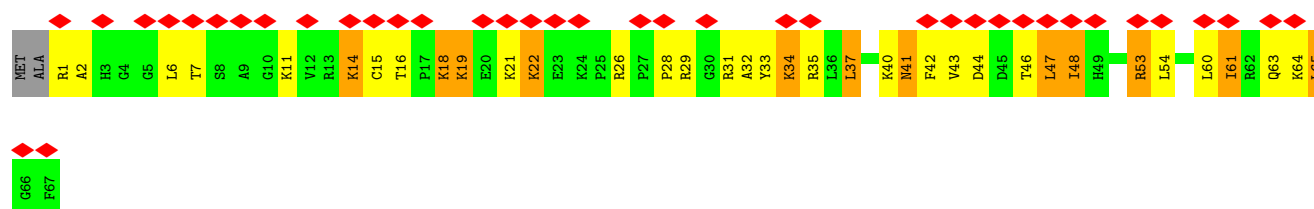
• Molecule 72: Ribosomal protein S28



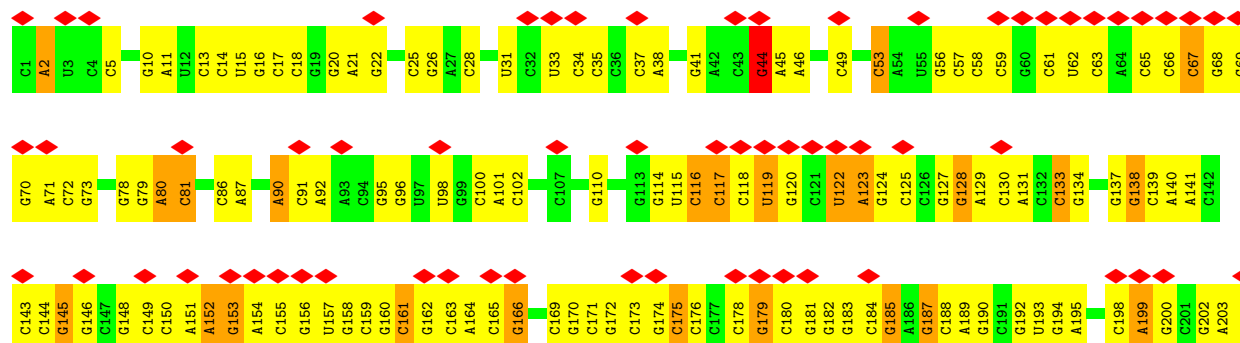
• Molecule 73: Ribosomal protein S29A

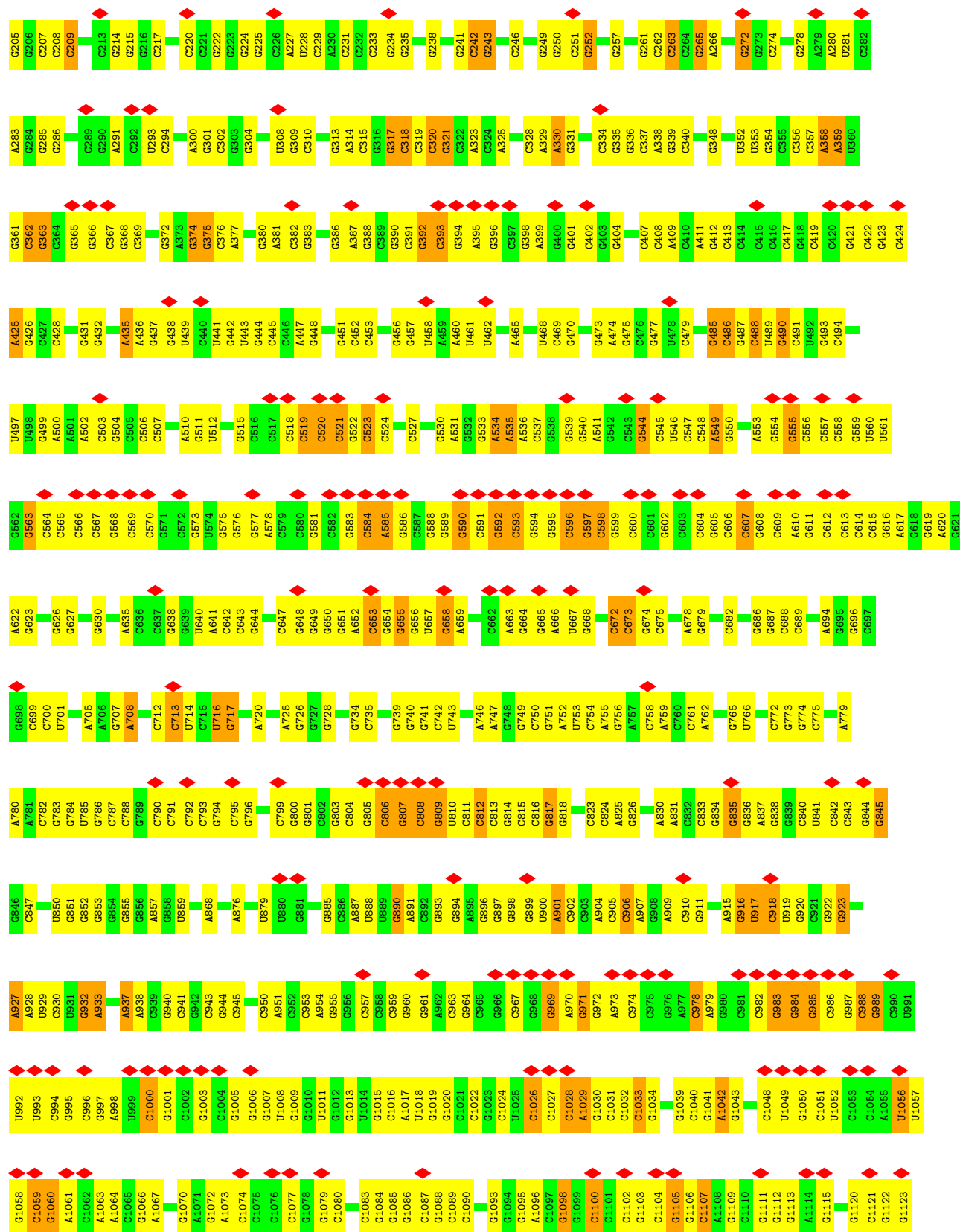


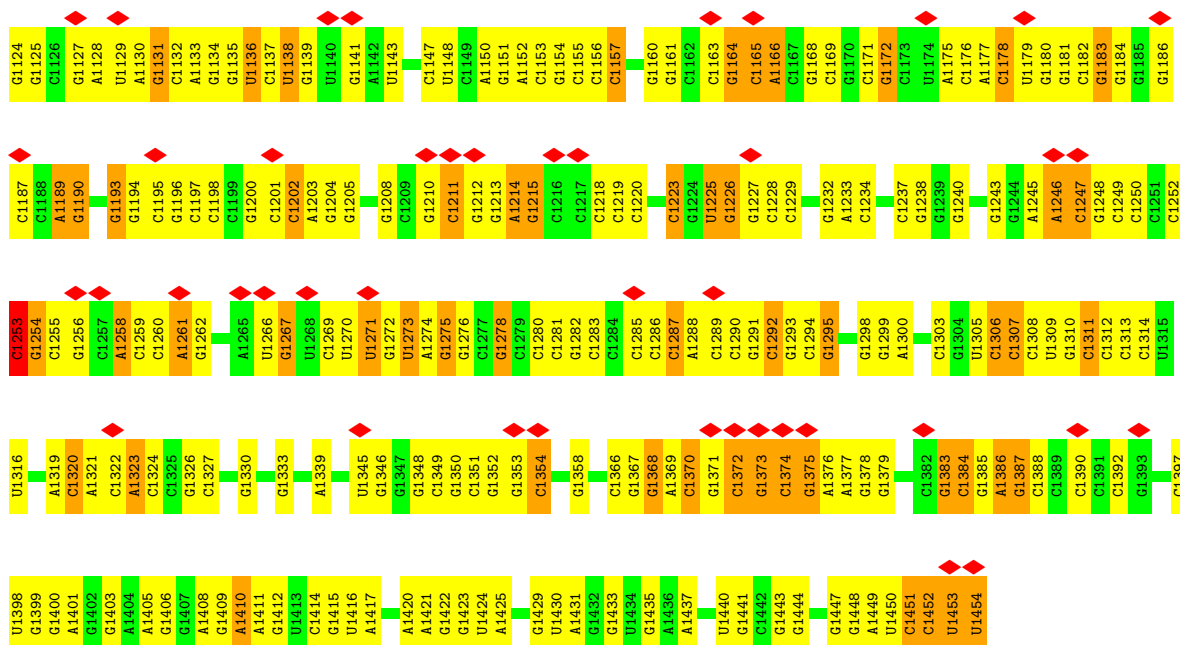
• Molecule 74: 40S ribosomal protein S30



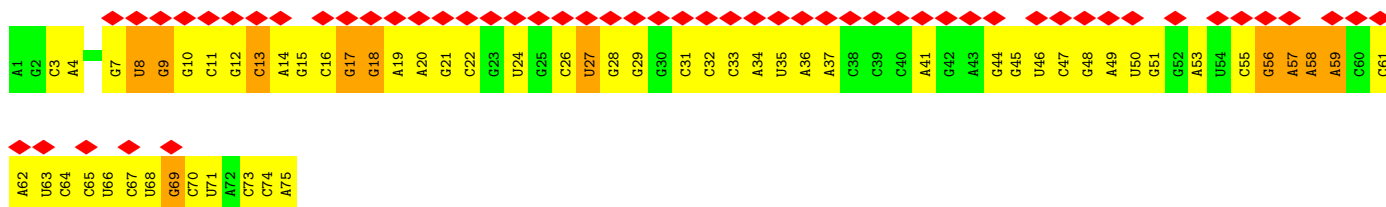
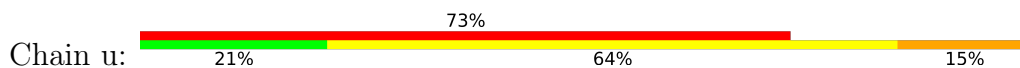
• Molecule 75: Small Subunit rRNA



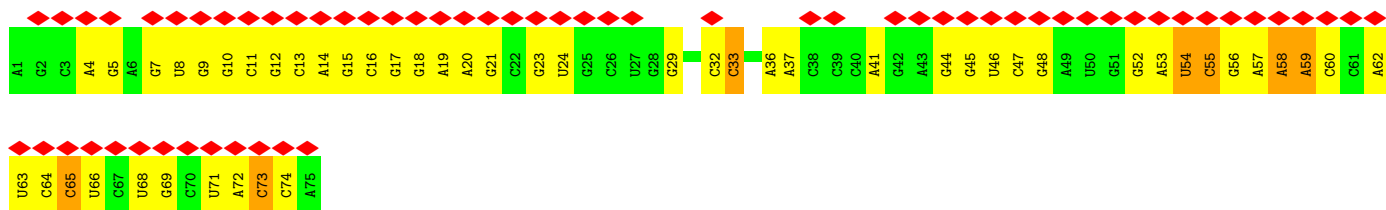
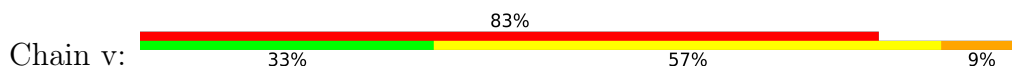




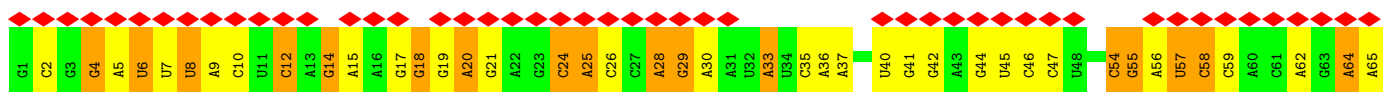
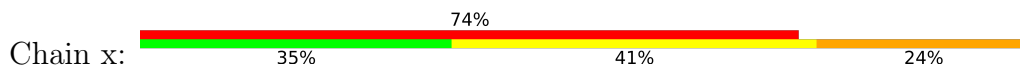
- Molecule 76: tRNA

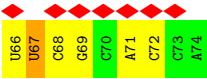


- Molecule 76: tRNA

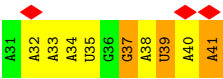
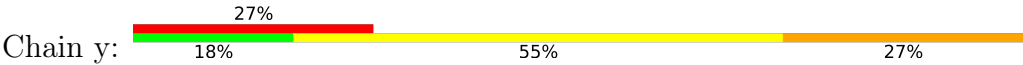


- Molecule 77: tRNA





● Molecule 78: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	4000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30.0	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	14.250	Depositor
Minimum map value	-7.956	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.83	Depositor
Map size (Å)	410.0, 410.0, 410.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	LA	0.91	0/1855	1.41	9/2494 (0.4%)
2	LB	0.91	0/3030	1.43	21/4091 (0.5%)
3	LC	0.90	0/2463	1.43	10/3342 (0.3%)
4	LD	0.54	0/3345	0.78	0/5217
5	LE	0.55	0/2773	0.78	0/4322
6	LF	0.87	1/2368 (0.0%)	1.43	10/3177 (0.3%)
7	LG	0.78	0/450	1.40	4/601 (0.7%)
8	LH	0.87	0/1783	1.46	8/2403 (0.3%)
9	LI	0.89	0/1494	1.42	6/2019 (0.3%)
10	LJ	0.90	0/1479	1.42	10/1997 (0.5%)
11	LK	0.89	0/1645	1.37	4/2202 (0.2%)
12	LL	0.88	0/1350	1.45	8/1813 (0.4%)
13	LM	0.89	0/1582	1.37	4/2118 (0.2%)
14	LN	0.85	0/1004	1.45	4/1344 (0.3%)
15	LO	0.87	0/1742	1.37	8/2334 (0.3%)
16	LP	0.87	0/1570	1.43	11/2105 (0.5%)
17	LQ	0.89	0/1257	1.44	6/1681 (0.4%)
18	LR	0.90	0/1425	1.45	6/1907 (0.3%)
19	LS	0.84	0/1564	1.37	3/2069 (0.1%)
20	LT	0.88	0/1457	1.37	6/1957 (0.3%)
21	LU	0.87	0/1240	1.45	11/1665 (0.7%)
22	LV	0.86	0/876	1.40	4/1177 (0.3%)
23	LW	0.92	0/1035	1.38	4/1396 (0.3%)
24	LX	0.86	0/526	1.52	7/700 (1.0%)
25	LY	0.92	0/933	1.38	3/1262 (0.2%)
26	LZ	0.91	0/1091	1.39	2/1454 (0.1%)
27	La	0.92	0/985	1.47	8/1328 (0.6%)
28	Lb	0.89	0/1208	1.40	3/1615 (0.2%)
29	Lc	0.89	0/463	1.44	5/612 (0.8%)
30	Ld	0.92	0/745	1.53	5/1008 (0.5%)
31	Le	0.87	0/803	1.36	3/1077 (0.3%)
32	Lf	0.88	0/1055	1.37	0/1407
33	Lg	0.90	0/793	1.56	8/1062 (0.8%)
34	Lh	0.93	0/849	1.43	5/1141 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Li	0.83	0/968	1.40	3/1286 (0.2%)
36	Lj	0.86	0/693	1.44	4/919 (0.4%)
37	Lk	0.88	0/705	1.42	5/934 (0.5%)
38	Ll	0.92	0/562	1.51	5/749 (0.7%)
39	Ln	0.98	0/1621	1.50	12/2183 (0.5%)
40	Lo	0.78	0/229	1.27	0/291
41	Lp	0.89	0/759	1.38	3/1004 (0.3%)
42	Lq	0.88	0/717	1.52	4/955 (0.4%)
43	Ls	0.93	0/392	1.44	2/522 (0.4%)
44	Lt	0.58	0/62213	0.81	47/97094 (0.0%)
45	SA	0.93	0/1587	1.46	7/2156 (0.3%)
46	SB	0.93	0/1671	1.45	9/2253 (0.4%)
47	SC	0.90	0/1662	1.40	7/2231 (0.3%)
48	SD	0.91	0/1882	1.45	8/2535 (0.3%)
49	SE	0.94	0/2131	1.41	5/2874 (0.2%)
50	SF	0.94	0/1409	1.44	8/1896 (0.4%)
51	SG	0.95	0/1789	1.42	7/2390 (0.3%)
52	SH	0.94	0/1508	1.40	3/2032 (0.1%)
53	SI	0.93	0/1331	1.41	5/1784 (0.3%)
54	SJ	0.92	0/1048	1.41	4/1412 (0.3%)
55	SK	0.90	0/1413	1.46	13/1886 (0.7%)
56	SL	0.91	0/917	1.37	4/1250 (0.3%)
57	SM	0.91	0/1245	1.39	5/1666 (0.3%)
58	SO	0.91	0/1103	1.41	7/1477 (0.5%)
59	SP	0.92	1/1215 (0.1%)	1.40	8/1632 (0.5%)
60	SQ	0.95	0/923	1.48	4/1239 (0.3%)
61	SR	0.94	0/934	1.45	7/1247 (0.6%)
62	ST	0.92	0/1192	1.43	7/1594 (0.4%)
63	SU	0.95	0/973	1.52	7/1300 (0.5%)
64	SV	0.90	0/1140	1.54	14/1529 (0.9%)
65	SW	0.92	0/1104	1.47	10/1484 (0.7%)
66	SX	0.91	0/869	1.45	3/1173 (0.3%)
67	SY	0.99	0/650	1.47	5/872 (0.6%)
68	Sb	0.90	0/967	1.50	11/1294 (0.9%)
69	Sc	0.90	0/603	1.49	5/802 (0.6%)
70	Sd	0.90	0/800	1.40	3/1077 (0.3%)
71	Se	1.00	0/643	1.43	5/871 (0.6%)
72	Sg	0.99	0/488	1.39	3/652 (0.5%)
73	Sh	0.84	0/409	1.43	2/542 (0.4%)
74	Sj	0.92	0/553	1.38	2/736 (0.3%)
75	St	0.58	0/34858	0.82	19/54401 (0.0%)
76	u	0.58	0/1795	0.86	1/2798 (0.0%)
76	v	0.57	0/1795	0.81	0/2798

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	x	0.56	0/1771	0.78	0/2758
78	y	0.56	0/270	0.88	1/419 (0.2%)
All	All	0.74	2/191745 (0.0%)	1.10	500/281094 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	LF	88	ILE	N-CA	5.47	1.50	1.46
59	SP	23	ALA	C-N	5.43	1.37	1.33

The worst 5 of 500 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	Lt	776	G	C2'-C3'-O3'	10.81	125.72	109.50
65	SW	56	ALA	N-CA-C	-9.88	101.72	113.88
64	SV	48	LYS	N-CA-C	-9.80	100.73	112.89
9	LI	167	LEU	N-CA-C	-9.73	101.97	114.04
15	LO	21	TYR	CB-CA-C	-9.64	95.75	110.88

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	LA	1823	0	1868	34	0
2	LB	2960	0	2996	63	0
3	LC	2412	0	2493	39	0
4	LD	2995	0	1534	11	0
5	LE	2480	0	1257	11	0
6	LF	2325	0	2381	49	0
7	LG	439	0	479	5	0
8	LH	1753	0	1789	28	0
9	LI	1468	0	1541	20	0
10	LJ	1452	0	1495	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	LK	1609	0	1629	26	0
12	LL	1325	0	1345	33	0
13	LM	1560	0	1651	23	0
14	LN	993	0	1059	17	0
15	LO	1699	0	1777	24	0
16	LP	1539	0	1576	35	0
17	LQ	1231	0	1265	31	0
18	LR	1402	0	1478	20	0
19	LS	1548	0	1651	30	0
20	LT	1423	0	1426	25	0
21	LU	1216	0	1245	24	0
22	LV	861	0	854	13	0
23	LW	1015	0	1057	17	0
24	LX	512	0	515	12	0
25	LY	913	0	959	16	0
26	LZ	1076	0	1140	20	0
27	La	968	0	1009	14	0
28	Lb	1179	0	1207	21	0
29	Lc	456	0	482	11	0
30	Ld	737	0	764	15	0
31	Le	791	0	839	17	0
32	Lf	1031	0	1084	18	0
33	Lg	778	0	816	14	0
34	Lh	834	0	865	21	0
35	Li	958	0	1054	13	0
36	Lj	684	0	742	12	0
37	Lk	689	0	683	13	0
38	Ll	558	0	612	15	0
39	Ln	1592	0	1667	68	0
40	Lo	227	0	272	0	0
41	Lp	748	0	798	6	0
42	Lq	708	0	753	27	0
43	Ls	388	0	401	12	0
44	Lt	55643	0	28281	265	0
45	SA	1553	0	1588	39	0
46	SB	1640	0	1696	40	0
47	SC	1636	0	1675	42	0
48	SD	1847	0	1905	44	0
49	SE	2085	0	2174	49	0
50	SF	1387	0	1406	37	0
51	SG	1768	0	1884	57	0
52	SH	1481	0	1544	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	SI	1311	0	1367	34	0
54	SJ	1031	0	1082	27	0
55	SK	1395	0	1485	28	0
56	SL	890	0	883	15	0
57	SM	1217	0	1242	27	0
58	SO	1088	0	1177	24	0
59	SP	1192	0	1265	30	0
60	SQ	911	0	922	32	0
61	SR	918	0	986	22	0
62	ST	1180	0	1250	29	0
63	SU	963	0	1015	23	0
64	SV	1124	0	1148	26	0
65	SW	1080	0	1106	29	0
66	SX	853	0	875	20	0
67	SY	642	0	642	12	0
68	Sb	952	0	1011	25	0
69	Sc	597	0	636	16	0
70	Sd	787	0	812	18	0
71	Se	629	0	623	13	0
72	Sg	486	0	519	13	0
73	Sh	401	0	396	15	0
74	Sj	543	0	587	14	0
75	St	31176	0	15856	254	0
76	u	1604	0	816	8	0
76	v	1604	0	816	6	0
77	x	1582	0	800	11	0
78	y	240	0	120	2	0
All	All	178791	0	134098	2089	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 2089 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LV:45:ILE:HG12	22:LV:52:VAL:HG12	1.44	1.00
39:Ln:196:LYS:HB2	39:Ln:200:ASN:HB2	1.45	0.95
53:SI:147:ARG:HH21	75:St:243:G:H5"	1.29	0.93
24:LX:11:SER:HB3	24:LX:54:LYS:HB2	1.53	0.88
6:LF:217:LEU:HB3	6:LF:225:TYR:HB2	1.53	0.87

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	239/251 (95%)	223 (93%)	15 (6%)	1 (0%)	30	67
2	LB	370/379 (98%)	349 (94%)	18 (5%)	3 (1%)	16	54
3	LC	307/316 (97%)	294 (96%)	13 (4%)	0	100	100
6	LF	287/297 (97%)	270 (94%)	15 (5%)	2 (1%)	18	56
7	LG	48/51 (94%)	44 (92%)	3 (6%)	1 (2%)	5	30
8	LH	215/235 (92%)	206 (96%)	8 (4%)	1 (0%)	24	63
9	LI	179/225 (80%)	166 (93%)	9 (5%)	4 (2%)	5	29
10	LJ	182/185 (98%)	165 (91%)	16 (9%)	1 (0%)	24	63
11	LK	193/210 (92%)	185 (96%)	7 (4%)	1 (0%)	24	63
12	LL	163/173 (94%)	155 (95%)	7 (4%)	1 (1%)	21	59
13	LM	191/234 (82%)	182 (95%)	7 (4%)	2 (1%)	12	48
14	LN	122/131 (93%)	117 (96%)	4 (3%)	1 (1%)	16	54
15	LO	199/204 (98%)	187 (94%)	12 (6%)	0	100	100
16	LP	185/197 (94%)	173 (94%)	11 (6%)	1 (0%)	24	63
17	LQ	151/164 (92%)	144 (95%)	7 (5%)	0	100	100
18	LR	176/179 (98%)	169 (96%)	6 (3%)	1 (1%)	21	59
19	LS	185/196 (94%)	180 (97%)	5 (3%)	0	100	100
20	LT	168/173 (97%)	162 (96%)	6 (4%)	0	100	100
21	LU	146/159 (92%)	134 (92%)	6 (4%)	6 (4%)	2	18
22	LV	102/124 (82%)	86 (84%)	16 (16%)	0	100	100
23	LW	130/142 (92%)	126 (97%)	4 (3%)	0	100	100
24	LX	58/189 (31%)	53 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	LY	111/141 (79%)	105 (95%)	4 (4%)	2 (2%)	6	34
26	LZ	131/135 (97%)	128 (98%)	3 (2%)	0	100	100
27	La	117/135 (87%)	110 (94%)	5 (4%)	2 (2%)	7	36
28	Lb	141/149 (95%)	133 (94%)	8 (6%)	0	100	100
29	Lc	53/62 (86%)	49 (92%)	3 (6%)	1 (2%)	6	32
30	Ld	96/109 (88%)	92 (96%)	3 (3%)	1 (1%)	12	48
31	Le	93/106 (88%)	87 (94%)	6 (6%)	0	100	100
32	Lf	123/136 (90%)	115 (94%)	8 (6%)	0	100	100
33	Lg	96/123 (78%)	89 (93%)	7 (7%)	0	100	100
34	Lh	102/120 (85%)	92 (90%)	7 (7%)	3 (3%)	3	23
35	Li	114/124 (92%)	109 (96%)	4 (4%)	1 (1%)	14	51
36	Lj	80/90 (89%)	73 (91%)	6 (8%)	1 (1%)	9	42
37	Lk	83/89 (93%)	76 (92%)	6 (7%)	1 (1%)	10	44
38	Ll	70/77 (91%)	67 (96%)	3 (4%)	0	100	100
39	Ln	194/217 (89%)	172 (89%)	15 (8%)	7 (4%)	2	20
40	Lo	23/25 (92%)	23 (100%)	0	0	100	100
41	Lp	89/106 (84%)	86 (97%)	2 (2%)	1 (1%)	11	46
42	Lq	89/94 (95%)	82 (92%)	5 (6%)	2 (2%)	5	29
43	Ls	45/127 (35%)	39 (87%)	4 (9%)	2 (4%)	2	17
45	SA	192/245 (78%)	173 (90%)	17 (9%)	2 (1%)	12	48
46	SB	211/242 (87%)	188 (89%)	21 (10%)	2 (1%)	14	51
47	SC	204/217 (94%)	188 (92%)	14 (7%)	2 (1%)	12	48
48	SD	226/248 (91%)	210 (93%)	13 (6%)	3 (1%)	9	42
49	SE	258/268 (96%)	235 (91%)	17 (7%)	6 (2%)	5	28
50	SF	175/190 (92%)	162 (93%)	10 (6%)	3 (2%)	7	36
51	SG	220/248 (89%)	207 (94%)	10 (4%)	3 (1%)	9	40
52	SH	182/190 (96%)	162 (89%)	19 (10%)	1 (0%)	24	63
53	SI	163/174 (94%)	150 (92%)	12 (7%)	1 (1%)	21	59
54	SJ	127/130 (98%)	113 (89%)	13 (10%)	1 (1%)	16	54
55	SK	168/189 (89%)	157 (94%)	10 (6%)	1 (1%)	21	59
56	SL	107/134 (80%)	88 (82%)	16 (15%)	3 (3%)	4	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	SM	143/154 (93%)	133 (93%)	9 (6%)	1 (1%)	18	56
58	SO	138/143 (96%)	133 (96%)	3 (2%)	2 (1%)	9	40
59	SP	148/154 (96%)	143 (97%)	4 (3%)	1 (1%)	18	56
60	SQ	122/145 (84%)	108 (88%)	11 (9%)	3 (2%)	4	26
61	SR	109/145 (75%)	99 (91%)	9 (8%)	1 (1%)	14	51
62	ST	149/158 (94%)	140 (94%)	6 (4%)	3 (2%)	6	31
63	SU	119/137 (87%)	112 (94%)	5 (4%)	2 (2%)	7	36
64	SV	140/154 (91%)	119 (85%)	14 (10%)	7 (5%)	1	16
65	SW	136/139 (98%)	131 (96%)	4 (3%)	1 (1%)	18	56
66	SX	105/126 (83%)	100 (95%)	5 (5%)	0	100	100
67	SY	83/89 (93%)	80 (96%)	3 (4%)	0	100	100
68	Sb	118/132 (89%)	109 (92%)	8 (7%)	1 (1%)	16	54
69	Sc	73/88 (83%)	63 (86%)	6 (8%)	4 (6%)	1	14
70	Sd	95/109 (87%)	83 (87%)	11 (12%)	1 (1%)	11	46
71	Se	78/81 (96%)	76 (97%)	2 (3%)	0	100	100
72	Sg	59/64 (92%)	52 (88%)	7 (12%)	0	100	100
73	Sh	46/51 (90%)	43 (94%)	3 (6%)	0	100	100
74	Sj	65/69 (94%)	58 (89%)	7 (11%)	0	100	100
All	All	10005/11192 (89%)	9312 (93%)	588 (6%)	105 (1%)	15	48

5 of 105 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	LA	15	VAL
2	LB	5	LYS
9	LI	184	VAL
27	La	49	ARG
27	La	98	VAL

5.3.2 Protein sidechains ⓘ

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	185/192 (96%)	119 (64%)	66 (36%)	0	1
2	LB	309/313 (99%)	177 (57%)	132 (43%)	0	0
3	LC	257/263 (98%)	164 (64%)	93 (36%)	0	1
6	LF	235/242 (97%)	130 (55%)	105 (45%)	0	0
7	LG	47/48 (98%)	28 (60%)	19 (40%)	0	0
8	LH	186/204 (91%)	119 (64%)	67 (36%)	0	1
9	LI	163/198 (82%)	104 (64%)	59 (36%)	0	1
10	LJ	163/164 (99%)	95 (58%)	68 (42%)	0	0
11	LK	167/177 (94%)	100 (60%)	67 (40%)	0	0
12	LL	141/149 (95%)	79 (56%)	62 (44%)	0	0
13	LM	165/197 (84%)	98 (59%)	67 (41%)	0	1
14	LN	106/111 (96%)	63 (59%)	43 (41%)	0	1
15	LO	174/175 (99%)	112 (64%)	62 (36%)	0	1
16	LP	158/165 (96%)	100 (63%)	58 (37%)	0	1
17	LQ	130/139 (94%)	78 (60%)	52 (40%)	0	1
18	LR	154/155 (99%)	90 (58%)	64 (42%)	0	0
19	LS	158/167 (95%)	98 (62%)	60 (38%)	0	1
20	LT	151/154 (98%)	90 (60%)	61 (40%)	0	0
21	LU	125/133 (94%)	72 (58%)	53 (42%)	0	0
22	LV	93/110 (84%)	47 (50%)	46 (50%)	0	0
23	LW	108/114 (95%)	67 (62%)	41 (38%)	0	1
24	LX	58/174 (33%)	36 (62%)	22 (38%)	0	1
25	LY	102/123 (83%)	62 (61%)	40 (39%)	0	1
26	LZ	114/115 (99%)	71 (62%)	43 (38%)	0	1
27	La	106/119 (89%)	59 (56%)	47 (44%)	0	0
28	Lb	124/127 (98%)	74 (60%)	50 (40%)	0	0
29	Lc	50/57 (88%)	28 (56%)	22 (44%)	0	0
30	Ld	83/92 (90%)	42 (51%)	41 (49%)	0	0
31	Le	85/92 (92%)	47 (55%)	38 (45%)	0	0
32	Lf	111/120 (92%)	67 (60%)	44 (40%)	0	1
33	Lg	82/103 (80%)	51 (62%)	31 (38%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Lh	90/100 (90%)	62 (69%)	28 (31%)	0	2
35	Li	102/107 (95%)	63 (62%)	39 (38%)	0	1
36	Lj	72/78 (92%)	40 (56%)	32 (44%)	0	0
37	Lk	71/74 (96%)	45 (63%)	26 (37%)	0	1
38	Ll	63/68 (93%)	26 (41%)	37 (59%)	0	0
39	Ln	173/189 (92%)	73 (42%)	100 (58%)	0	0
40	Lo	22/22 (100%)	10 (46%)	12 (54%)	0	0
41	Lp	81/93 (87%)	43 (53%)	38 (47%)	0	0
42	Lq	71/73 (97%)	36 (51%)	35 (49%)	0	0
43	Ls	43/110 (39%)	22 (51%)	21 (49%)	0	0
45	SA	169/217 (78%)	104 (62%)	65 (38%)	0	1
46	SB	177/201 (88%)	91 (51%)	86 (49%)	0	0
47	SC	172/182 (94%)	89 (52%)	83 (48%)	0	0
48	SD	206/220 (94%)	116 (56%)	90 (44%)	0	0
49	SE	228/232 (98%)	121 (53%)	107 (47%)	0	0
50	SF	148/157 (94%)	93 (63%)	55 (37%)	0	1
51	SG	192/213 (90%)	87 (45%)	105 (55%)	0	0
52	SH	165/170 (97%)	78 (47%)	87 (53%)	0	0
53	SI	141/148 (95%)	73 (52%)	68 (48%)	0	0
54	SJ	114/115 (99%)	55 (48%)	59 (52%)	0	0
55	SK	152/164 (93%)	79 (52%)	73 (48%)	0	0
56	SL	98/119 (82%)	55 (56%)	43 (44%)	0	0
57	SM	131/136 (96%)	82 (63%)	49 (37%)	0	1
58	SO	112/114 (98%)	60 (54%)	52 (46%)	0	0
59	SP	125/130 (96%)	76 (61%)	49 (39%)	0	1
60	SQ	86/113 (76%)	46 (54%)	40 (46%)	0	0
61	SR	101/128 (79%)	51 (50%)	50 (50%)	0	0
62	ST	125/130 (96%)	67 (54%)	58 (46%)	0	0
63	SU	108/123 (88%)	57 (53%)	51 (47%)	0	0
64	SV	119/131 (91%)	61 (51%)	58 (49%)	0	0
65	SW	114/115 (99%)	56 (49%)	58 (51%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	SX	96/110 (87%)	50 (52%)	46 (48%)	0	0
67	SY	68/72 (94%)	36 (53%)	32 (47%)	0	0
68	Sb	104/113 (92%)	54 (52%)	50 (48%)	0	0
69	Sc	67/79 (85%)	28 (42%)	39 (58%)	0	0
70	Sd	91/103 (88%)	55 (60%)	36 (40%)	0	1
71	Se	72/73 (99%)	46 (64%)	26 (36%)	0	1
72	Sg	54/57 (95%)	22 (41%)	32 (59%)	0	0
73	Sh	42/45 (93%)	28 (67%)	14 (33%)	0	2
74	Sj	57/58 (98%)	26 (46%)	31 (54%)	0	0
All	All	8712/9574 (91%)	4929 (57%)	3783 (43%)	0	0

5 of 3783 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	Ll	8	GLU
67	SY	74	SER
47	SC	130	ARG
66	SX	104	ILE
60	SQ	143	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 221 such sidechains are listed below:

Mol	Chain	Res	Type
38	Ll	3	ASN
47	SC	91	ASN
74	Sj	58	ASN
63	SU	77	GLN
39	Ln	119	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	LD	139/142 (97%)	64 (46%)	5 (3%)
44	Lt	2587/2697 (95%)	1153 (44%)	0
5	LE	115/121 (95%)	52 (45%)	4 (3%)
75	St	1453/1454 (99%)	785 (54%)	0
76	u	74/75 (98%)	53 (71%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
76	v	74/75 (98%)	49 (66%)	0
77	x	73/74 (98%)	46 (63%)	0
78	y	10/11 (90%)	8 (80%)	0
All	All	4525/4649 (97%)	2210 (48%)	9 (0%)

5 of 2210 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	LD	3	A
4	LD	8	C
4	LD	9	C
4	LD	10	G
4	LD	12	C

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	LE	110	U
5	LE	114	G
4	LD	87	A
4	LD	117	C
5	LE	38	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

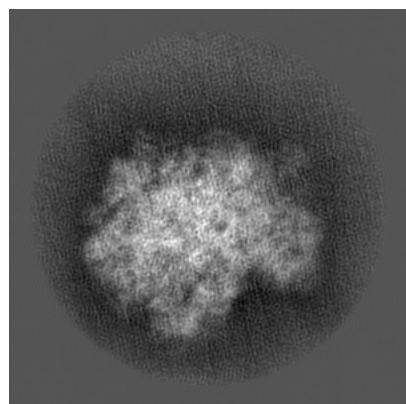
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16226. These allow visual inspection of the internal detail of the map and identification of artifacts.

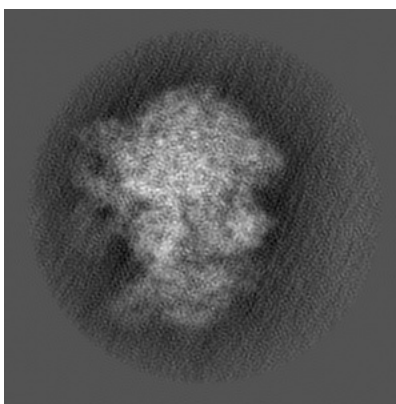
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

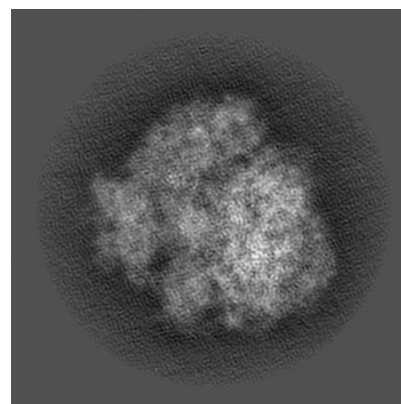
6.1.1 Primary map



X

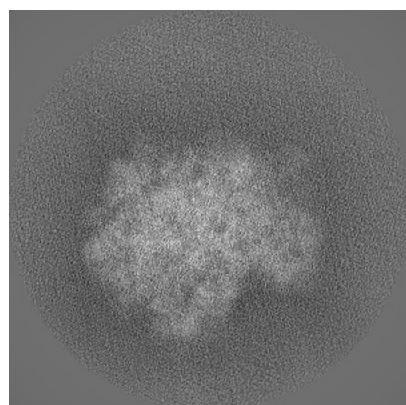


Y

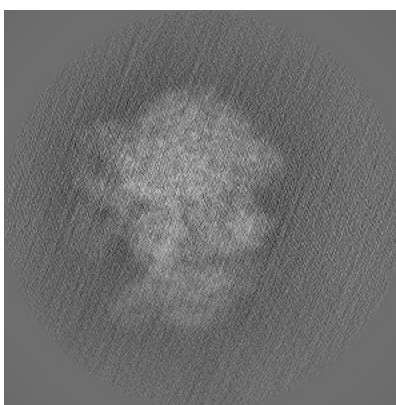


Z

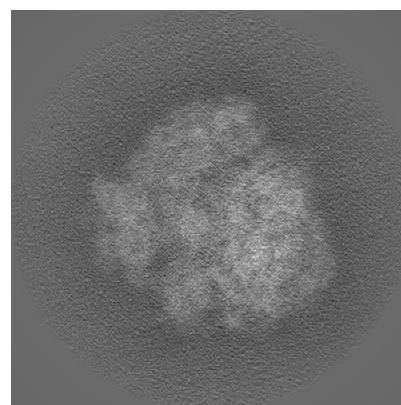
6.1.2 Raw map



X



Y

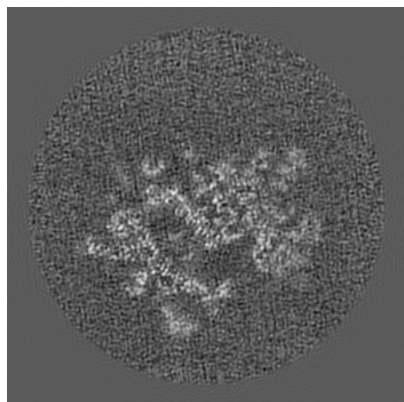


Z

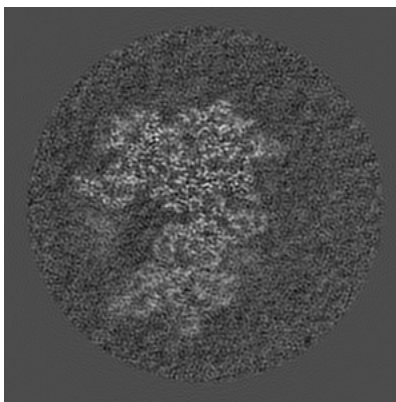
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

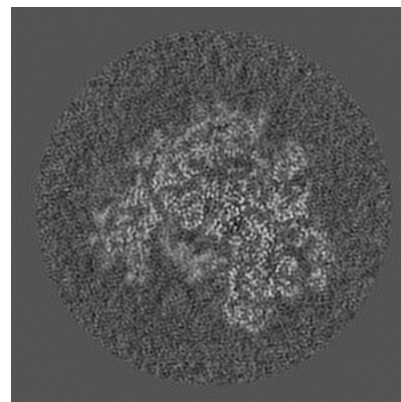
6.2.1 Primary map



X Index: 250

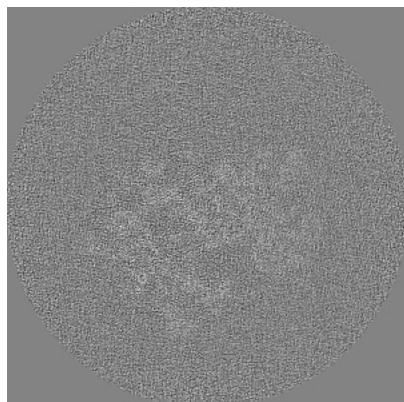


Y Index: 250

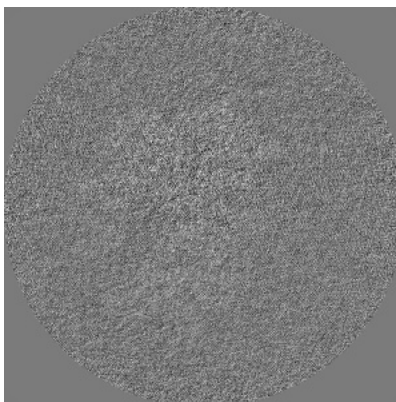


Z Index: 250

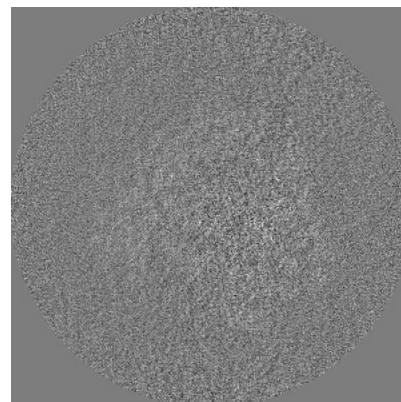
6.2.2 Raw map



X Index: 250



Y Index: 250

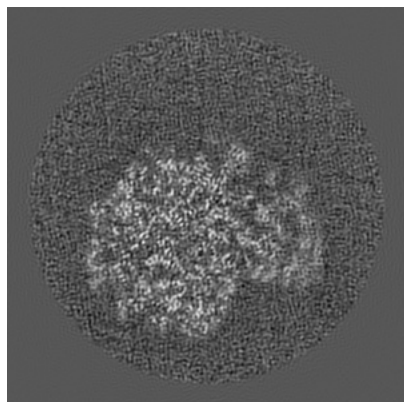


Z Index: 250

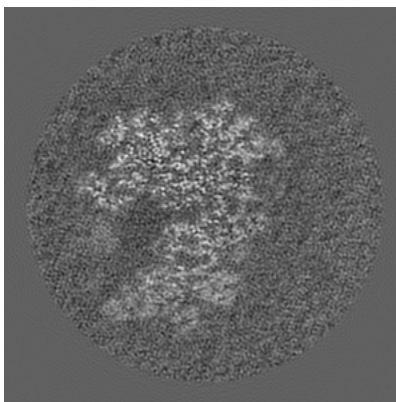
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

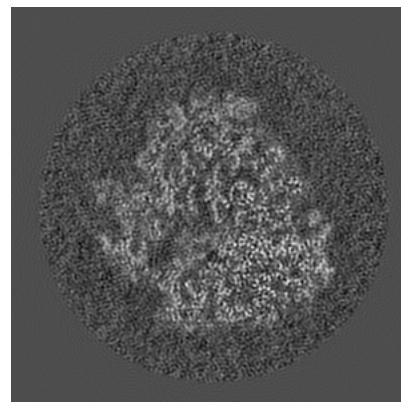
6.3.1 Primary map



X Index: 277

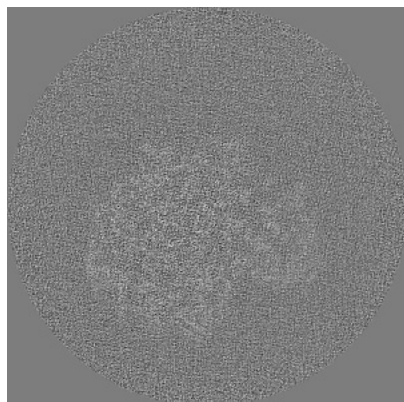


Y Index: 253

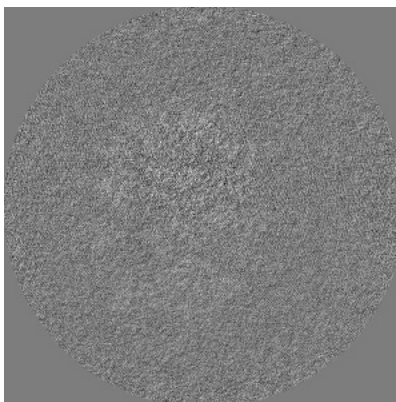


Z Index: 208

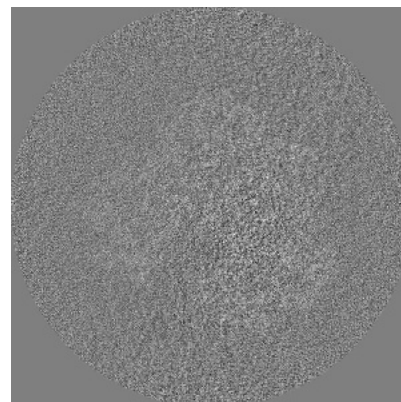
6.3.2 Raw map



X Index: 281



Y Index: 243

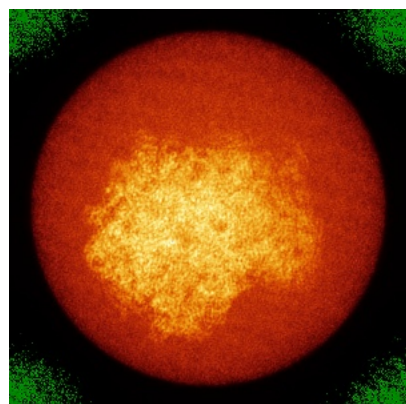


Z Index: 233

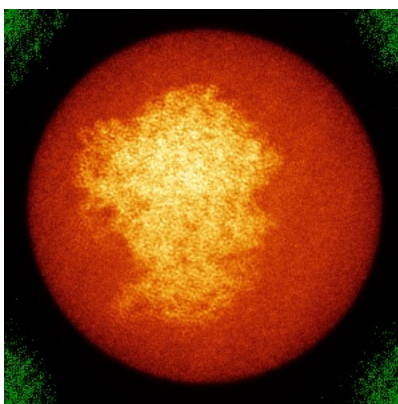
The images above show the largest variance slices of the map in three orthogonal directions.

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

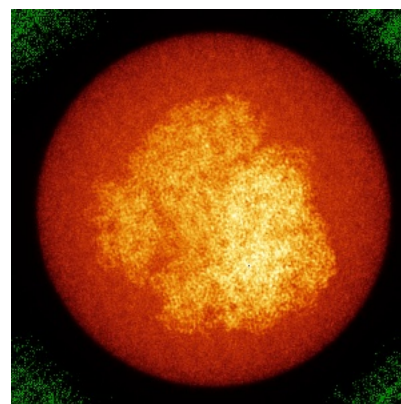
6.4.1 Primary map



X

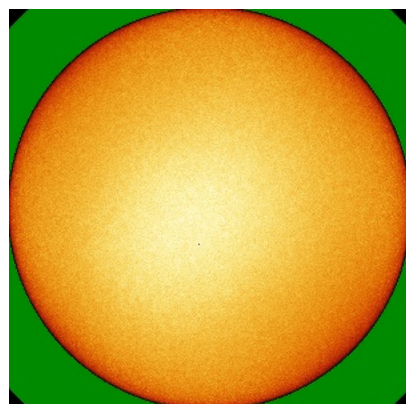


Y

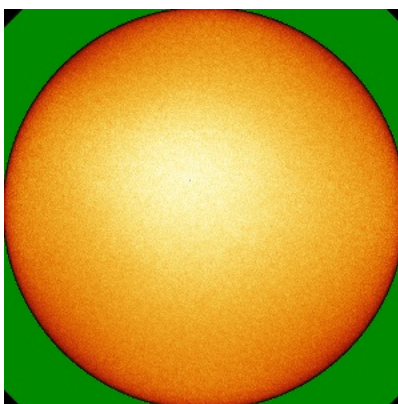


Z

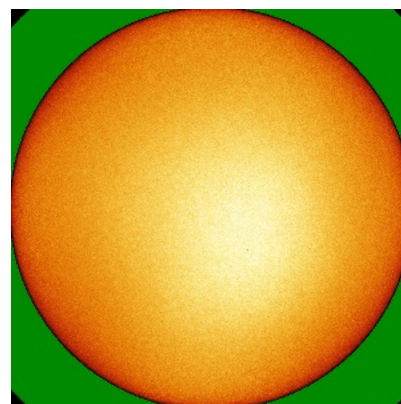
6.4.2 Raw map



X



Y



Z

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

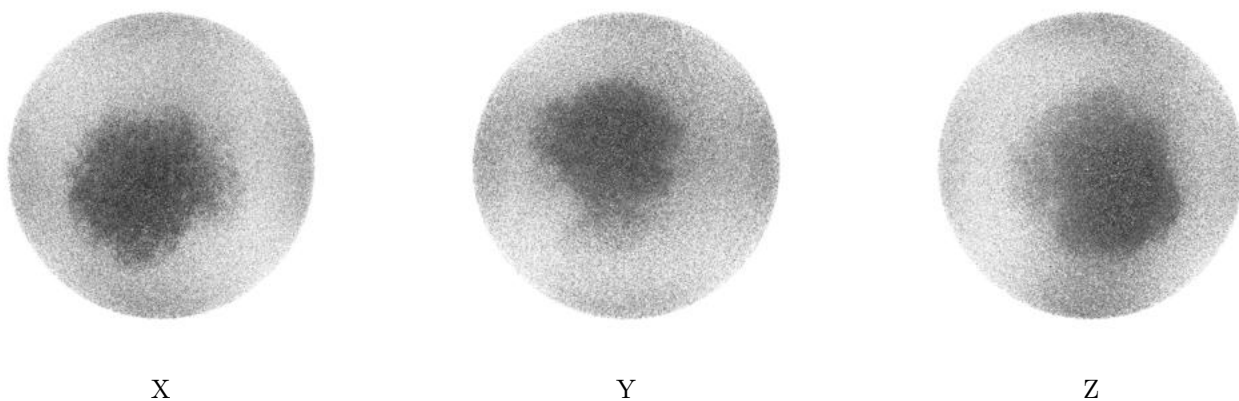
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.83. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

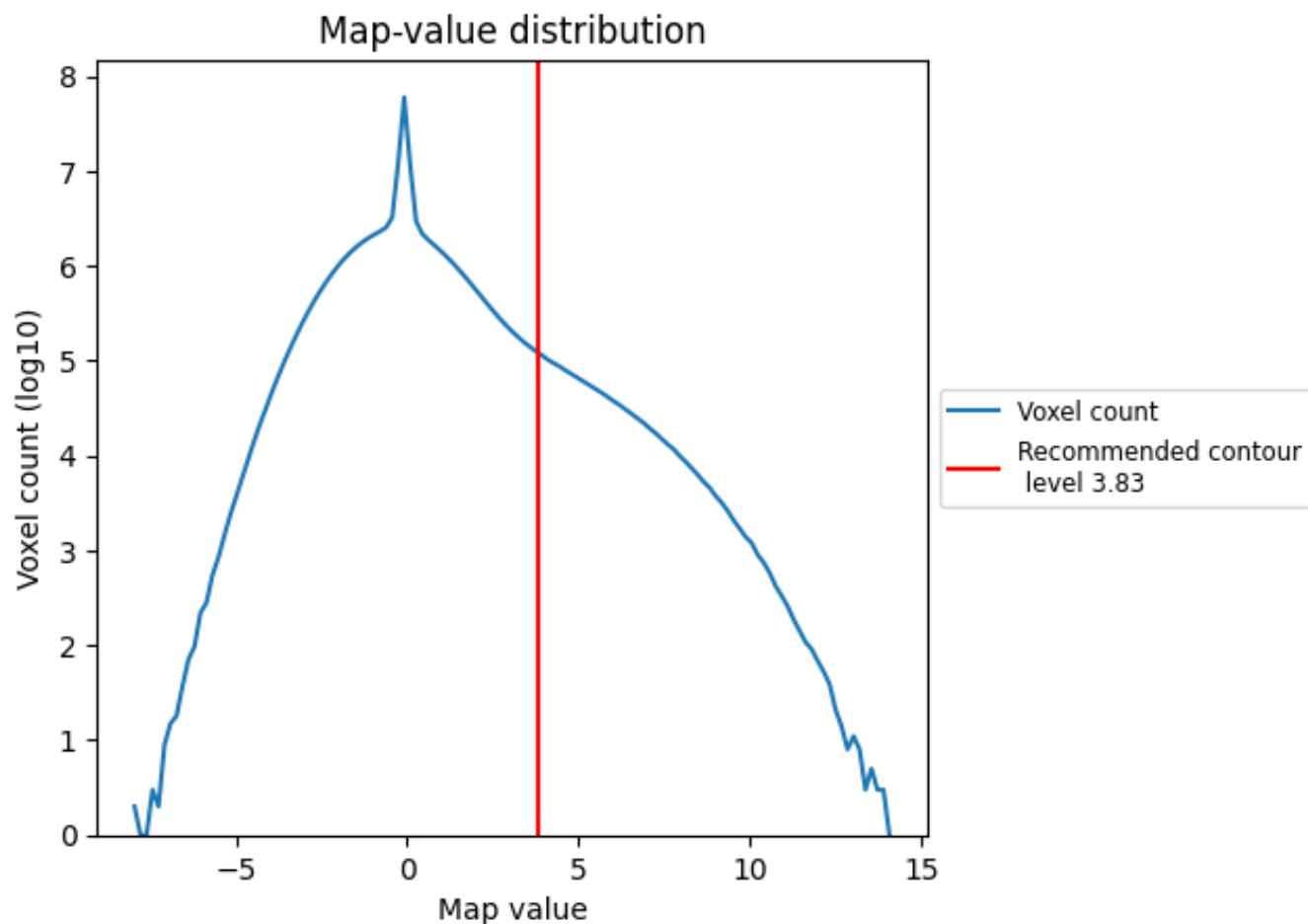
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

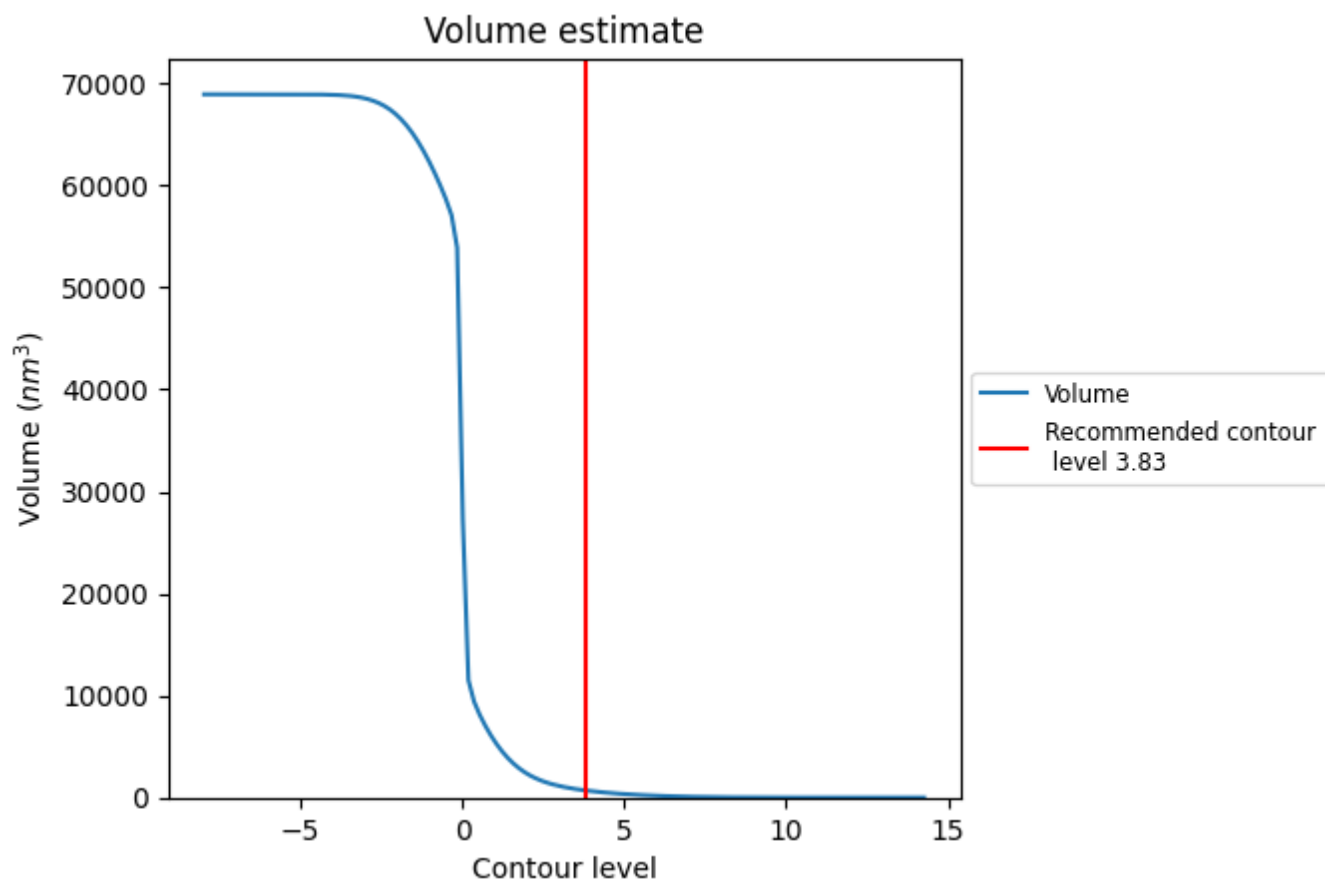
This section contains the results of statistical analysis of the map.

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.

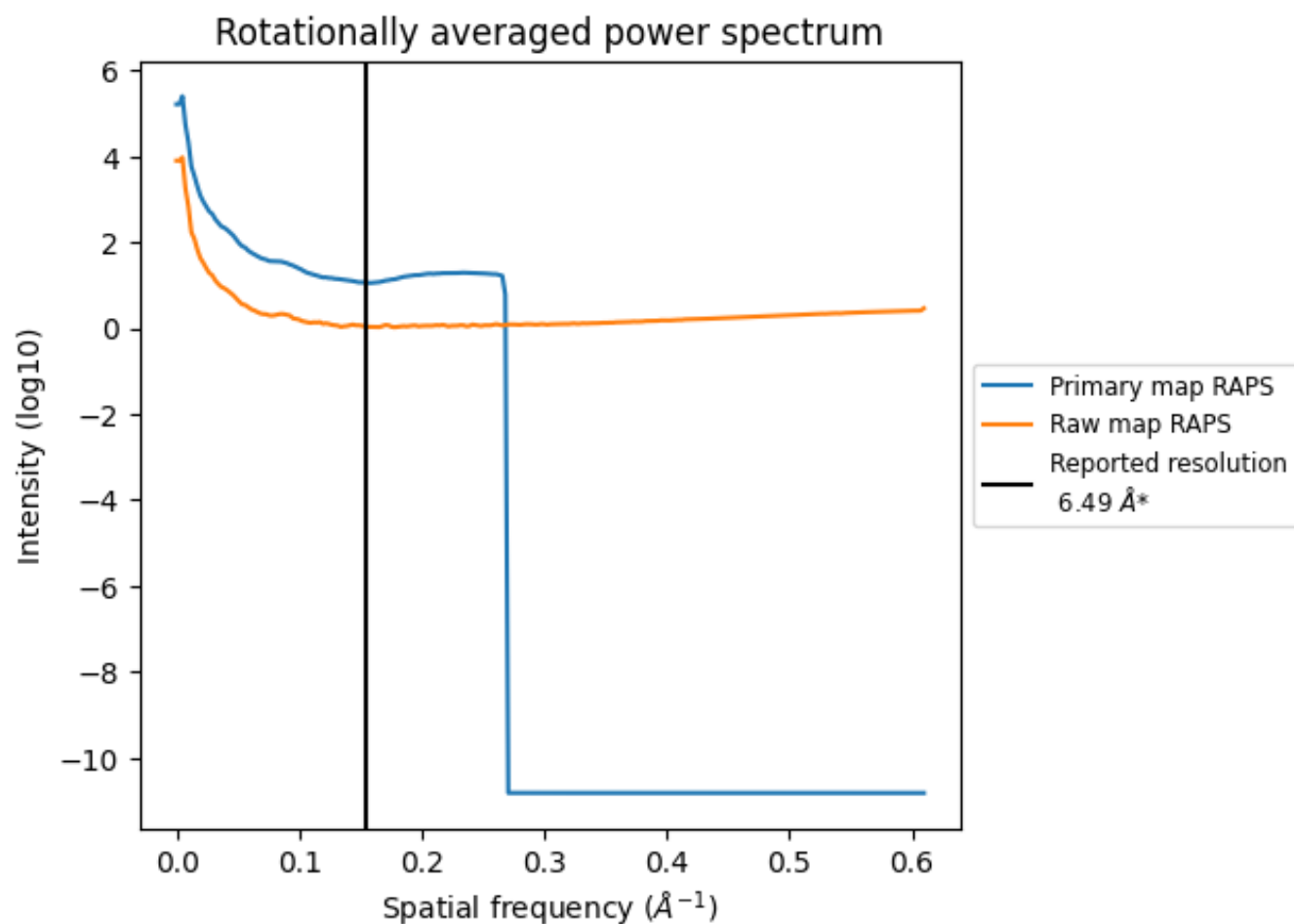
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 689 nm³; this corresponds to an approximate mass of 623 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

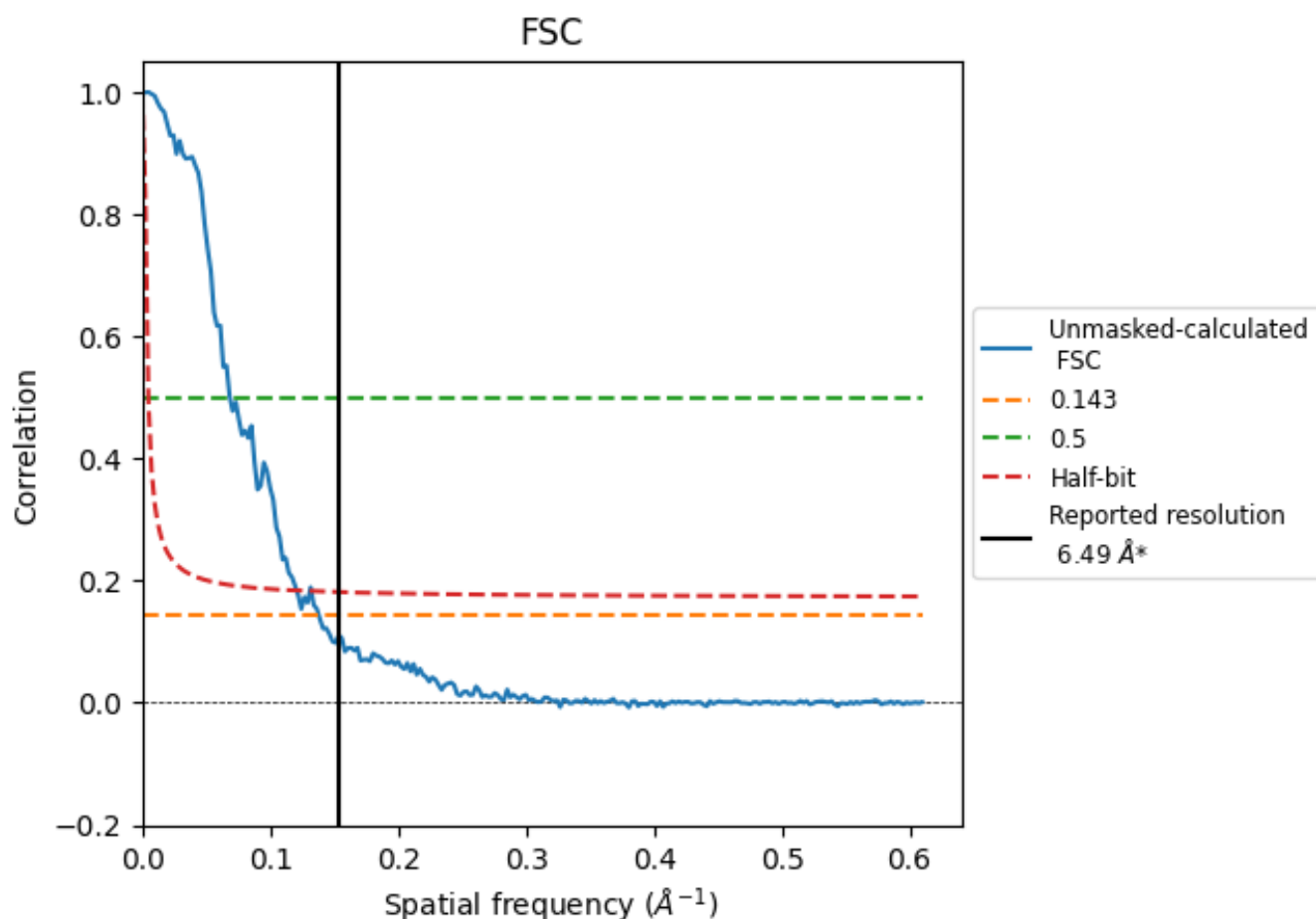


*Reported resolution corresponds to spatial frequency of 0.154 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.154 Å⁻¹

8.2 Resolution estimates [i](#)

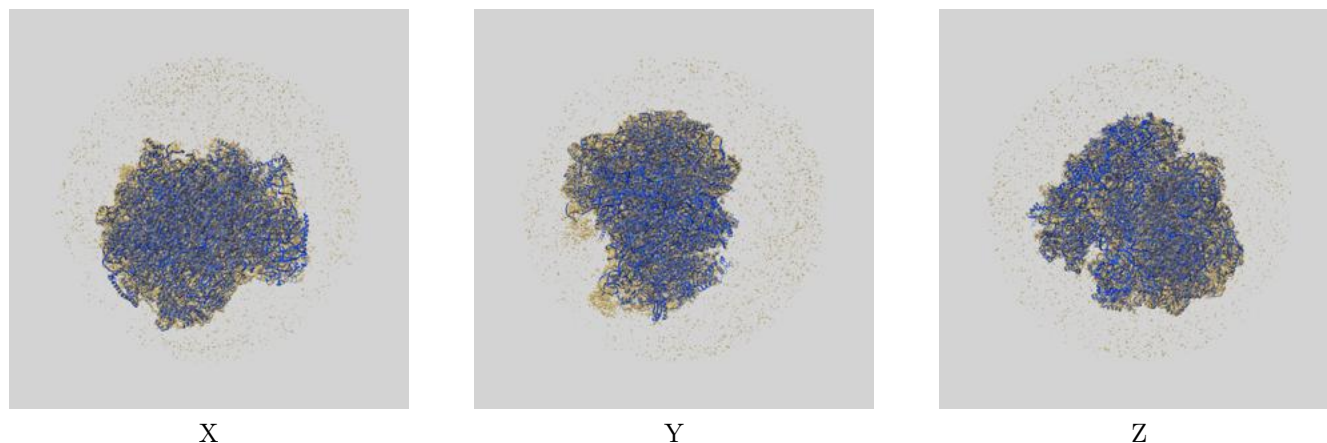
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.49	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.24	14.60	8.28

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.24 differs from the reported value 6.49 by more than 10 %

9 Map-model fit [i](#)

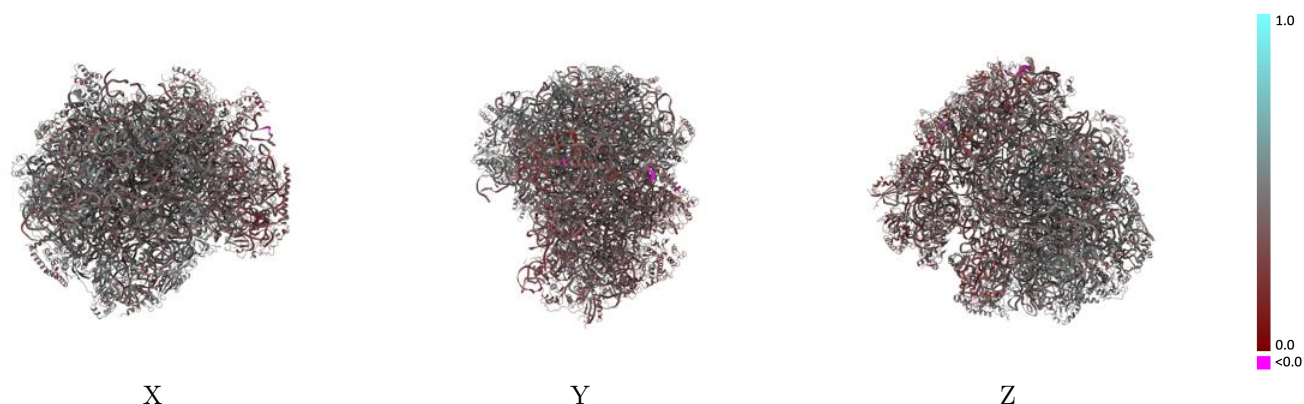
This section contains information regarding the fit between EMDB map EMD-16226 and PDB model 8BSJ. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

9.1 Map-model overlay [i](#)



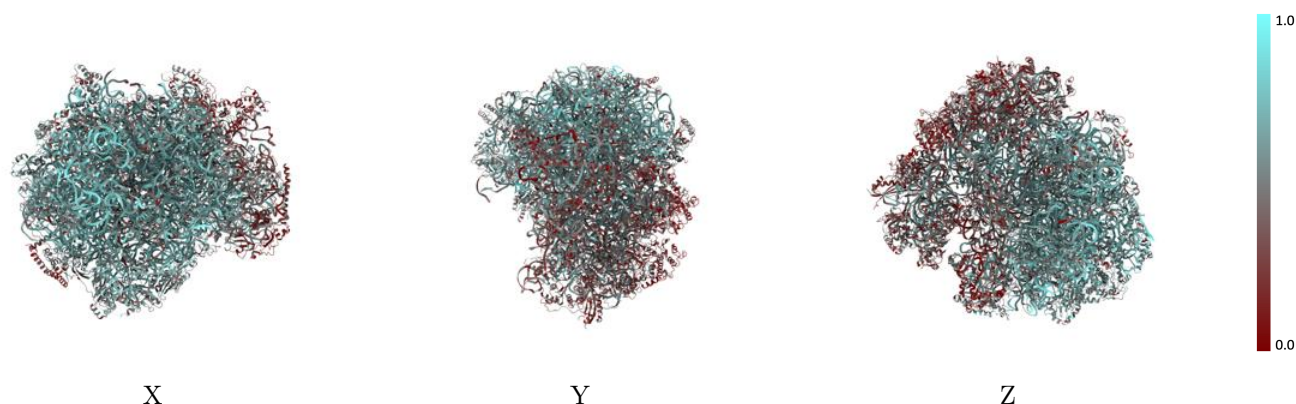
The images above show the 3D surface view of the map at the recommended contour level 3.83 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



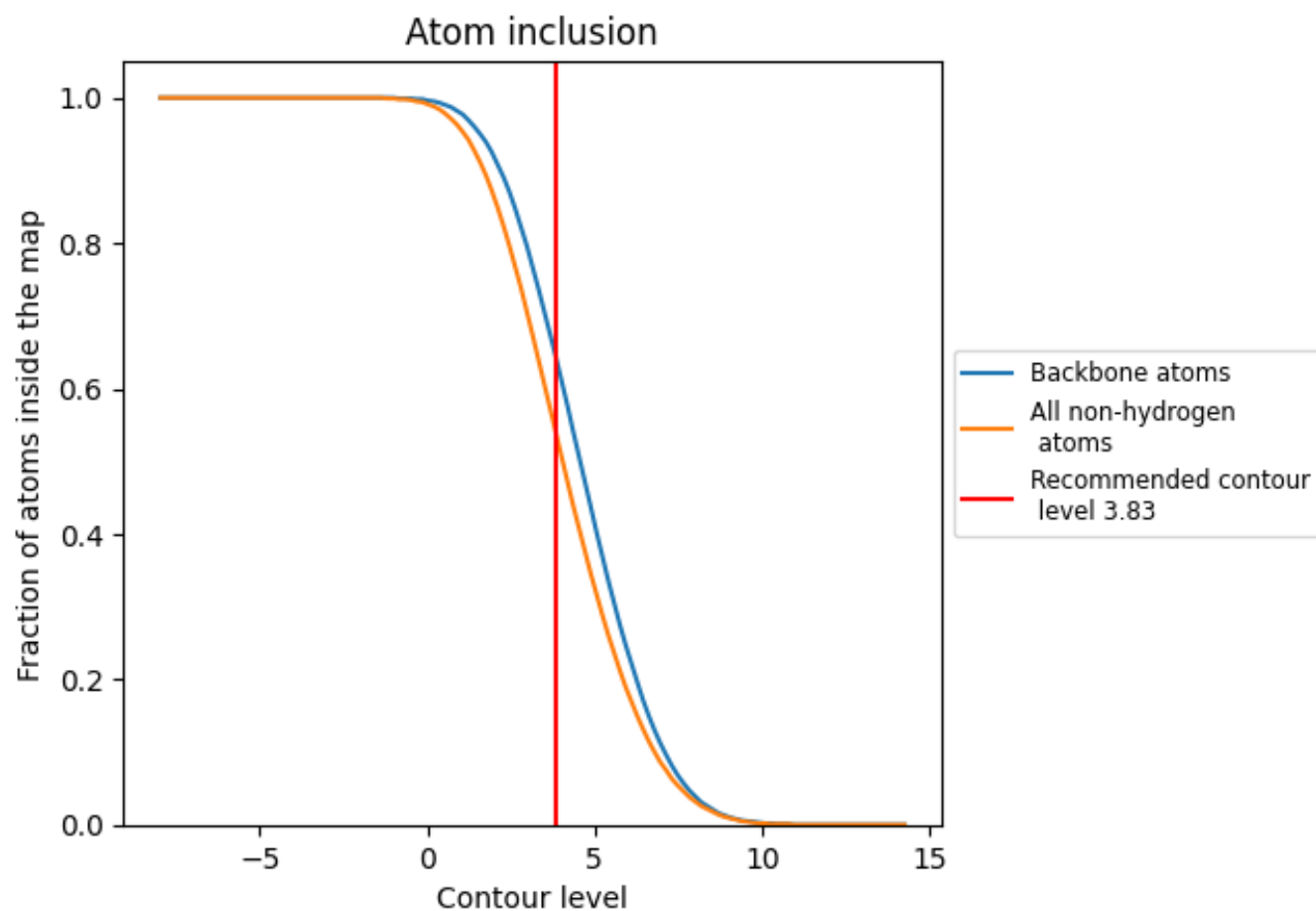
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.83).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 54% 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 (3.83) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5420	 0.4110
LA	 0.5730	 0.4930
LB	 0.5620	 0.4800
LC	 0.5610	 0.4650
LD	 0.7260	 0.4240
LE	 0.7230	 0.4220
LF	 0.5070	 0.4570
LG	 0.5530	 0.4690
LH	 0.4790	 0.4460
LI	 0.5130	 0.4590
LJ	 0.5290	 0.4700
LK	 0.4930	 0.4560
LL	 0.4870	 0.4350
LM	 0.5760	 0.4730
LN	 0.5390	 0.4540
LO	 0.6270	 0.4890
LP	 0.5420	 0.4600
LQ	 0.5760	 0.4840
LR	 0.5600	 0.4800
LS	 0.4890	 0.4440
LT	 0.5580	 0.4710
LU	 0.5350	 0.4690
LV	 0.4500	 0.4060
LW	 0.5470	 0.4750
LX	 0.5820	 0.4640
LY	 0.5730	 0.4740
LZ	 0.6030	 0.4720
La	 0.4130	 0.4140
Lb	 0.5960	 0.4850
Lc	 0.5430	 0.4690
Ld	 0.4660	 0.4390
Le	 0.5560	 0.4780
Lf	 0.5560	 0.4700
Lg	 0.5710	 0.4710
Lh	 0.5070	 0.4700



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Chain	Atom inclusion	Q-score
Li	 0.5330	 0.4500
Lj	 0.5040	 0.4610
Lk	 0.5870	 0.4800
Ll	 0.3930	 0.3960
Ln	 0.1170	 0.2900
Lo	 0.4620	 0.4630
Lp	 0.5660	 0.4800
Lq	 0.5040	 0.4620
Ls	 0.5570	 0.4540
Lt	 0.6930	 0.4240
SA	 0.2680	 0.3480
SB	 0.3610	 0.3900
SC	 0.3250	 0.3900
SD	 0.3860	 0.4040
SE	 0.3040	 0.3750
SF	 0.3320	 0.3960
SG	 0.2540	 0.3630
SH	 0.1900	 0.3450
SI	 0.3820	 0.4260
SJ	 0.3560	 0.4050
SK	 0.3600	 0.3740
SL	 0.3000	 0.3410
SM	 0.3290	 0.4300
SO	 0.3600	 0.4360
SP	 0.3350	 0.3910
SQ	 0.3910	 0.4280
SR	 0.2680	 0.3640
ST	 0.3340	 0.3740
SU	 0.1770	 0.3350
SV	 0.3250	 0.3670
SW	 0.3540	 0.3710
SX	 0.2590	 0.3550
SY	 0.2870	 0.3830
Sb	 0.2860	 0.3570
Sc	 0.2730	 0.3660
Sd	 0.4070	 0.4350
Se	 0.1880	 0.3510
Sg	 0.2740	 0.4070
Sh	 0.4140	 0.4050
Sj	 0.3290	 0.3860
St	 0.5470	 0.3630
u	 0.2660	 0.2870

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Chain	Atom inclusion	Q-score
v	 0.2790	 0.3040
x	 0.2890	 0.2980
y	 0.4790	 0.3830