



wwPDB EM Validation Summary Report ⓘ

Oct 6, 2024 – 10:09 am BST

PDB ID : 8BSJ
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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

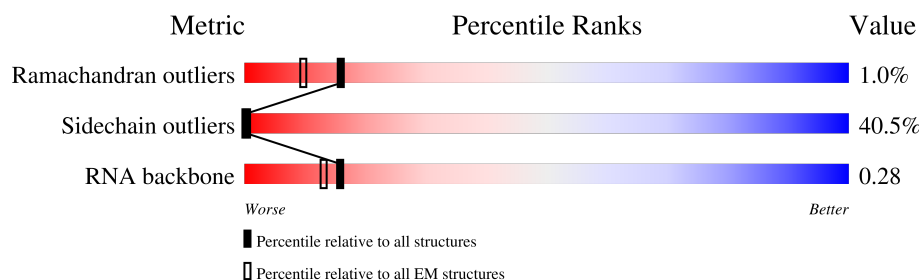
1 Overall quality at a glance

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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	<div> <div>14%</div> <div>73%</div> <div>24%</div> <div>.</div> </div>
2	LB	379	<div> <div>16%</div> <div>68%</div> <div>31%</div> <div>.</div> </div>
3	LC	316	<div> <div>19%</div> <div>69%</div> <div>29%</div> <div>.</div> </div>
4	LD	142	<div> <div>52%</div> <div>46%</div> <div>.</div> </div>
5	LE	121	<div> <div>54%</div> <div>42%</div> <div>.</div> </div>
6	LF	297	<div> <div>28%</div> <div>65%</div> <div>32%</div> <div>.</div> </div>
7	LG	51	<div> <div>24%</div> <div>67%</div> <div>27%</div> <div>.</div> </div>
8	LH	235	<div> <div>31%</div> <div>66%</div> <div>26%</div> <div>8%</div> </div>

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Mol	Chain	Length	Quality of chain
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	
29	Lc	62	
30	Ld	109	
31	Le	106	
32	Lf	136	
33	Lg	123	

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Mol	Chain	Length	Quality of chain
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	
54	SJ	130	
55	SK	189	
56	SL	134	
57	SM	154	
58	SO	143	

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Mol	Chain	Length	Quality of chain
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	
78	y	11	

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		

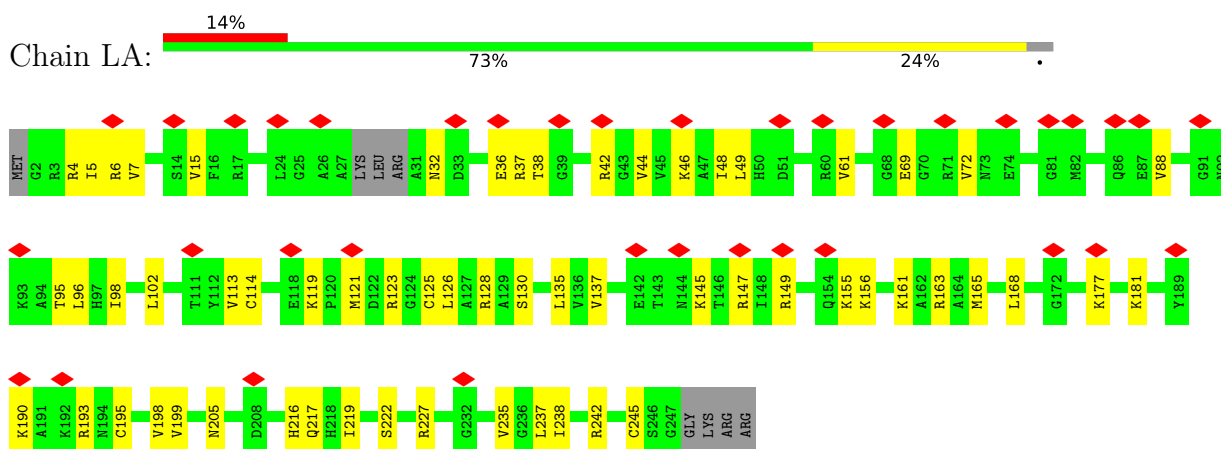
- Molecule 78 is a RNA chain called mRNA.

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

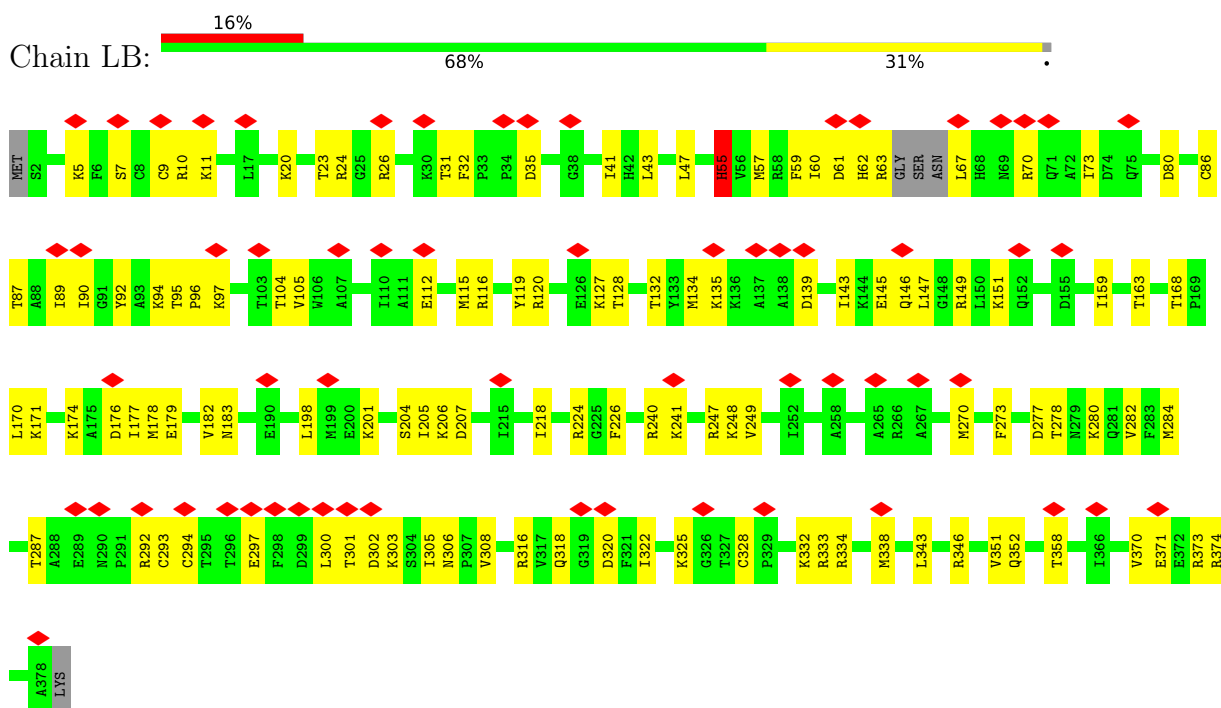
3 Residue-property plots

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.

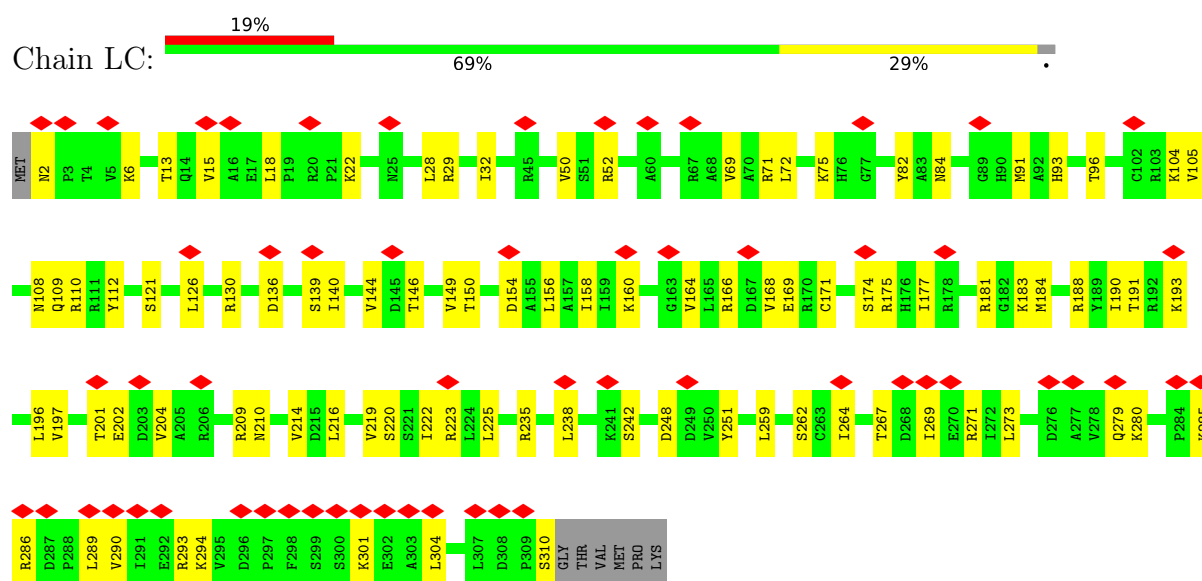
• Molecule 1: Ribosomal protein L2



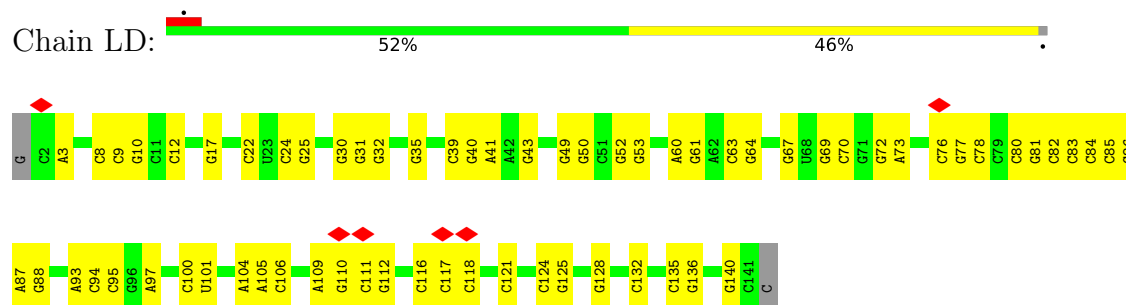
• Molecule 2: Ribosomal protein L3



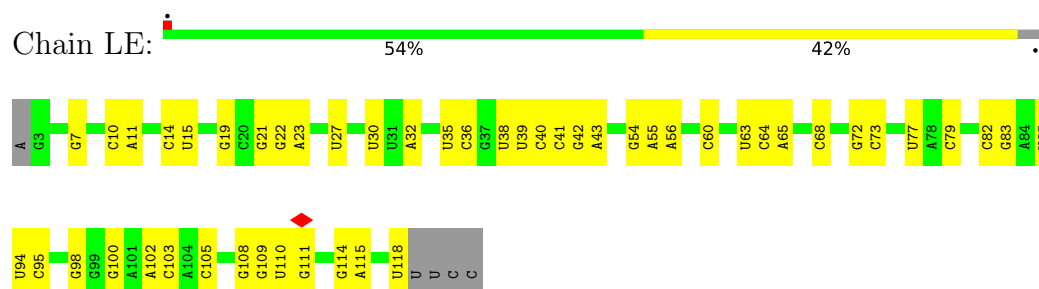
• Molecule 3: Ribosomal protein L4



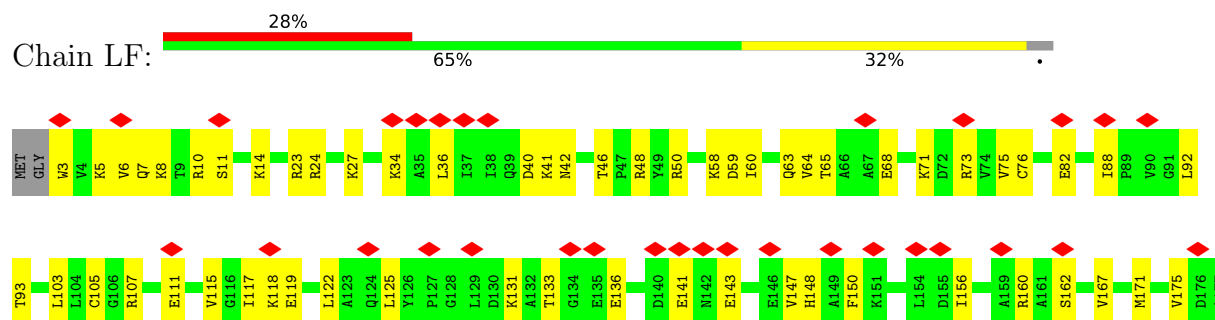
• Molecule 4: 5.8S rRNA

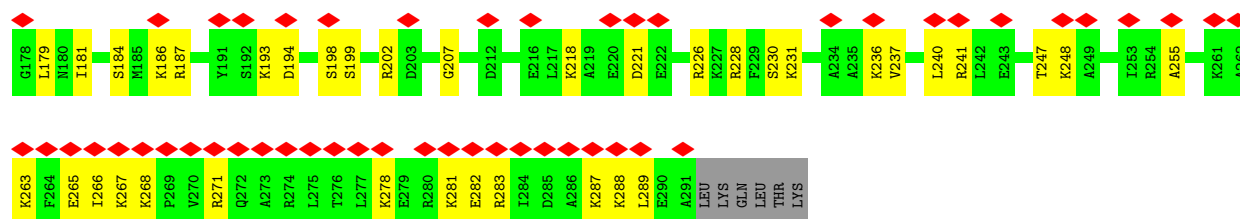


• Molecule 5: 5S rRNA

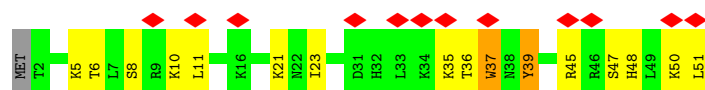


• Molecule 6: Ribosomal protein L5

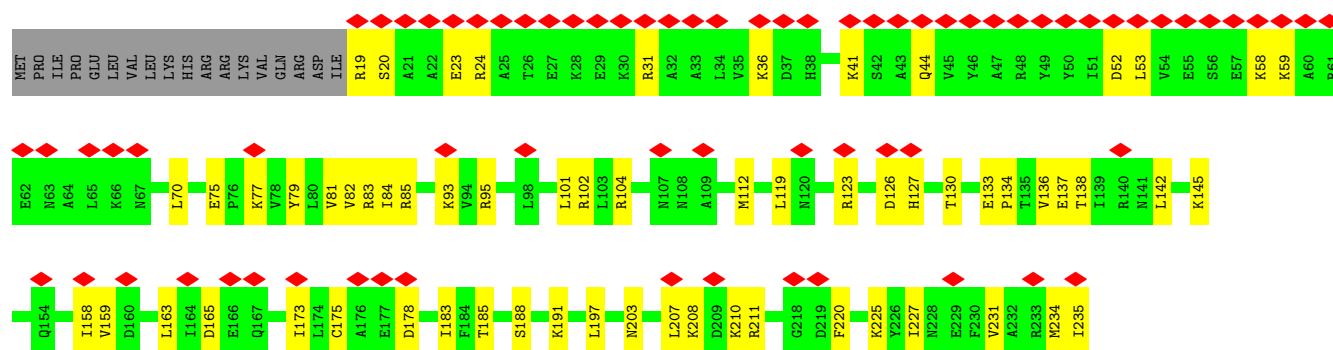




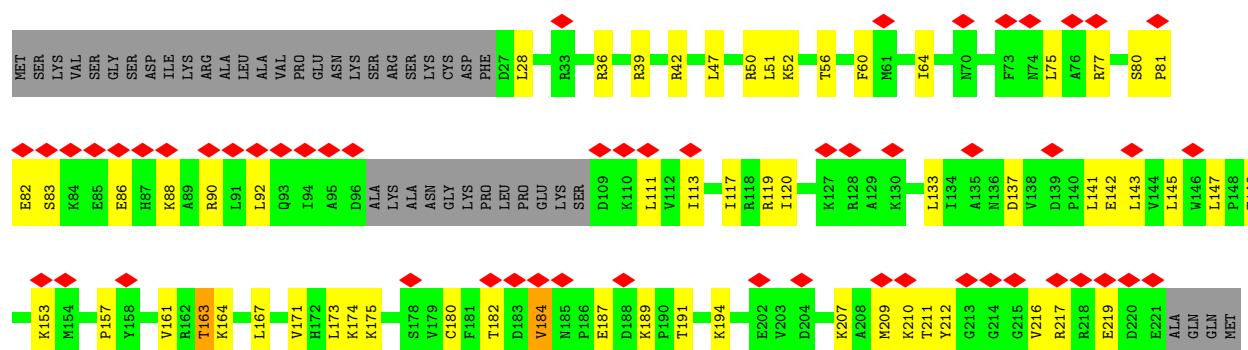
• Molecule 7: Ribosomal protein L39



• Molecule 8: Ribosomal protein L7

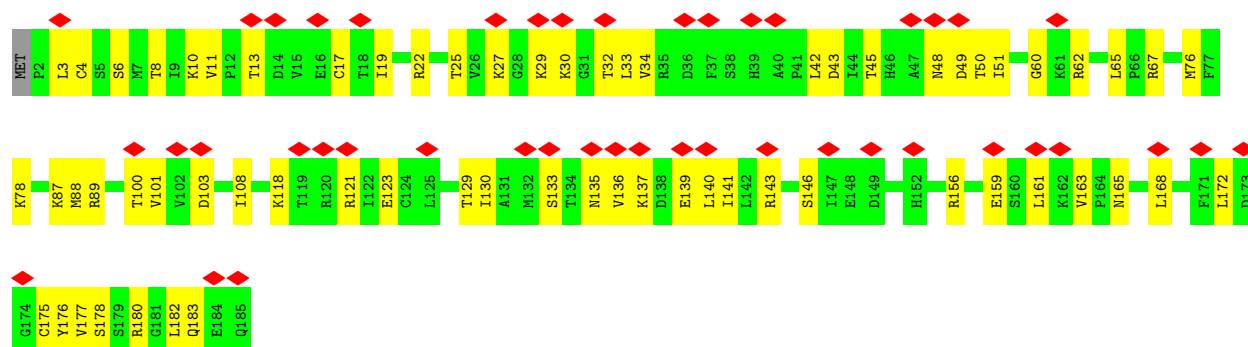


• Molecule 9: 60S ribosomal protein L7a



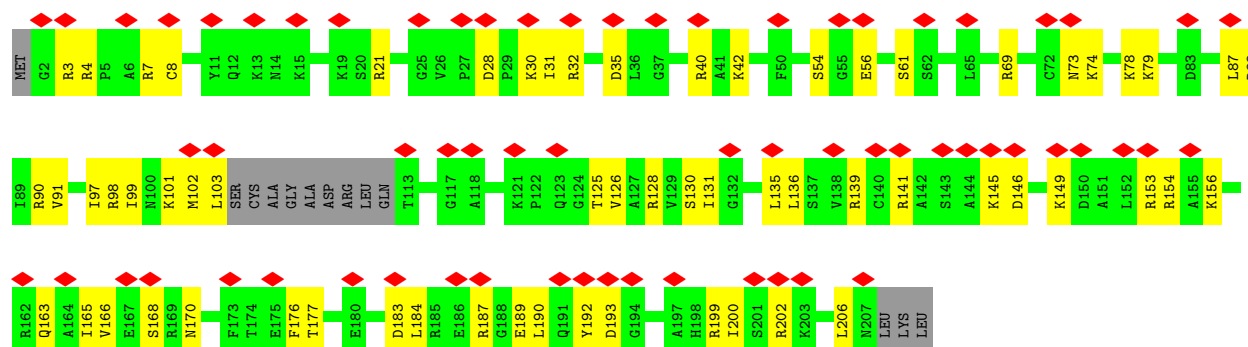
• Molecule 10: Ribosomal protein L6





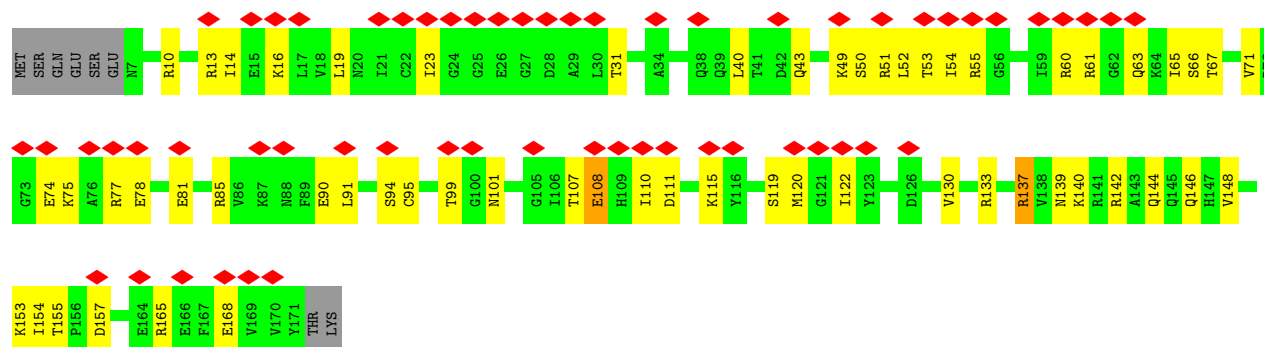
• Molecule 11: Ribosomal protein L10

Chain LK: 31% 64% 30% 6%



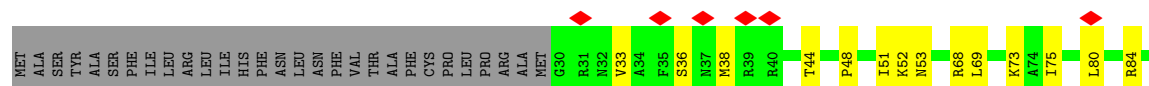
• Molecule 12: Ribosomal protein L11

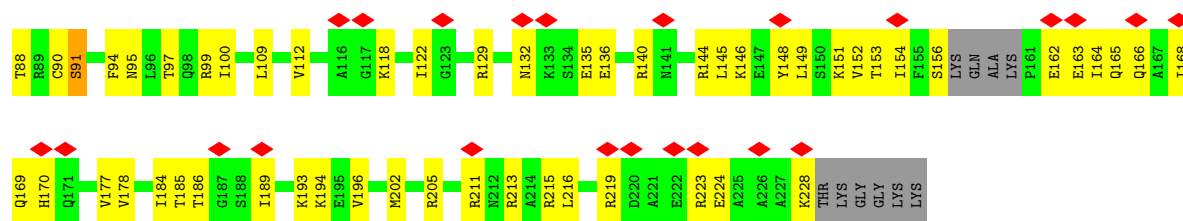
Chain LL: 34% 62% 32% 5%



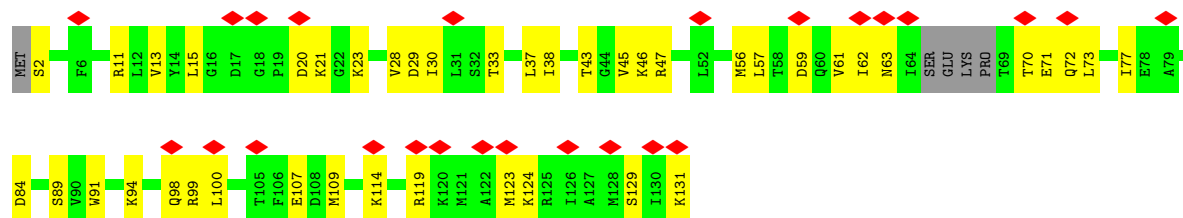
• Molecule 13: 60S ribosomal protein L13

Chain LM: 12% 54% 29% 17%

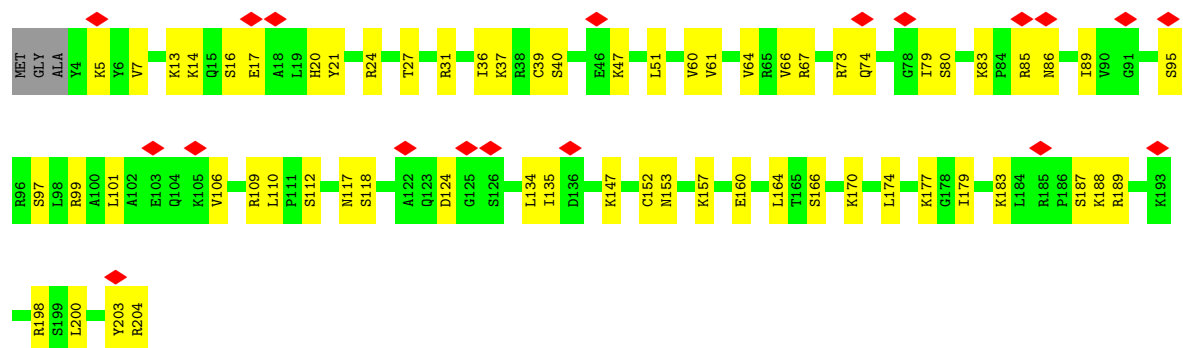




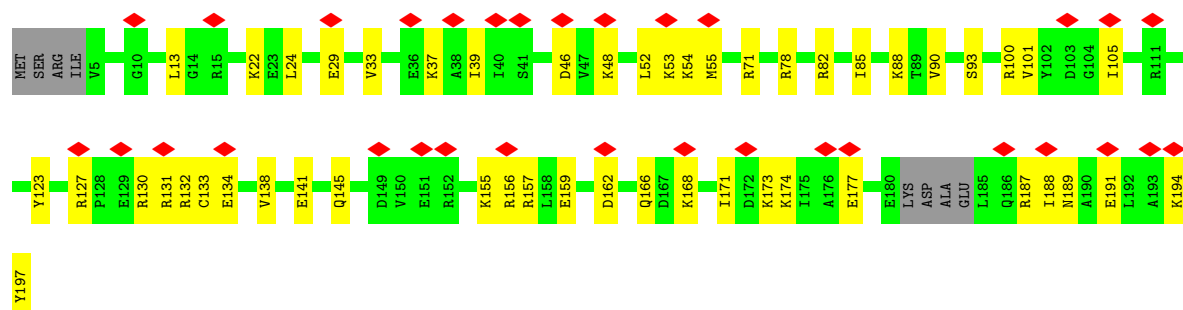
• Molecule 14: Ribosomal protein L14



• Molecule 15: Ribosomal protein L15

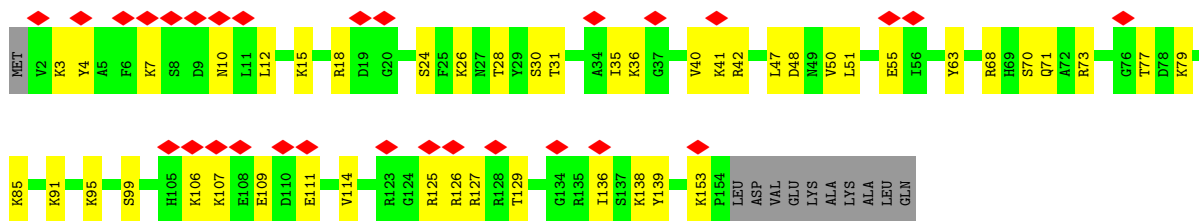


• Molecule 16: Ribosomal protein L13a

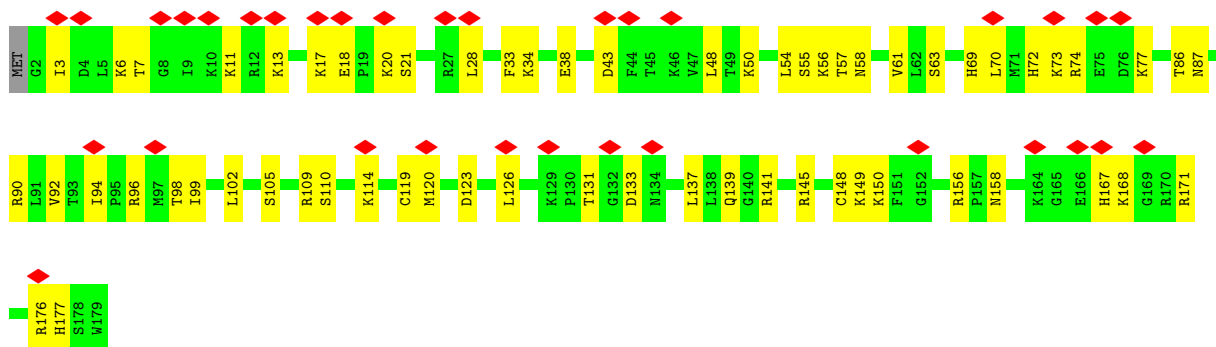


• Molecule 17: Ribosomal protein L17

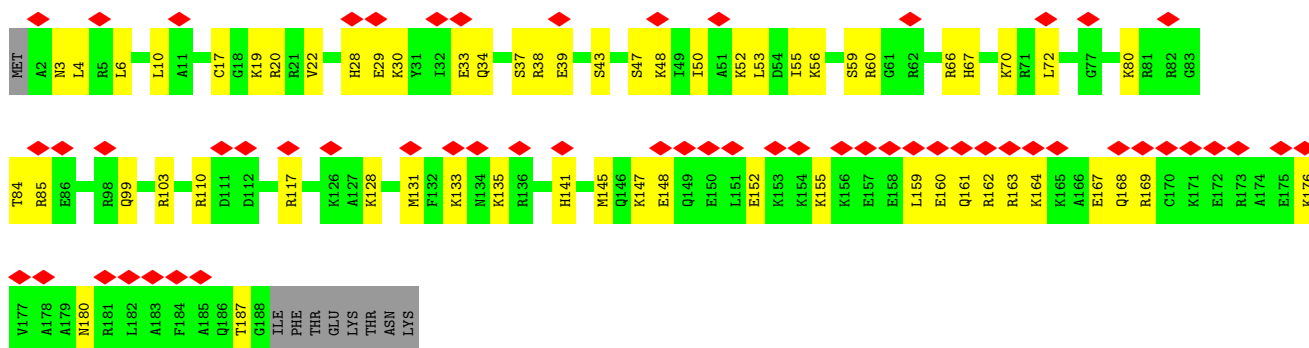




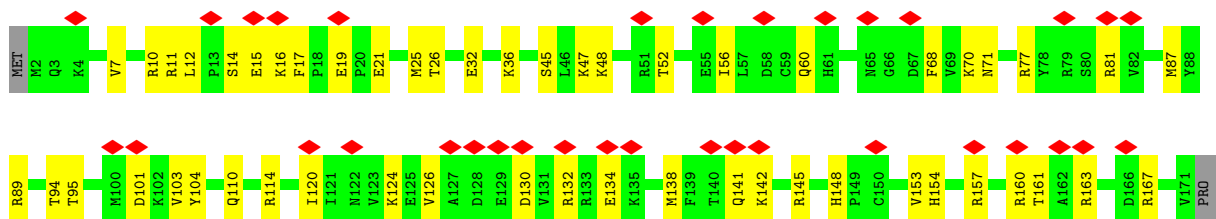
• Molecule 18: Ribosomal protein L18



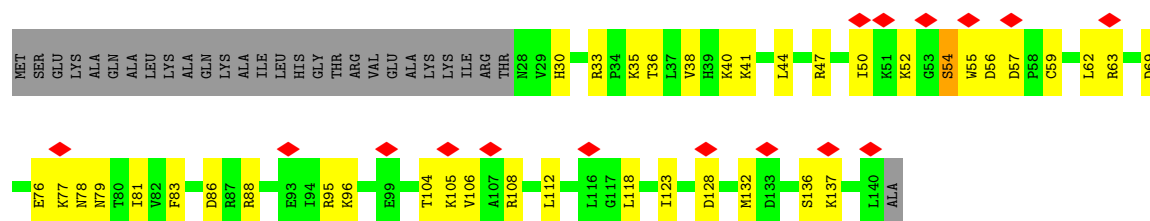
• Molecule 19: Ribosomal protein L19



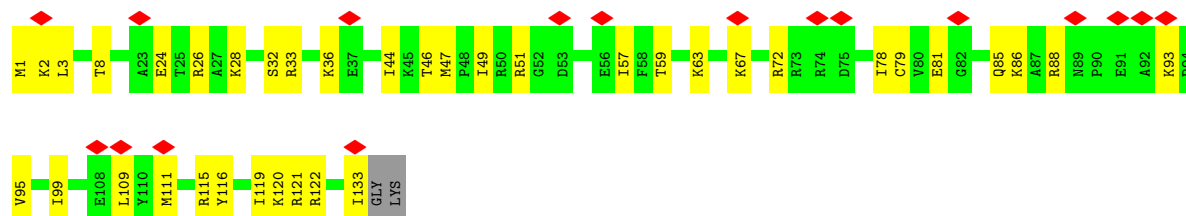
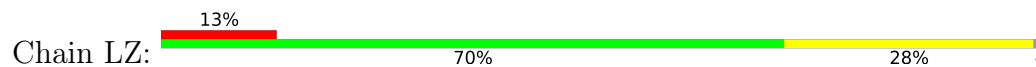
• Molecule 20: 60S ribosomal protein L18a



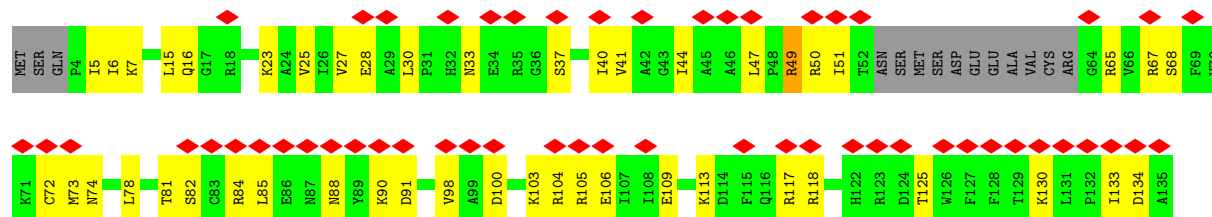
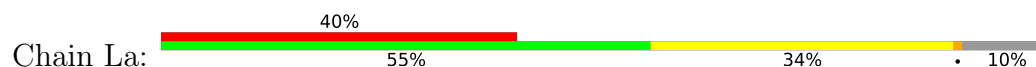
• Molecule 21: Ribosomal protein L21



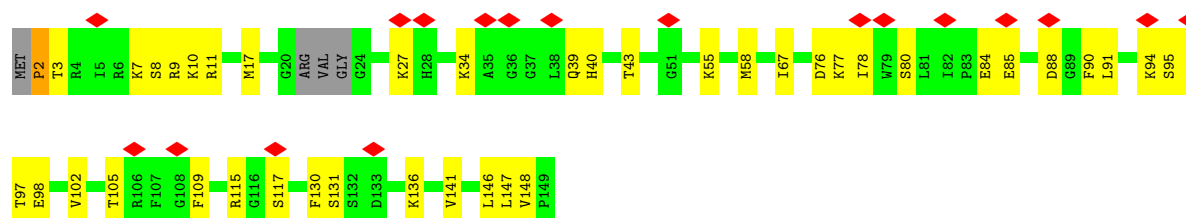
• Molecule 26: Ribosomal protein L26



• Molecule 27: 60S ribosomal protein L27



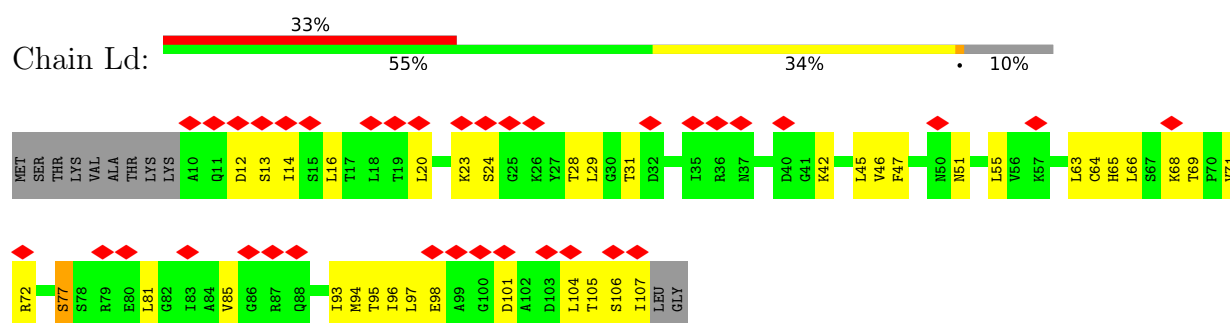
• Molecule 28: Ribosomal protein L27a



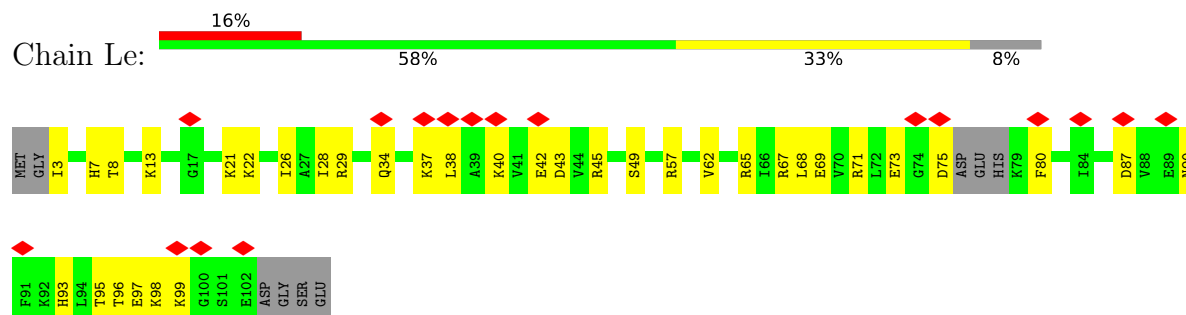
• Molecule 29: 60S ribosomal protein L29



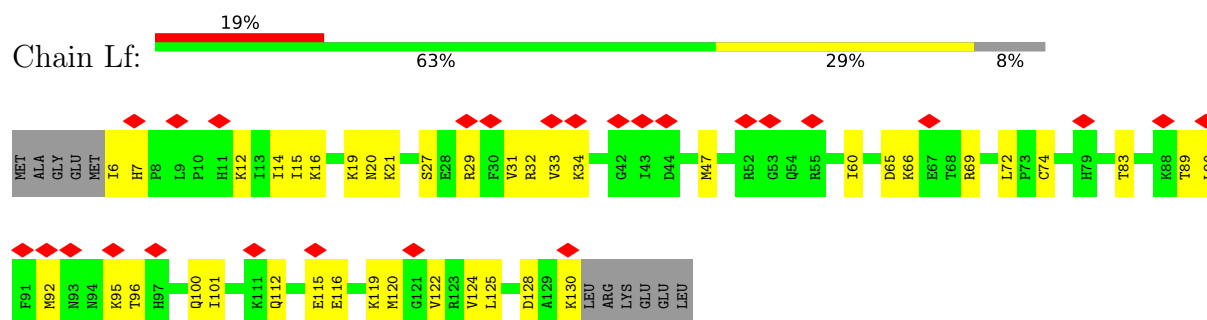
• Molecule 30: Ribosomal protein L30



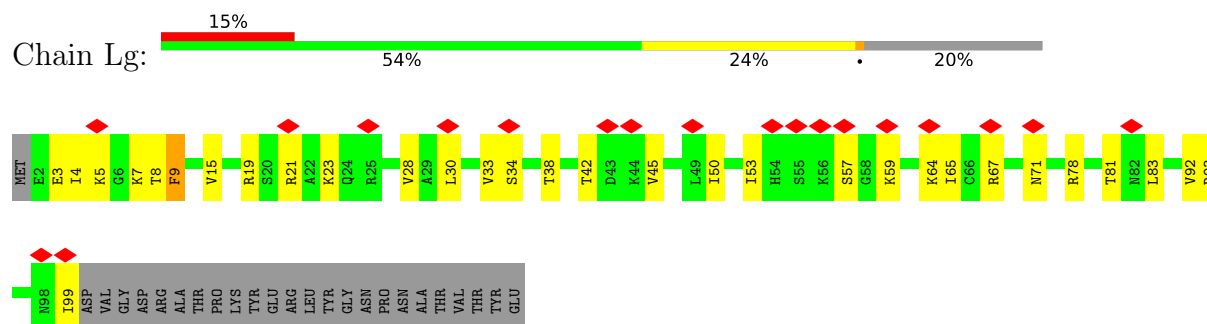
• Molecule 31: Ribosomal protein L31B



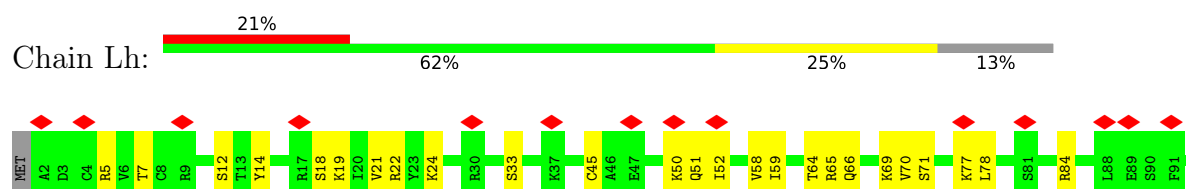
• Molecule 32: Ribosomal protein L32

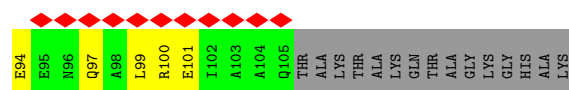


• Molecule 33: Ribosomal protein L35a

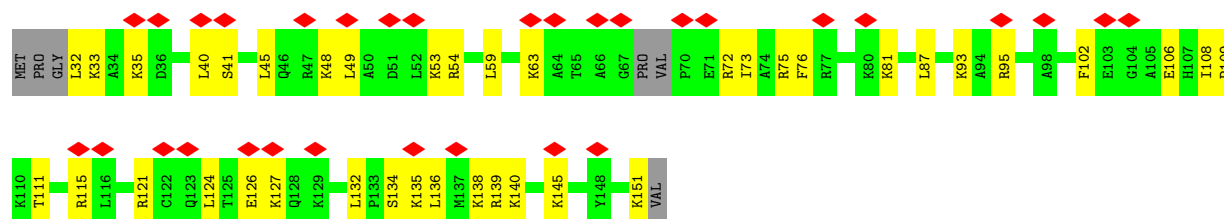


• Molecule 34: Ribosomal protein L34

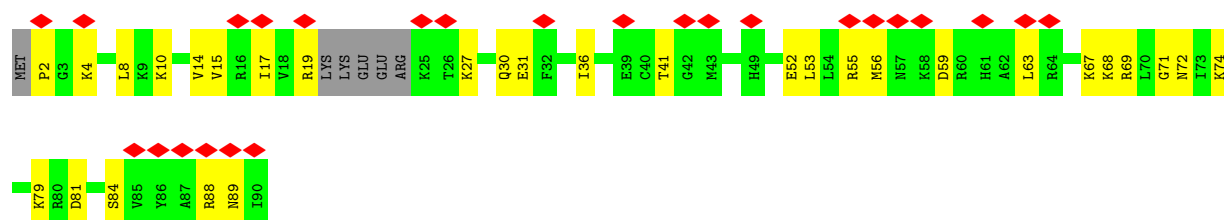




• Molecule 35: Ribosomal protein L29



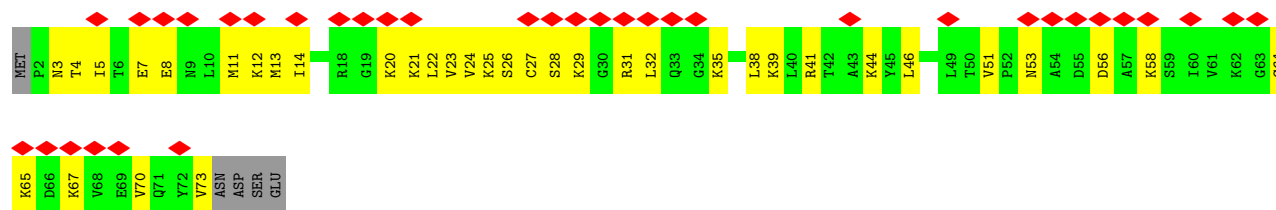
• Molecule 36: Ribosomal protein L36-1



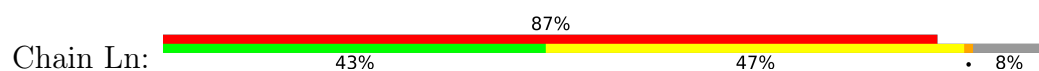
• Molecule 37: Ribosomal protein L37

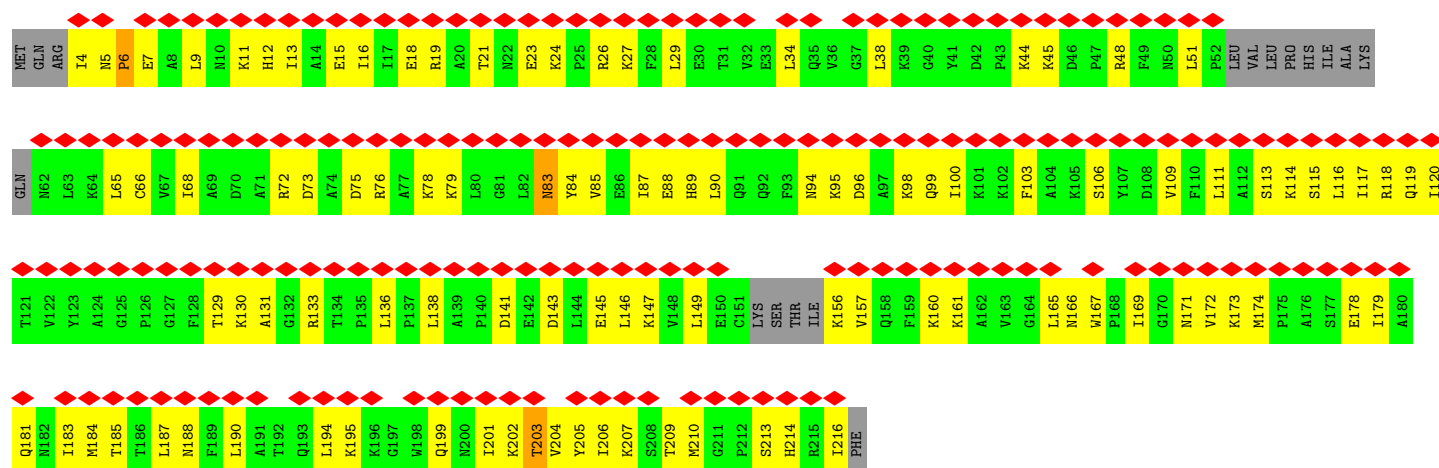


• Molecule 38: Ribosomal L38e

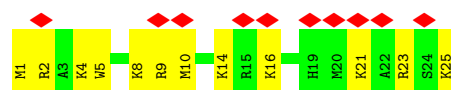
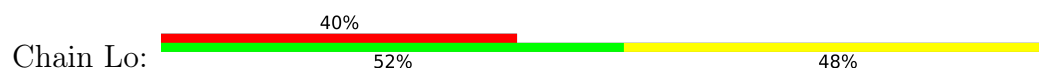


• Molecule 39: Ribosomal protein L10a

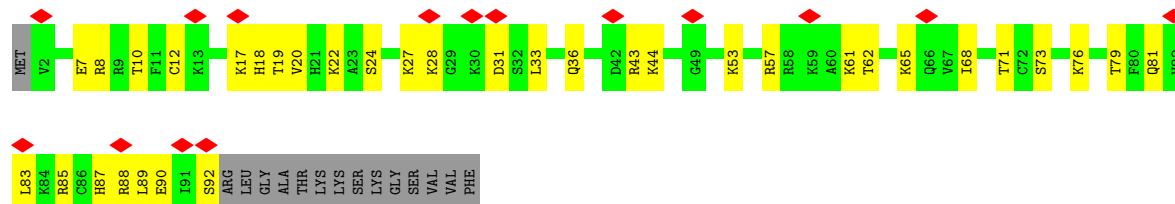




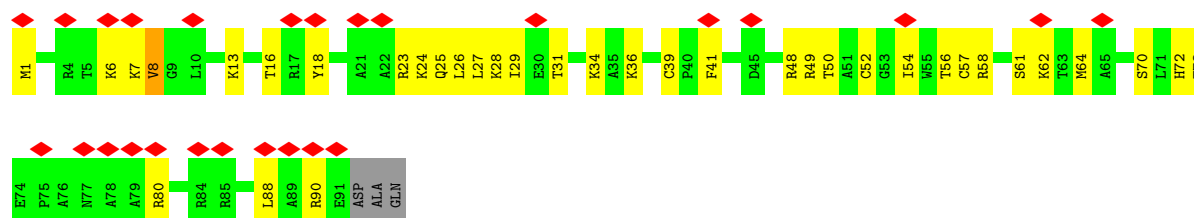
• Molecule 40: 60S ribosomal protein L41



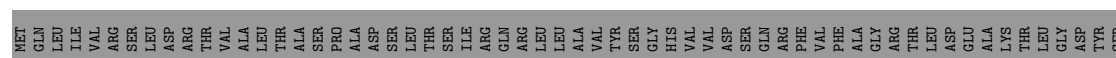
• Molecule 41: Ribosomal protein L44

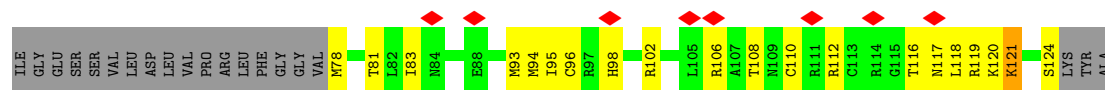


• Molecule 42: Ribosomal protein L37a

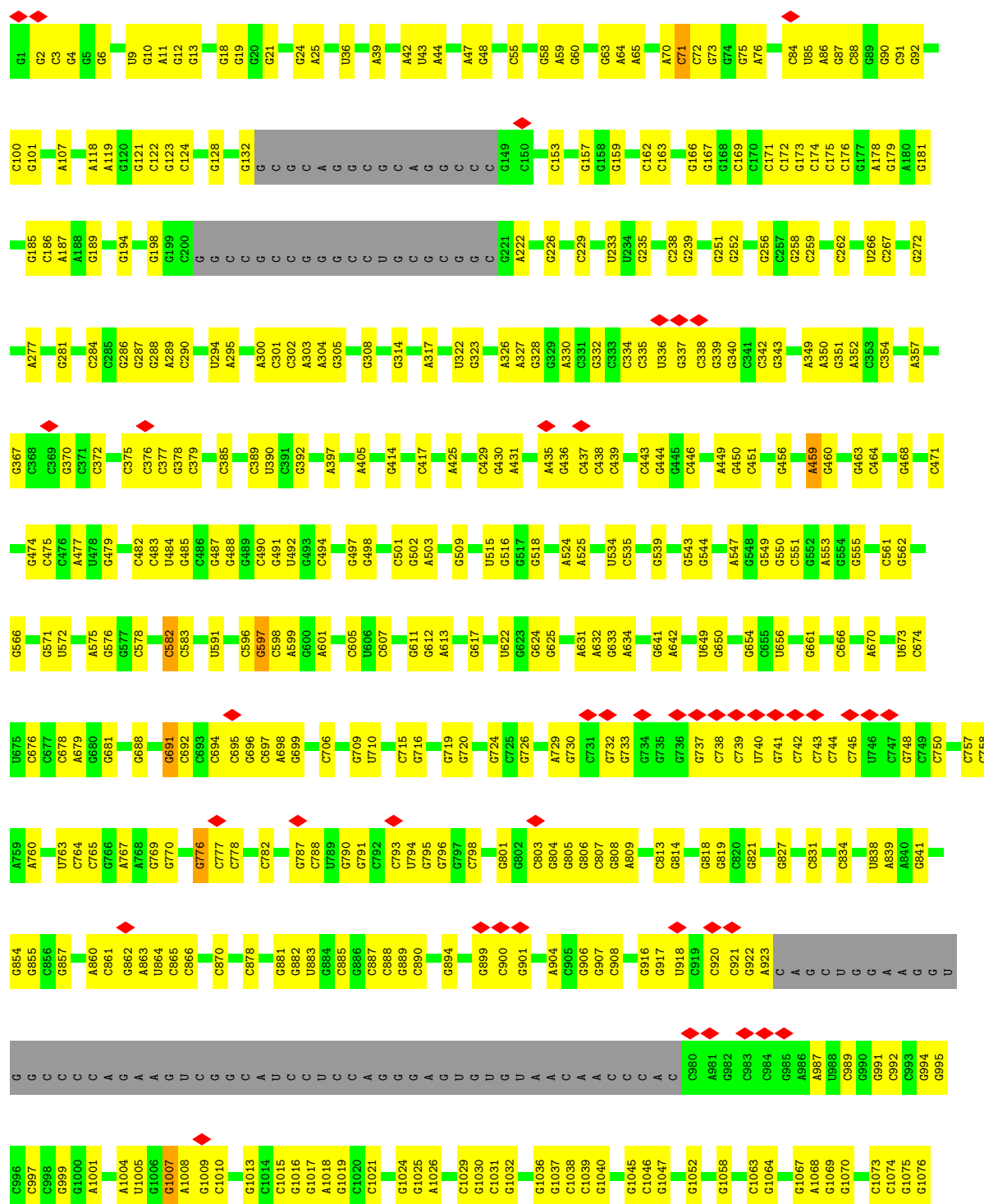


• Molecule 43: Ubiquitin/Ribosomal protein L40e

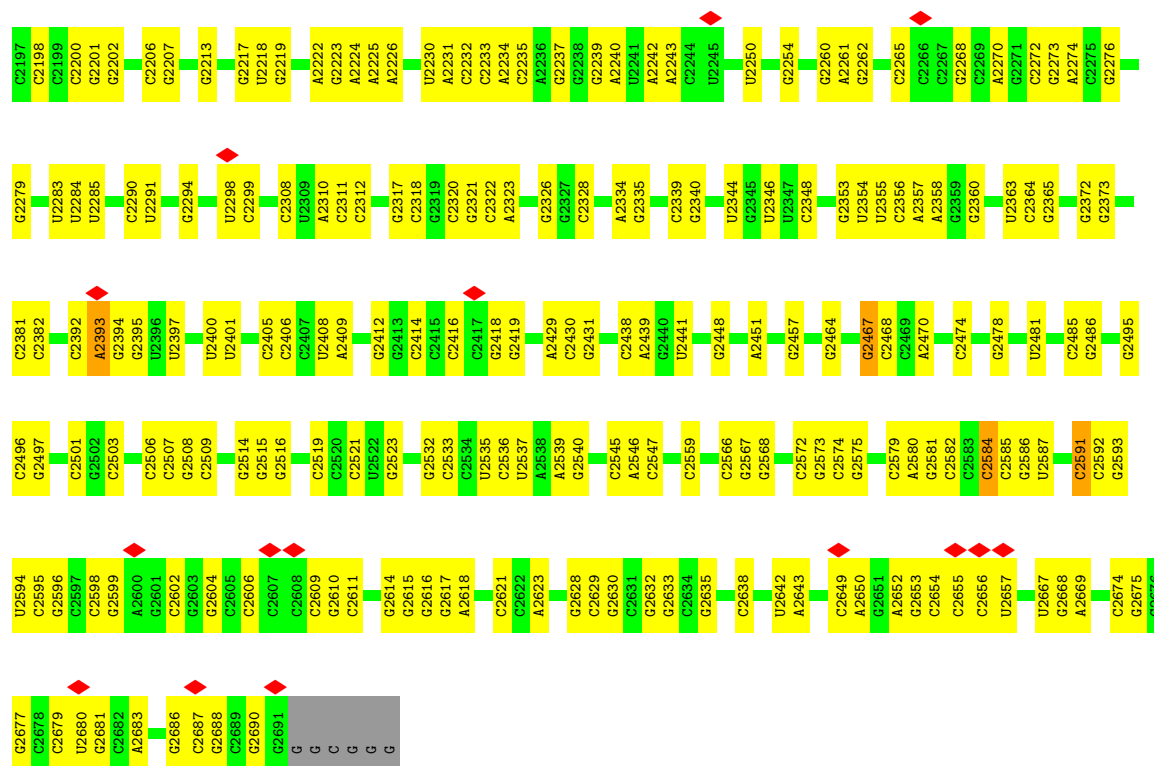




• Molecule 44: Large Subunit rRNA



G2103	A2104	C2105	G2106	U2107	C2108	C2109	C2012	C2013	A2017	C2018	C2019	C2022	C2023	G2027	G2030	G2031	G2032	A2033	G2034	G2039	G2048	C2049	G2050	C2051	G2052	A2059	C2060	A2061	C2062	G2065	A2066	C2067	C2068	C2150	C2151	G2152	U2153	G2157	C2161	C2168	C2177	C2184	G2185	A2186	U2187	U2190	U2191	C2192	G2193	C2195	C2196					
G1945	C1946	G1947	C1948	A1949	C1950	A1951	G1952	G1953	G1954	G1955	A1956	G1957	G1958	C1959	C1960	G1961	C1962	G1963	C1964	C1965	C1966	C1967	U1968	G1969	A1970	G1971	A1972	C1973	A1974	C1975	C1976	C1977	U1978	G1979	A1980	C1981	G1982	G1983	C1984	C1985	G1986	C1987	G1988	G1989	C1990	G1991	G1992	C1993	C1994	U1999	C2000	G2005	C2008	G2009	C2010	C2011
G1865	C1866	C1873	G1874	G1875	C1876	G1881	G1882	G1883	G1884	C1885	A1886	A1887	G1888	A1889	A1890	G1891	A1892	C1893	U1897	U1898	U1899	A1900	G1901	G1902	C1903	G1906	A1907	C1910	C1914	C1915	C1916	G1917	U1922	G1927	G1928	C1929	G1930	G1931	G1932	C1933	C1934	G1935	G1936	C1937	C1938	G1939	G1940	C1941	G1942	C1943	A1944					
C1693	C1694	A1695	C1696	C1697	G1698	C1702	G1706	A1707	G1711	C1715	G1716	G1717	C1718	G1727	G1728	U1729	A1730	A1731	A1732	C1733	G1734	G1735	G1736	G1737	G1738	G1739	G1740	G1741	A1744	C1745	U1748	G1749	A1750	G1751	U1752	C1753	U1754	U1757	G1760	G1761	G1764	A1767	A1768	A1769	U1770	U1774	C1775									
G1600	A1601	A1602	C1603	G1604	G1605	A1606	G1611	U1615	C1618	G1619	A1620	G1621	U1622	U1626	A1627	C1628	U1629	A1630	G1631	A1632	A1633	A1634	G1641	G1646	A1647	G1648	G1649	A1655	C1658	G1659	G1662	C1663	U1664	G1665	G1666	C1669	G1670	A1671	C1672	G1673	A1676	C1680	G1687	U1688	A1692											
C1510	G1511	G1512	C1513	A1514	G1515	C1516	G1517	A1518	A1519	G1524	C1525	G1530	C1536	G1537	G1538	C1550	A1553	A1554	C1558	A1562	A1563	A1564	A1565	G1566	G1567	A1568	G1569	U1570	G1571	C1575	U1576	G1577	A1578	C1579	G1580	C	G1581	C1582	G1585	C1586	G1590	U1591	C1592	A1593	G1594	A1595	A1596	C1597								
G1429	G1430	C1431	C1432	G1435	U1438	G1439	A1440	A1441	A1442	G1448	G1449	G1452	G1453	G1454	C1455	C1456	C1460	C1464	C1467	G1468	U1469	A1470	C1471	C1472	G1473	A1474	C1475	C1476	G1477	A1478	G1479	G1480	C1481	G1482	G1483	G1484	A1485	C1486	C1489	G1490	G1491	G1492	C1495	C1498	A1499	G1507	C1508	G1509								
A1328	C1329	G1330	G1337	G1338	G1339	C1345	G1346	G1349	C1350	G1355	G1361	G1365	C1366	G1380	A1381	C1382	G1383	U1386	U1387	G1388	C1389	G1390	C1391	A1394	G1395	A1396	G1401	G1406	G1407	G1410	C1411	G1412	G1413	A1414	C	C	C1417	C1418	G1419	C1420	G1421	C1422	G1423	U1424	C1427	C1428										
C1249	C1250	A1171	C1251	G1252	C1253	G1256	U1257	C1258	G1259	A1260	A1261	C1262	G1263	G1264	G1265	G1266	G1272	C1273	G1274	G1275	A1276	G1277	A1278	C1279	U1280	G1284	G1285	A1286	G1290	C1291	C1296	C1297	C1298	G1299	C1300	G1301	C1306	G1307	C1308	C1309	C1310	G1311	C1312	C1313	C1314	C1317	G1318	A1322	C1323	G1326	C1327					
G1169	G1170	A1171	C1251	G1252	A1173	U1178	U1179	C1180	C1181	G1185	C1186	G1187	G1191	C1192	G1195	A1106	G1109	U1115	G1116	G1117	G1203	G1204	G1205	U1206	G1207	G1212	C1215	U1126	C1217	U1217	G1220	C1221	G1222	G1225	G1226	A1230	A1231	G1232	A1233	G1236	G1237	G1238	A1239	A1240	G1241	G1242	G1243	G1244	C1245	G	U	G1248				
G1077	G1078	G1079	C1080	G1081	G1084	G1087	G1088	C1089	G1095	G1096	C1100	G1105	A1106	G1109	U1115	G1116	G1117	C1120	A1121	G1122	C1125	U1126	C1127	G1132	C1133	A1134	G1135	U1136	C1139	C1140	G1141	G1142	U1143	A1144	C1150	G1151	C1152	C1153	C1154	G1159	G1164	A1165	G1166	G1167	G1168											

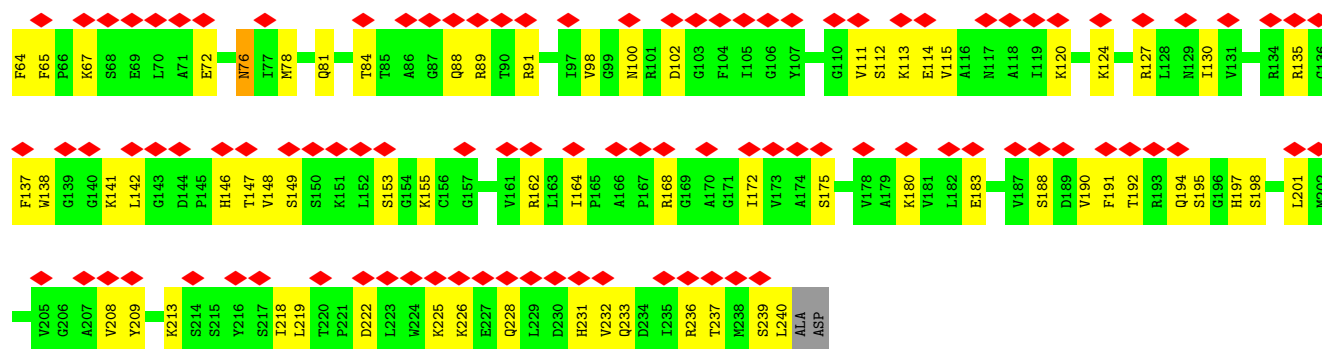


• Molecule 45: 40S ribosomal protein SA

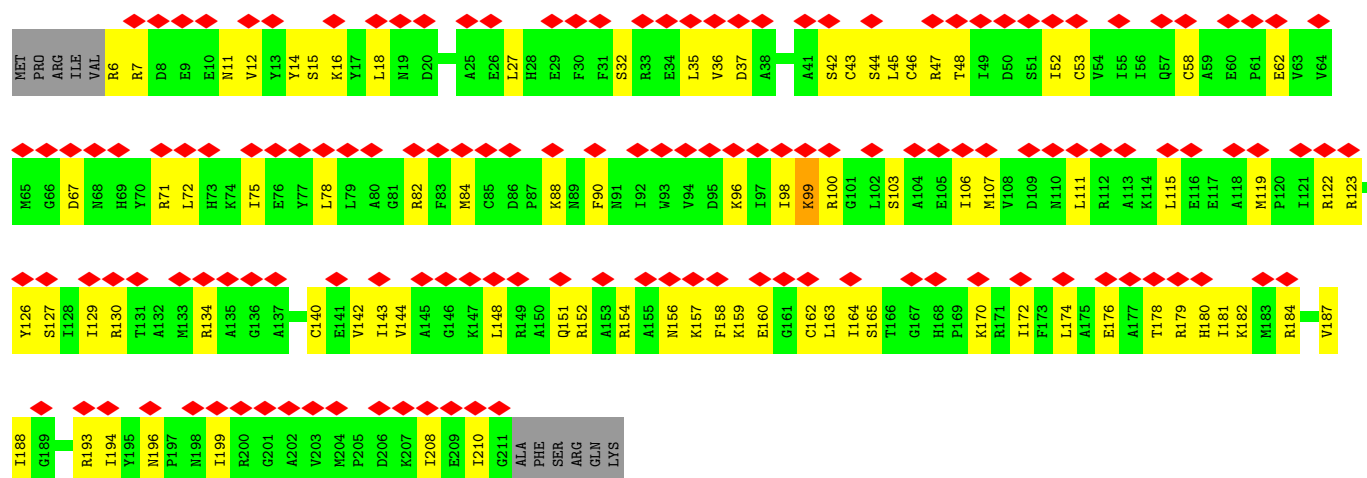


• Molecule 46: Ribosomal protein S2

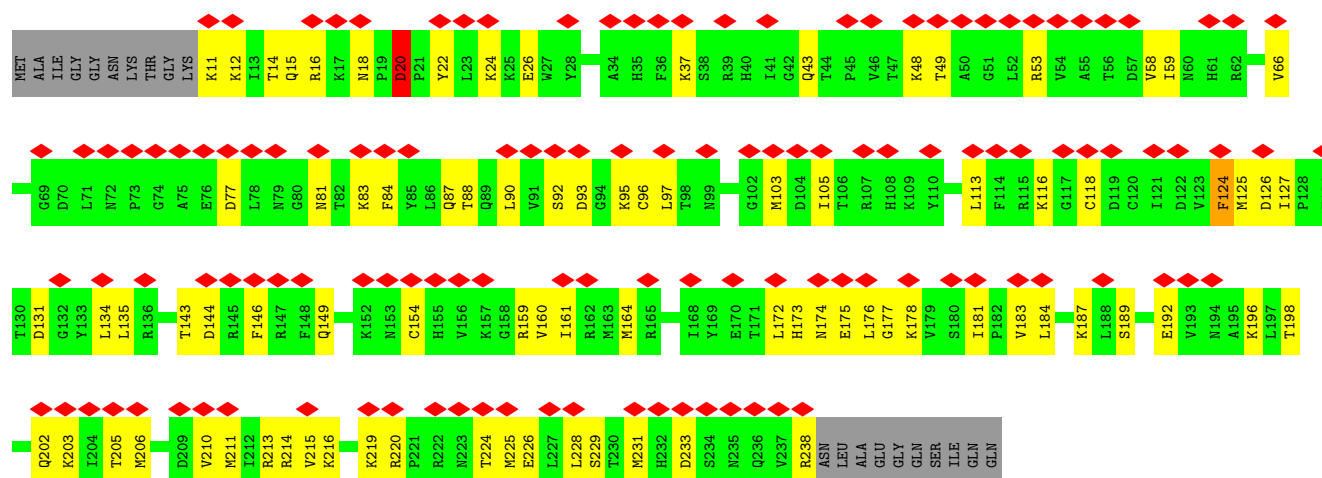




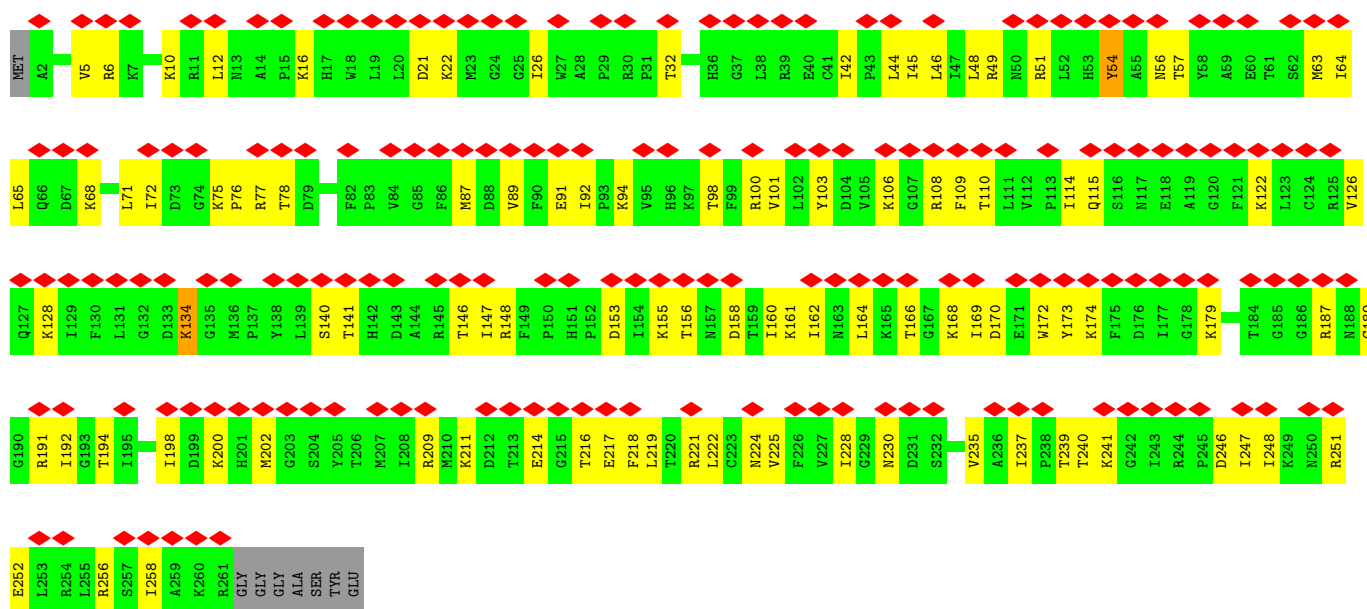
• Molecule 47: Ribosomal protein S3



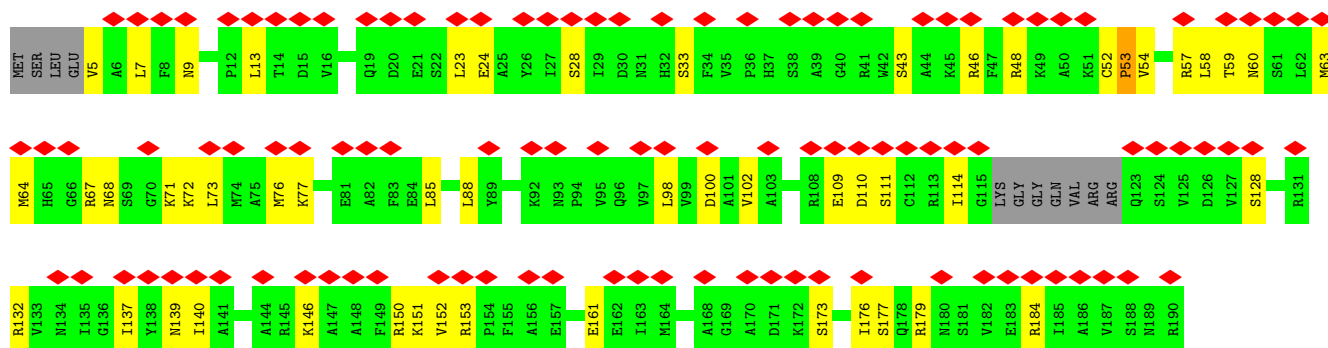
• Molecule 48: 40S ribosomal protein S3a



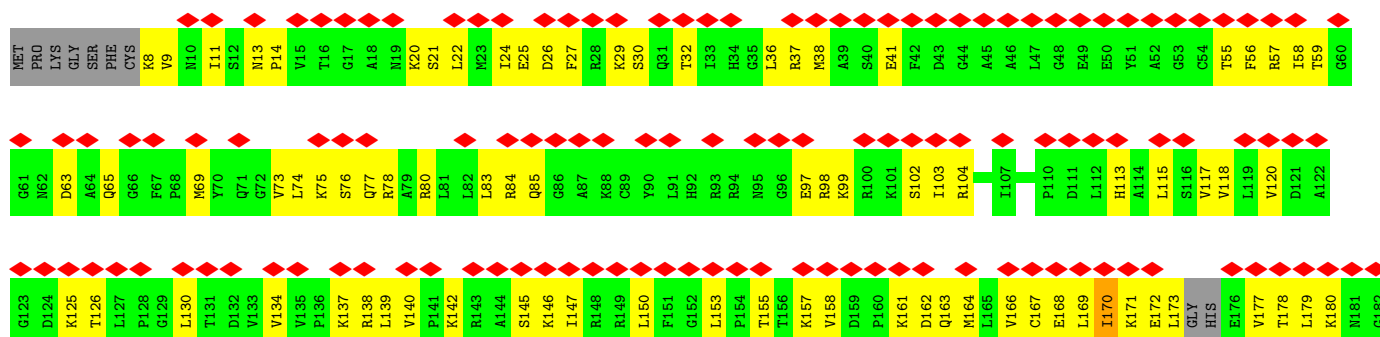
• Molecule 49: 40S ribosomal protein S4

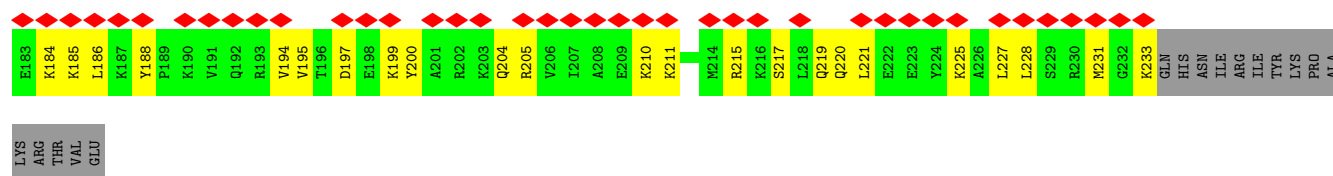


• Molecule 50: Ribosomal protein S5

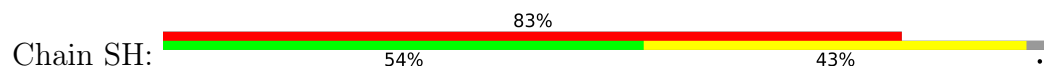


• Molecule 51: 40S ribosomal protein S6

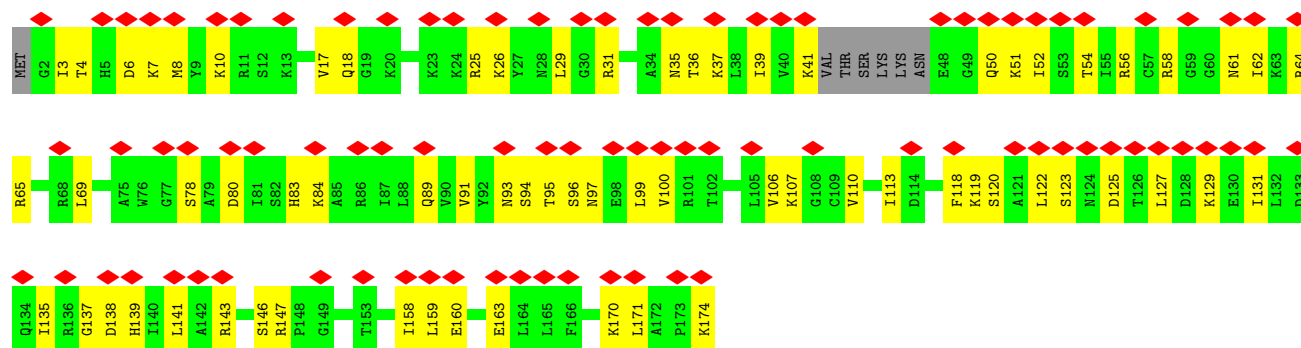




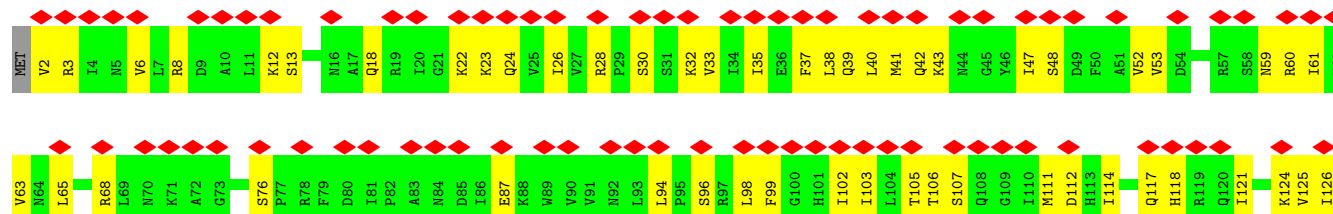
• Molecule 52: 40S ribosomal protein S7

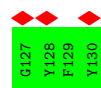


• Molecule 53: 40S ribosomal protein S8

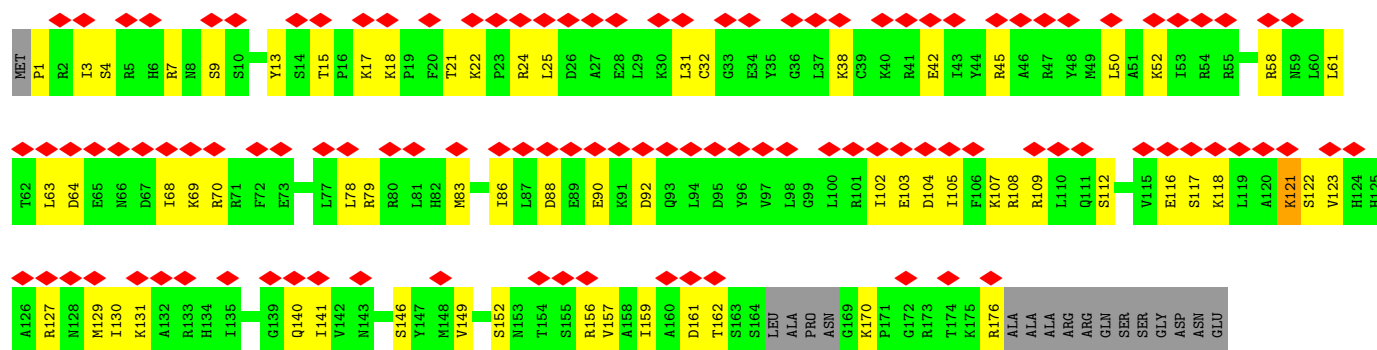


• Molecule 54: Ribosomal protein S15A

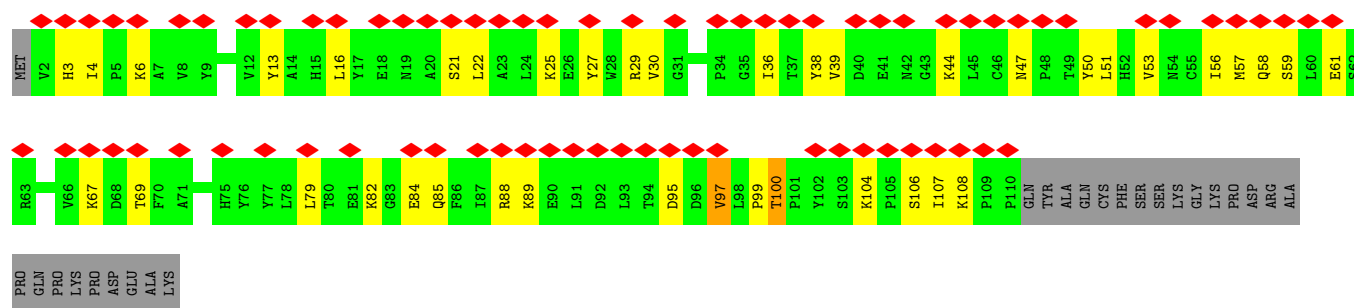




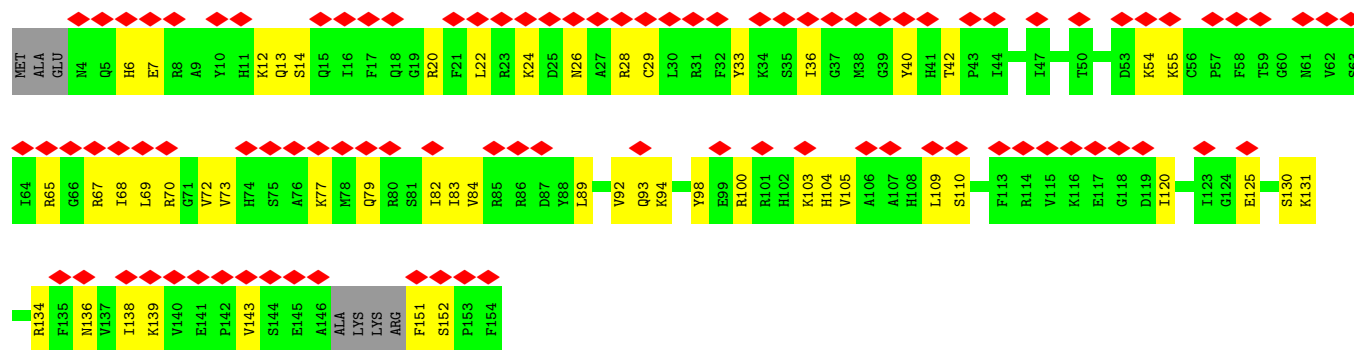
• Molecule 55: Ribosomal protein S9



• Molecule 56: Ribosomal protein S10B

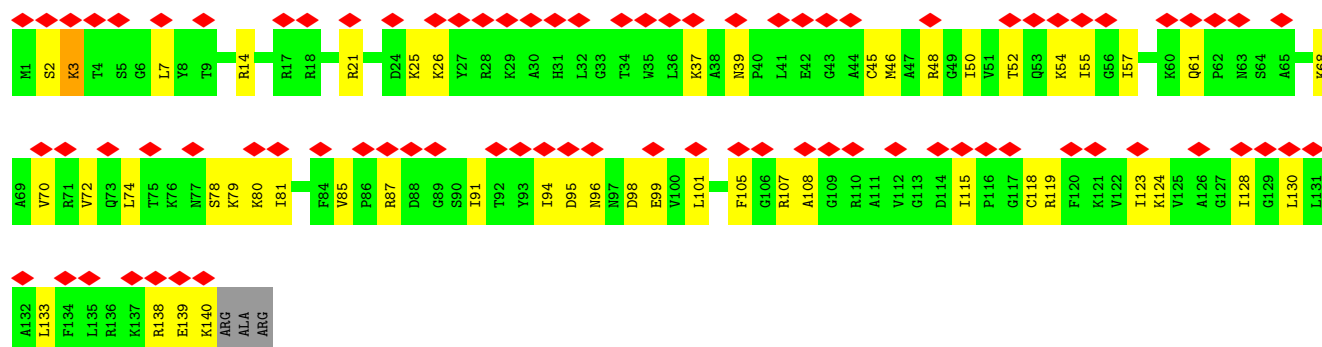


• Molecule 57: Ribosomal protein S11

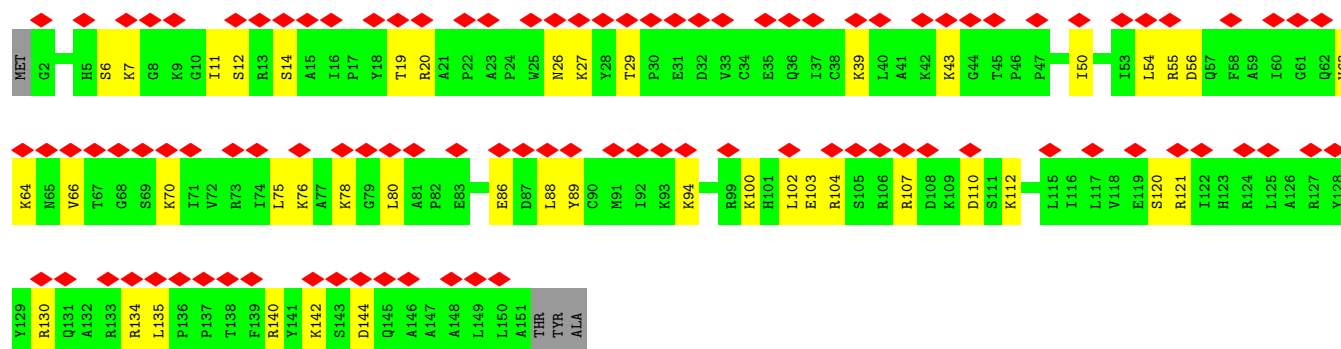


• Molecule 58: SSU ribosomal protein S12P

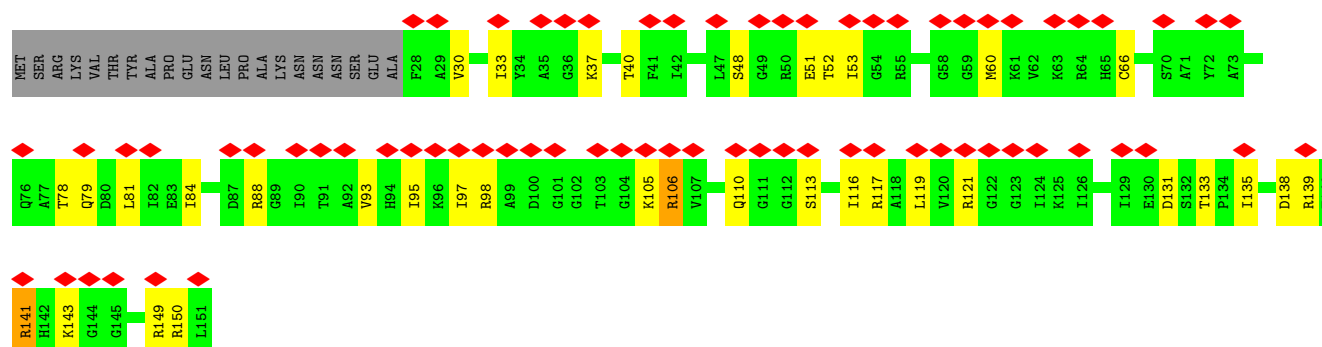




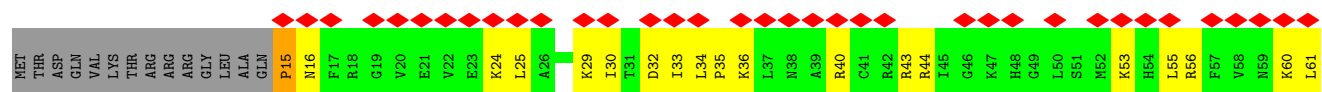
• Molecule 59: Ribosomal protein S13

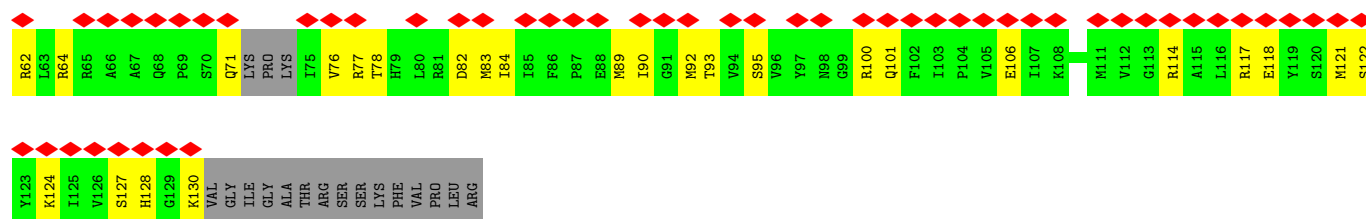


• Molecule 60: Ribosomal protein S14

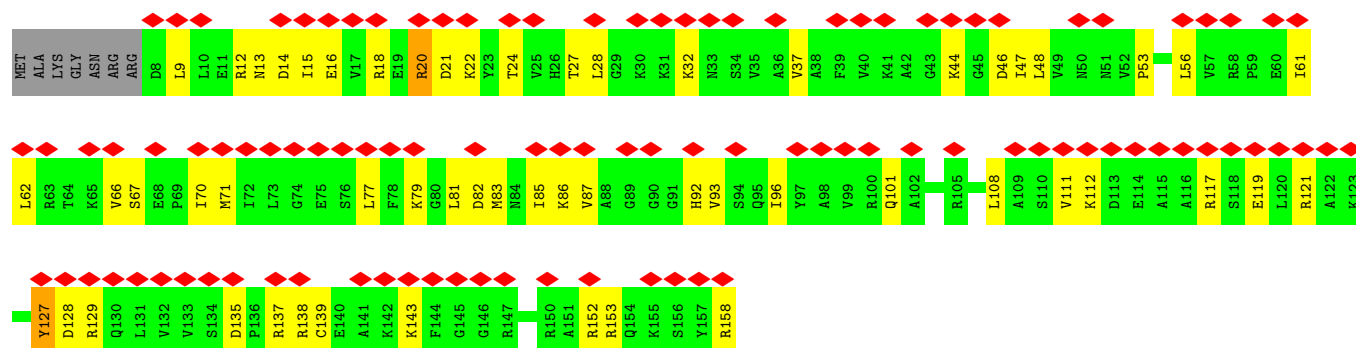


• Molecule 61: Ribosomal protein S15

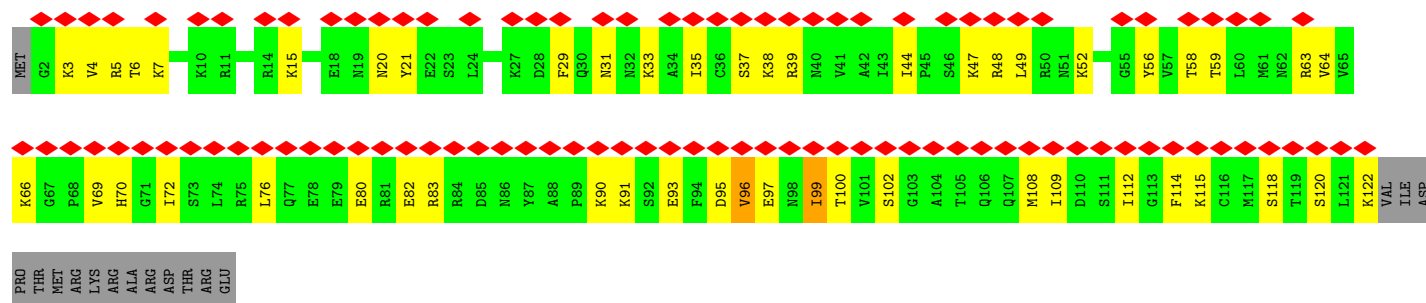
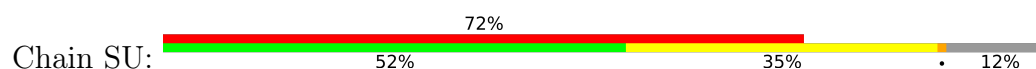




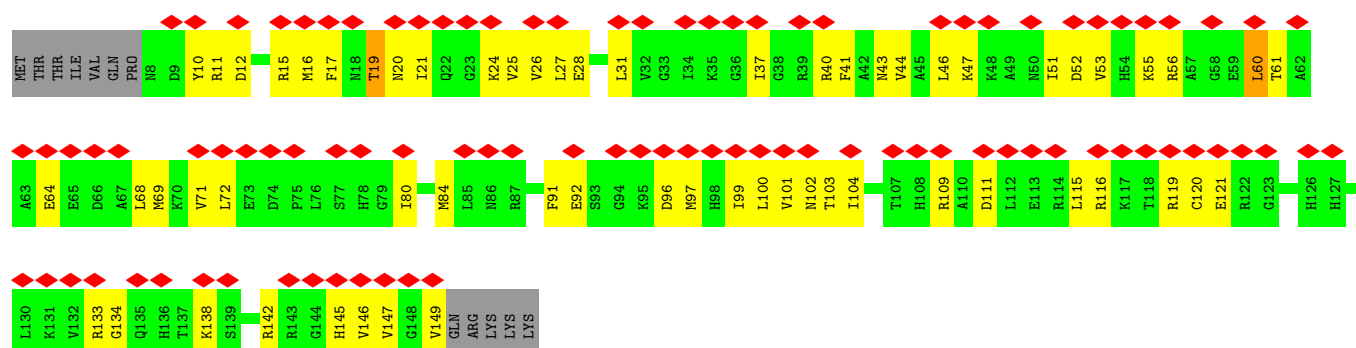
• Molecule 62: Ribosomal protein S16



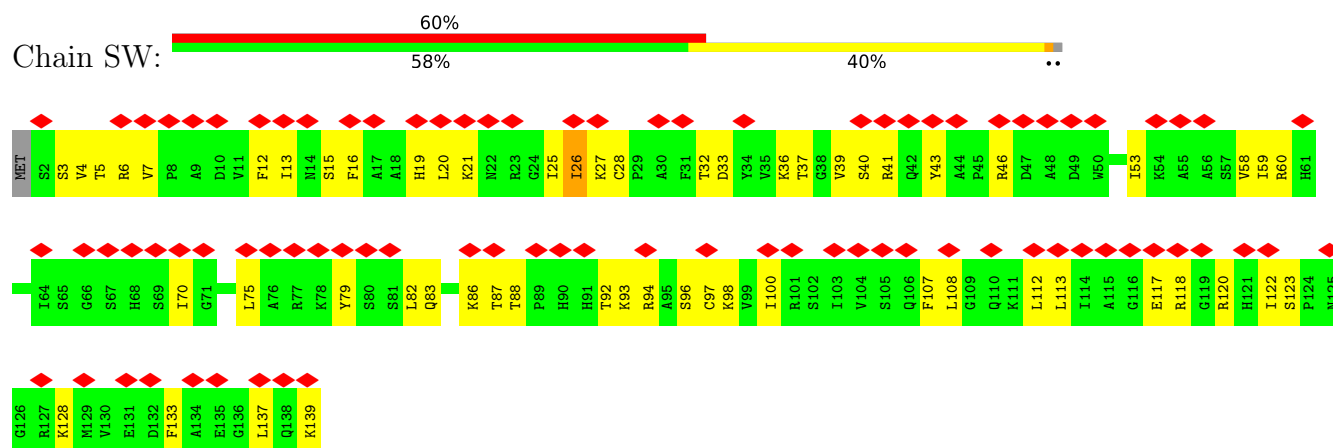
• Molecule 63: Ribosomal protein S17



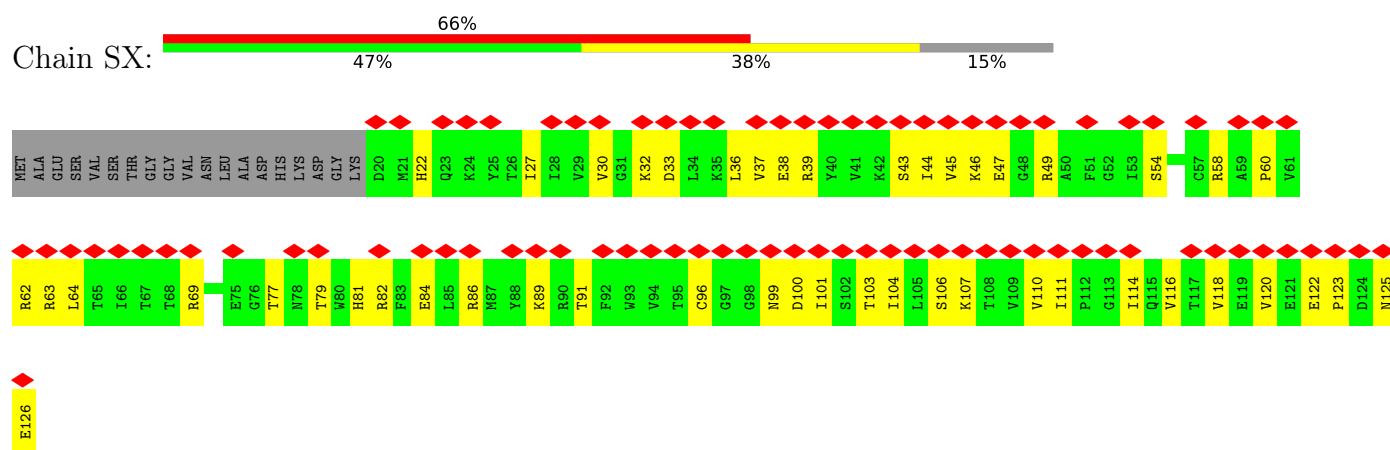
• Molecule 64: Ribosomal protein S18



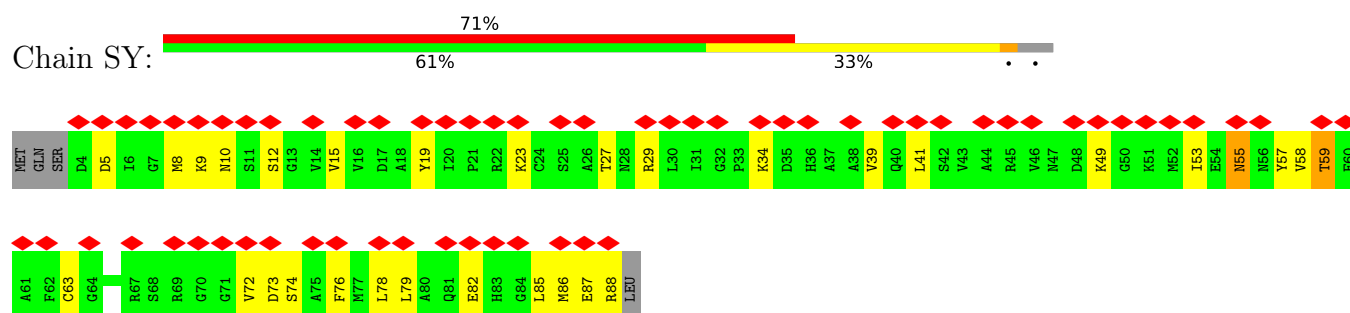
- Molecule 65: Ribosomal protein S19e



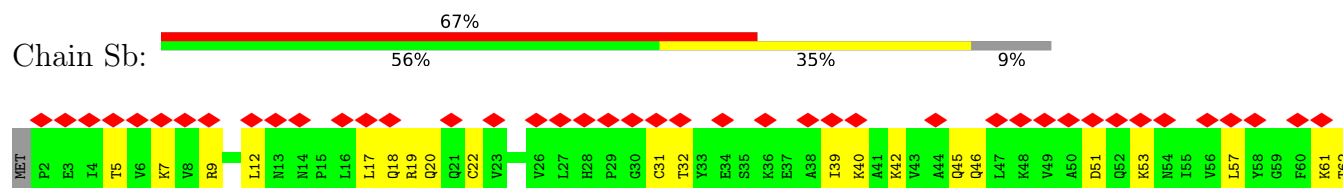
- Molecule 66: Ribosomal protein S20



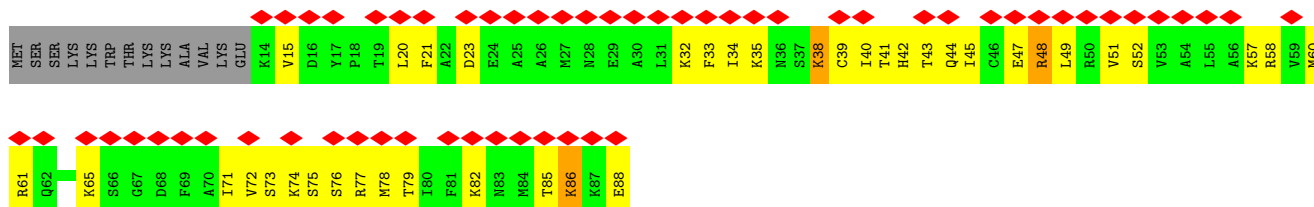
- Molecule 67: 40S ribosomal protein S21



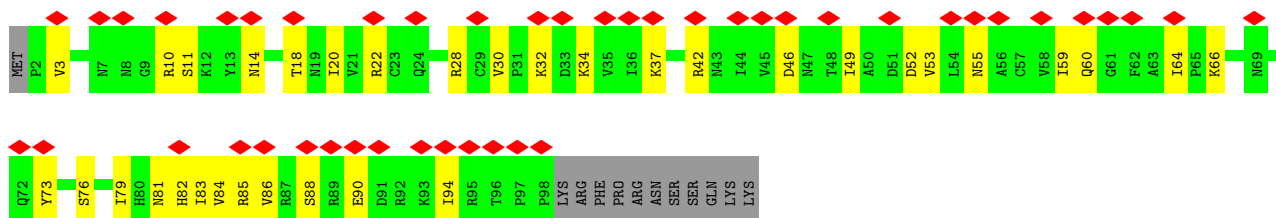
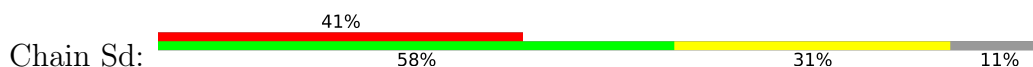
- Molecule 68: Ribosomal protein S24



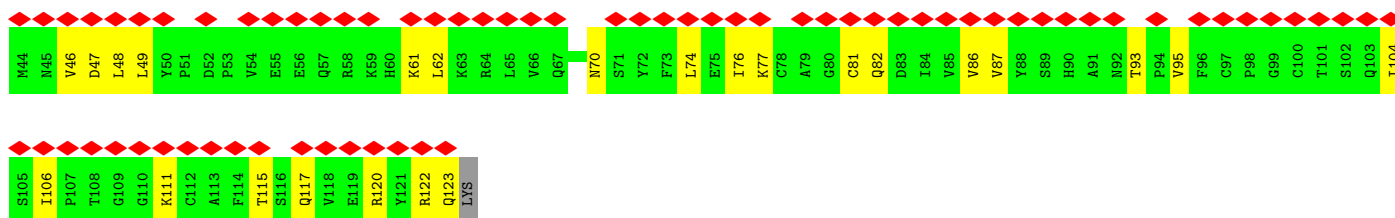
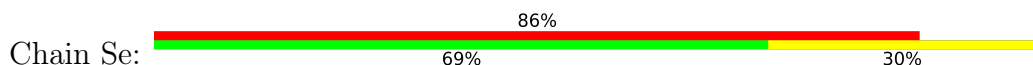
- Molecule 69: 40S ribosomal protein S25



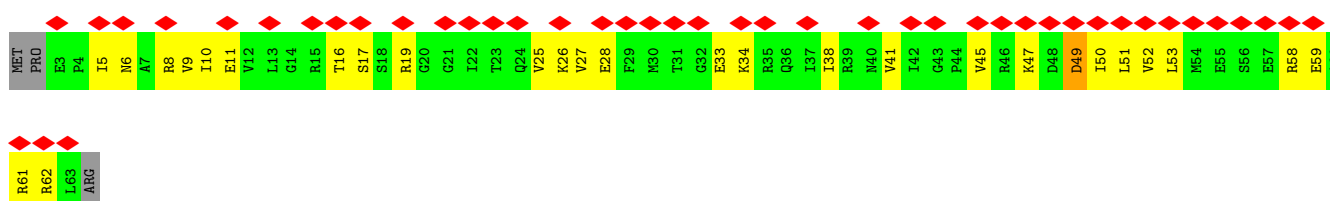
- Molecule 70: 40S ribosomal protein S26



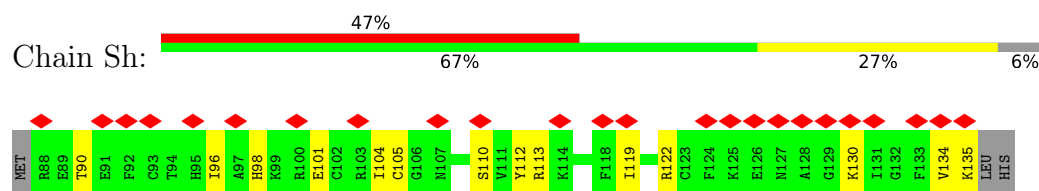
- Molecule 71: Ribosomal protein S27



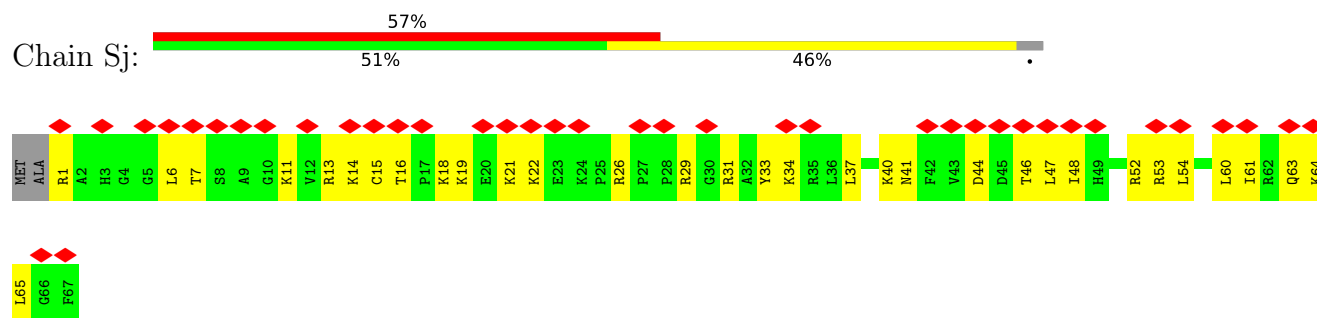
- Molecule 72: Ribosomal protein S28



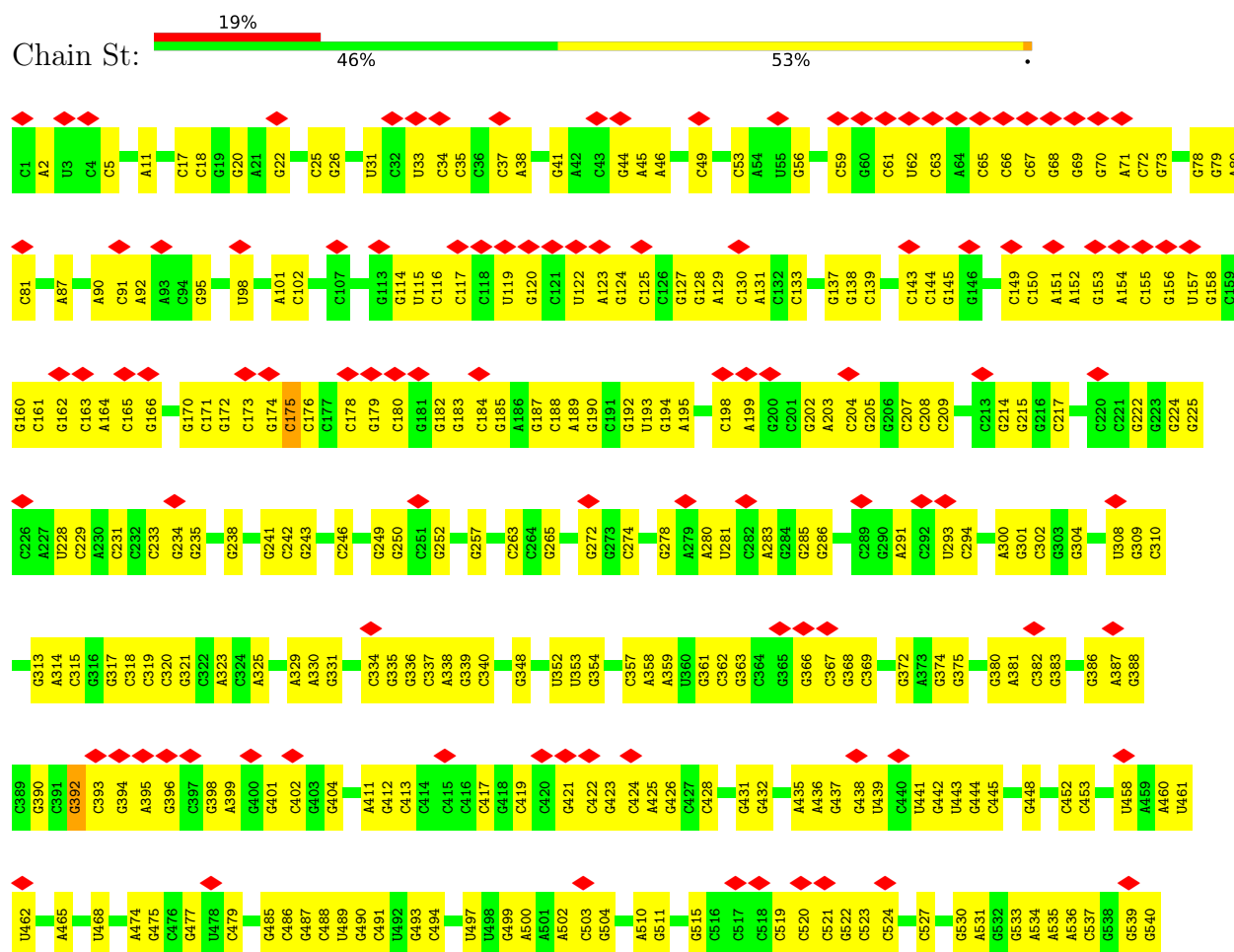
- Molecule 73: Ribosomal protein S29A



- Molecule 74: 40S ribosomal protein S30

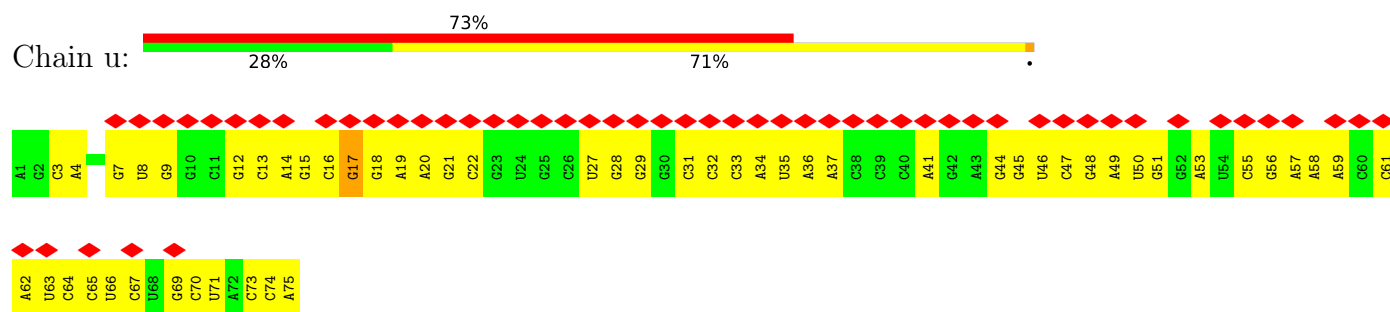


- Molecule 75: Small Subunit rRNA

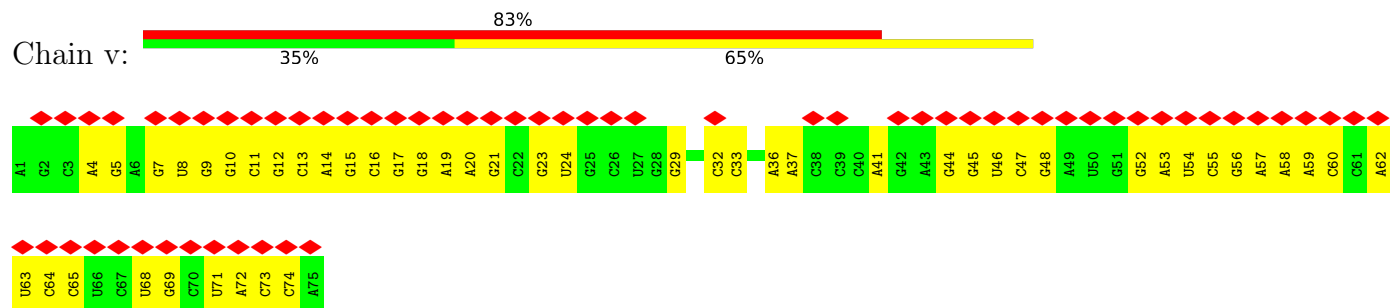




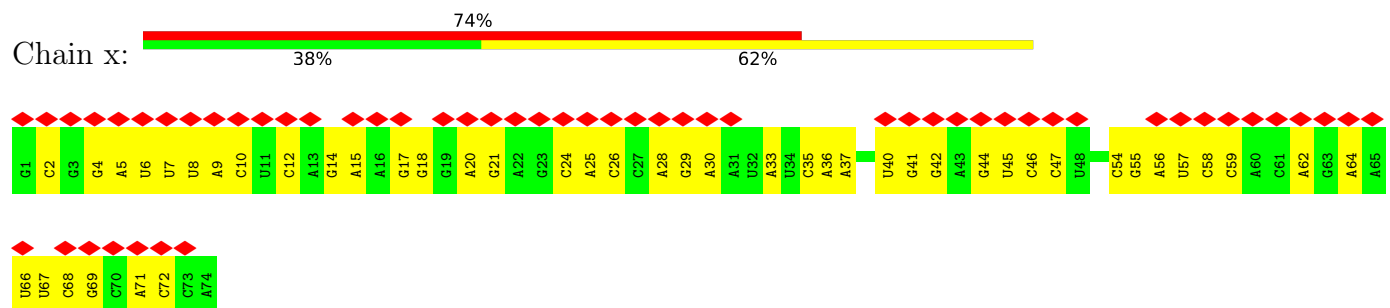
- Molecule 76: tRNA



- 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 [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	LA	0.59	0/1855	0.85	0/2494
2	LB	0.57	0/3030	0.85	2/4091 (0.0%)
3	LC	0.59	0/2463	0.83	1/3342 (0.0%)
4	LD	0.56	0/3345	0.83	0/5217
5	LE	0.57	0/2773	0.83	0/4322
6	LF	0.57	0/2368	0.83	0/3177
7	LG	0.52	0/450	0.81	1/601 (0.2%)
8	LH	0.57	0/1783	0.82	0/2403
9	LI	0.58	0/1494	0.83	0/2019
10	LJ	0.59	0/1479	0.84	0/1997
11	LK	0.58	0/1645	0.82	0/2202
12	LL	0.58	0/1350	0.83	1/1813 (0.1%)
13	LM	0.59	0/1582	0.80	0/2118
14	LN	0.56	0/1004	0.82	0/1344
15	LO	0.58	0/1742	0.83	1/2334 (0.0%)
16	LP	0.57	0/1570	0.83	0/2105
17	LQ	0.59	0/1257	0.87	1/1681 (0.1%)
18	LR	0.60	0/1425	0.83	0/1907
19	LS	0.56	0/1564	0.78	0/2069
20	LT	0.57	0/1457	0.84	1/1957 (0.1%)
21	LU	0.55	0/1240	0.87	1/1665 (0.1%)
22	LV	0.58	0/876	0.84	0/1177
23	LW	0.59	0/1035	0.83	1/1396 (0.1%)
24	LX	0.58	0/526	0.99	2/700 (0.3%)
25	LY	0.58	0/933	0.82	0/1262
26	LZ	0.60	0/1091	0.82	0/1454
27	La	0.59	0/985	0.86	0/1328
28	Lb	0.59	0/1208	0.86	1/1615 (0.1%)
29	Lc	0.59	0/463	0.90	1/612 (0.2%)
30	Ld	0.61	0/745	0.84	1/1008 (0.1%)
31	Le	0.57	0/803	0.77	0/1077
32	Lf	0.58	0/1055	0.80	0/1407
33	Lg	0.58	0/793	0.90	1/1062 (0.1%)
34	Lh	0.59	0/849	0.87	0/1141

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Li	0.55	0/968	0.79	0/1286
36	Lj	0.56	0/693	0.86	0/919
37	Lk	0.61	0/705	0.85	0/934
38	Ll	0.59	0/562	0.86	0/749
39	Ln	0.63	0/1621	0.90	0/2183
40	Lo	0.50	0/229	0.79	0/291
41	Lp	0.57	0/759	0.83	0/1004
42	Lq	0.57	0/717	0.92	0/955
43	Ls	0.58	0/392	0.93	0/522
44	Lt	0.60	0/62213	0.87	33/97094 (0.0%)
45	SA	0.59	0/1587	0.85	0/2156
46	SB	0.62	0/1671	0.85	0/2253
47	SC	0.60	0/1662	0.82	1/2231 (0.0%)
48	SD	0.58	0/1882	0.85	2/2535 (0.1%)
49	SE	0.60	0/2131	0.85	0/2874
50	SF	0.63	0/1409	0.86	0/1896
51	SG	0.61	0/1789	0.85	0/2390
52	SH	0.62	0/1508	0.82	0/2032
53	SI	0.59	0/1331	0.86	0/1784
54	SJ	0.60	0/1048	0.83	0/1412
55	SK	0.60	0/1413	0.85	1/1886 (0.1%)
56	SL	0.59	0/917	0.83	0/1250
57	SM	0.59	0/1245	0.84	1/1666 (0.1%)
58	SO	0.58	0/1103	0.78	0/1477
59	SP	0.59	0/1215	0.79	0/1632
60	SQ	0.62	0/923	0.87	0/1239
61	SR	0.61	0/934	0.88	1/1247 (0.1%)
62	ST	0.61	0/1192	0.84	0/1594
63	SU	0.62	0/973	0.84	0/1300
64	SV	0.59	0/1140	0.93	1/1529 (0.1%)
65	SW	0.61	0/1104	0.84	0/1484
66	SX	0.61	0/869	0.84	2/1173 (0.2%)
67	SY	0.64	0/650	0.91	2/872 (0.2%)
68	Sb	0.59	0/967	0.87	0/1294
69	Sc	0.59	0/603	0.86	0/802
70	Sd	0.59	0/800	0.85	0/1077
71	Se	0.63	0/643	0.82	0/871
72	Sg	0.63	0/488	0.83	1/652 (0.2%)
73	Sh	0.57	0/409	0.83	0/542
74	Sj	0.58	0/553	0.83	0/736
75	St	0.61	0/34858	0.88	11/54401 (0.0%)
76	u	0.60	0/1795	0.90	2/2798 (0.1%)
76	v	0.59	0/1795	0.83	0/2798

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	x	0.57	0/1771	0.80	0/2758
78	y	0.54	0/270	0.93	1/419 (0.2%)
All	All	0.60	0/191745	0.86	75/281094 (0.0%)

There are no bond length outliers.

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	Lt	1252	G	C2'-C3'-O3'	8.39	127.96	109.50
44	Lt	691	G	C2'-C3'-O3'	8.07	127.25	109.50
57	SM	98	TYR	CB-CA-C	-8.05	94.31	110.40
29	Lc	50	ASP	CB-CA-C	7.91	126.22	110.40
44	Lt	1448	G	C2'-C3'-O3'	7.68	126.39	109.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	239/251 (95%)	223 (93%)	15 (6%)	1 (0%)	30	68
2	LB	370/379 (98%)	349 (94%)	18 (5%)	3 (1%)	16	55
3	LC	307/316 (97%)	294 (96%)	13 (4%)	0	100	100
6	LF	287/297 (97%)	270 (94%)	15 (5%)	2 (1%)	19	57
7	LG	48/51 (94%)	44 (92%)	3 (6%)	1 (2%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	LH	215/235 (92%)	206 (96%)	8 (4%)	1 (0%)	25	64
9	LI	179/225 (80%)	166 (93%)	9 (5%)	4 (2%)	5	29
10	LJ	182/185 (98%)	165 (91%)	16 (9%)	1 (0%)	25	64
11	LK	193/210 (92%)	185 (96%)	7 (4%)	1 (0%)	25	64
12	LL	163/173 (94%)	155 (95%)	7 (4%)	1 (1%)	22	60
13	LM	191/234 (82%)	182 (95%)	7 (4%)	2 (1%)	13	49
14	LN	122/131 (93%)	117 (96%)	4 (3%)	1 (1%)	16	55
15	LO	199/204 (98%)	187 (94%)	12 (6%)	0	100	100
16	LP	185/197 (94%)	173 (94%)	11 (6%)	1 (0%)	25	64
17	LQ	151/164 (92%)	144 (95%)	7 (5%)	0	100	100
18	LR	176/179 (98%)	169 (96%)	6 (3%)	1 (1%)	22	60
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
25	LY	111/141 (79%)	105 (95%)	4 (4%)	2 (2%)	7	35
26	LZ	131/135 (97%)	128 (98%)	3 (2%)	0	100	100
27	La	117/135 (87%)	110 (94%)	5 (4%)	2 (2%)	7	37
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%)	13	49
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%)	10	43
37	Lk	83/89 (93%)	76 (92%)	6 (7%)	1 (1%)	11	44
38	Ll	70/77 (91%)	67 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	Ln	194/217 (89%)	172 (89%)	15 (8%)	7 (4%)	3	20
40	Lo	23/25 (92%)	23 (100%)	0	0	100	100
41	Lp	89/106 (84%)	86 (97%)	2 (2%)	1 (1%)	12	47
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%)	13	49
46	SB	211/242 (87%)	188 (89%)	21 (10%)	2 (1%)	14	51
47	SC	204/217 (94%)	188 (92%)	14 (7%)	2 (1%)	13	49
48	SD	226/248 (91%)	210 (93%)	13 (6%)	3 (1%)	10	43
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	37
51	SG	220/248 (89%)	207 (94%)	10 (4%)	3 (1%)	9	41
52	SH	182/190 (96%)	162 (89%)	19 (10%)	1 (0%)	25	64
53	SI	163/174 (94%)	150 (92%)	12 (7%)	1 (1%)	22	60
54	SJ	127/130 (98%)	113 (89%)	13 (10%)	1 (1%)	16	55
55	SK	168/189 (89%)	157 (94%)	10 (6%)	1 (1%)	22	60
56	SL	107/134 (80%)	88 (82%)	16 (15%)	3 (3%)	4	24
57	SM	143/154 (93%)	133 (93%)	9 (6%)	1 (1%)	19	57
58	SO	138/143 (96%)	133 (96%)	3 (2%)	2 (1%)	9	41
59	SP	148/154 (96%)	143 (97%)	4 (3%)	1 (1%)	19	57
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	37
64	SV	140/154 (91%)	119 (85%)	14 (10%)	7 (5%)	1	16
65	SW	136/139 (98%)	131 (96%)	4 (3%)	1 (1%)	19	57
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	55
69	Sc	73/88 (83%)	63 (86%)	6 (8%)	4 (6%)	1	14
70	Sd	95/109 (87%)	83 (87%)	11 (12%)	1 (1%)	12	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	16	49

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%)	126 (68%)	59 (32%)	0	2
2	LB	309/313 (99%)	194 (63%)	115 (37%)	0	0
3	LC	257/263 (98%)	166 (65%)	91 (35%)	0	1
6	LF	235/242 (97%)	142 (60%)	93 (40%)	0	0
7	LG	47/48 (98%)	31 (66%)	16 (34%)	0	1
8	LH	186/204 (91%)	125 (67%)	61 (33%)	0	2
9	LI	163/198 (82%)	106 (65%)	57 (35%)	0	1
10	LJ	163/164 (99%)	99 (61%)	64 (39%)	0	0
11	LK	167/177 (94%)	105 (63%)	62 (37%)	0	0
12	LL	141/149 (95%)	83 (59%)	58 (41%)	0	0
13	LM	165/197 (84%)	98 (59%)	67 (41%)	0	0
14	LN	106/111 (96%)	64 (60%)	42 (40%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
15	LO	174/175 (99%)	113 (65%)	61 (35%)	0	1	
16	LP	158/165 (96%)	108 (68%)	50 (32%)	0	2	
17	LQ	130/139 (94%)	85 (65%)	45 (35%)	0	1	
18	LR	154/155 (99%)	93 (60%)	61 (40%)	0	0	
19	LS	158/167 (95%)	99 (63%)	59 (37%)	0	0	
20	LT	151/154 (98%)	100 (66%)	51 (34%)	0	1	
21	LU	125/133 (94%)	78 (62%)	47 (38%)	0	0	
22	LV	93/110 (84%)	56 (60%)	37 (40%)	0	0	
23	LW	108/114 (95%)	70 (65%)	38 (35%)	0	1	
24	LX	58/174 (33%)	34 (59%)	24 (41%)	0	0	
25	LY	102/123 (83%)	63 (62%)	39 (38%)	0	0	
26	LZ	114/115 (99%)	76 (67%)	38 (33%)	0	1	
27	La	106/119 (89%)	60 (57%)	46 (43%)	0	0	
28	Lb	124/127 (98%)	82 (66%)	42 (34%)	0	1	
29	Lc	50/57 (88%)	30 (60%)	20 (40%)	0	0	
30	Ld	83/92 (90%)	46 (55%)	37 (45%)	0	0	
31	Le	85/92 (92%)	50 (59%)	35 (41%)	0	0	
32	Lf	111/120 (92%)	71 (64%)	40 (36%)	0	1	
33	Lg	82/103 (80%)	51 (62%)	31 (38%)	0	0	
34	Lh	90/100 (90%)	63 (70%)	27 (30%)	0	2	
35	Li	102/107 (95%)	64 (63%)	38 (37%)	0	0	
36	Lj	72/78 (92%)	43 (60%)	29 (40%)	0	0	
37	Lk	71/74 (96%)	47 (66%)	24 (34%)	0	1	
38	Ll	63/68 (93%)	27 (43%)	36 (57%)	0	0	
39	Ln	173/189 (92%)	71 (41%)	102 (59%)	0	0	
40	Lo	22/22 (100%)	10 (46%)	12 (54%)	0	0	
41	Lp	81/93 (87%)	47 (58%)	34 (42%)	0	0	
42	Lq	71/73 (97%)	36 (51%)	35 (49%)	0	0	
43	Ls	43/110 (39%)	24 (56%)	19 (44%)	0	0	
45	SA	169/217 (78%)	107 (63%)	62 (37%)	0	1	
46	SB	177/201 (88%)	96 (54%)	81 (46%)	0	0	

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	SC	172/182 (94%)	89 (52%)	83 (48%)	0	0
48	SD	206/220 (94%)	122 (59%)	84 (41%)	0	0
49	SE	228/232 (98%)	130 (57%)	98 (43%)	0	0
50	SF	148/157 (94%)	98 (66%)	50 (34%)	0	1
51	SG	192/213 (90%)	90 (47%)	102 (53%)	0	0
52	SH	165/170 (97%)	84 (51%)	81 (49%)	0	0
53	SI	141/148 (95%)	73 (52%)	68 (48%)	0	0
54	SJ	114/115 (99%)	62 (54%)	52 (46%)	0	0
55	SK	152/164 (93%)	89 (59%)	63 (41%)	0	0
56	SL	98/119 (82%)	59 (60%)	39 (40%)	0	0
57	SM	131/136 (96%)	82 (63%)	49 (37%)	0	0
58	SO	112/114 (98%)	64 (57%)	48 (43%)	0	0
59	SP	125/130 (96%)	83 (66%)	42 (34%)	0	1
60	SQ	86/113 (76%)	51 (59%)	35 (41%)	0	0
61	SR	101/128 (79%)	57 (56%)	44 (44%)	0	0
62	ST	125/130 (96%)	70 (56%)	55 (44%)	0	0
63	SU	108/123 (88%)	58 (54%)	50 (46%)	0	0
64	SV	119/131 (91%)	64 (54%)	55 (46%)	0	0
65	SW	114/115 (99%)	57 (50%)	57 (50%)	0	0
66	SX	96/110 (87%)	50 (52%)	46 (48%)	0	0
67	SY	68/72 (94%)	37 (54%)	31 (46%)	0	0
68	Sb	104/113 (92%)	59 (57%)	45 (43%)	0	0
69	Sc	67/79 (85%)	29 (43%)	38 (57%)	0	0
70	Sd	91/103 (88%)	58 (64%)	33 (36%)	0	1
71	Se	72/73 (99%)	48 (67%)	24 (33%)	0	1
72	Sg	54/57 (95%)	26 (48%)	28 (52%)	0	0
73	Sh	42/45 (93%)	28 (67%)	14 (33%)	0	1
74	Sj	57/58 (98%)	25 (44%)	32 (56%)	0	0
All	All	8712/9574 (91%)	5181 (60%)	3531 (40%)	0	0

5 of 3531 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	Lo	23	ARG
49	SE	114	ILE
74	Sj	21	LYS
65	SW	32	THR
42	Lq	49	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 111 such sidechains are listed below:

Mol	Chain	Res	Type
37	Lk	28	HIS
72	Sg	24	GLN
46	SB	76	ASN
71	Se	92	ASN
63	SU	20	ASN

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%)	1139 (44%)	0
5	LE	115/121 (95%)	50 (43%)	4 (3%)
75	St	1453/1454 (99%)	780 (53%)	0
76	u	74/75 (98%)	53 (71%)	0
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%)	2189 (48%)	9 (0%)

5 of 2189 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

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Mol	Chain	Res	Type
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 [i](#)

There are no chain breaks in this entry.

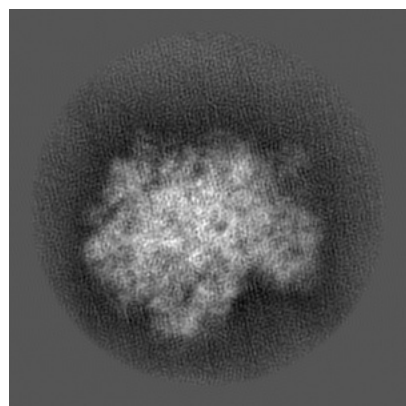
6 Map visualisation [i](#)

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.

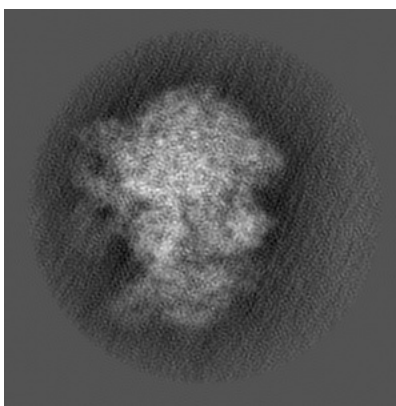
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

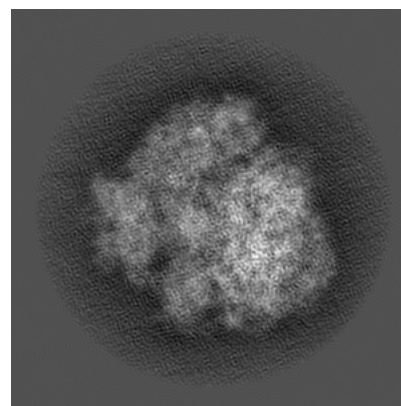
6.1.1 Primary map



X

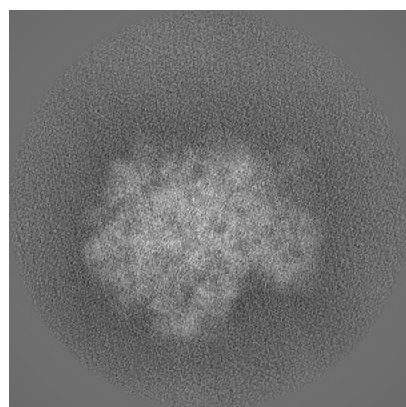


Y

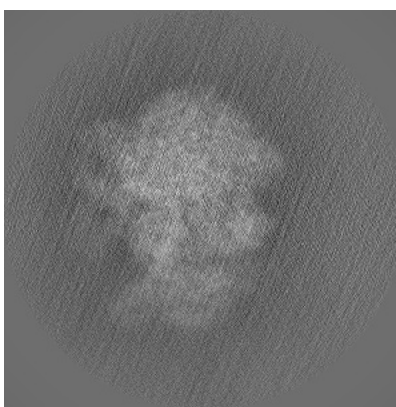


Z

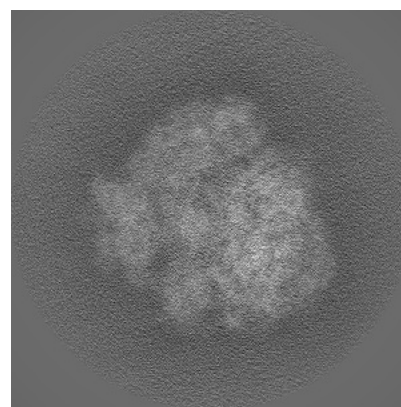
6.1.2 Raw map



X



Y

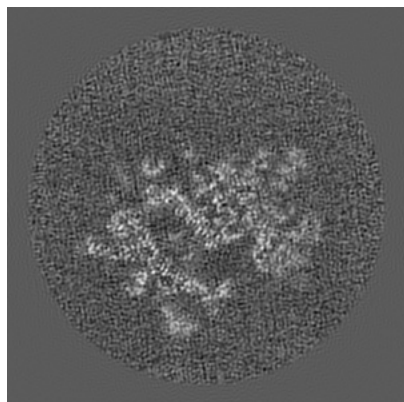


Z

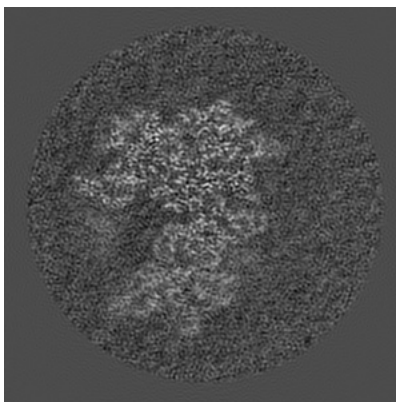
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

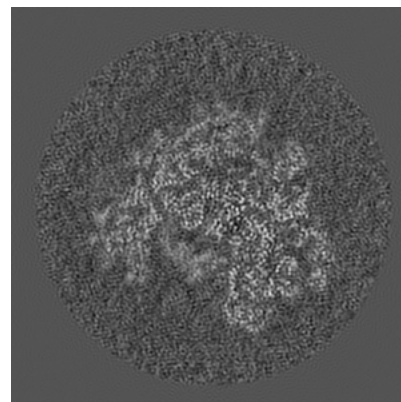
6.2.1 Primary map



X Index: 250

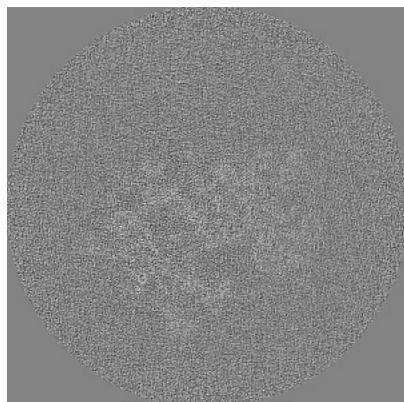


Y Index: 250

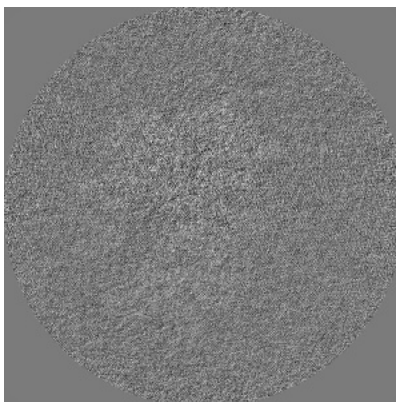


Z Index: 250

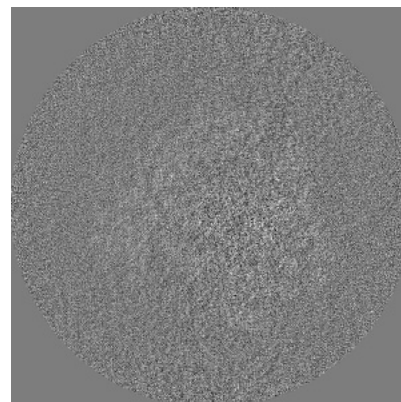
6.2.2 Raw map



X Index: 250



Y Index: 250

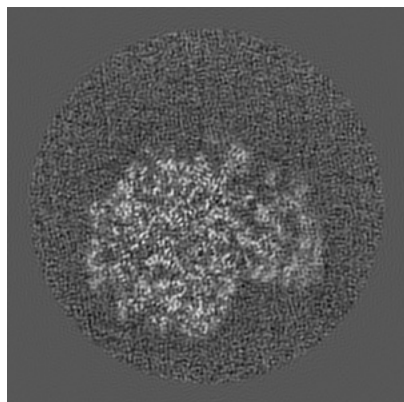


Z Index: 250

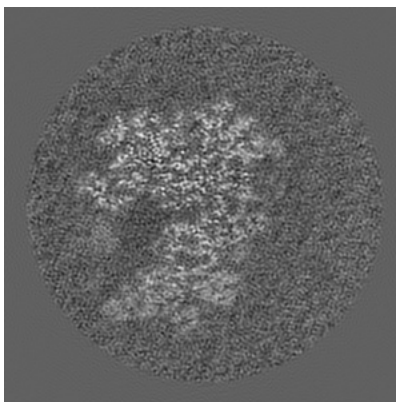
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

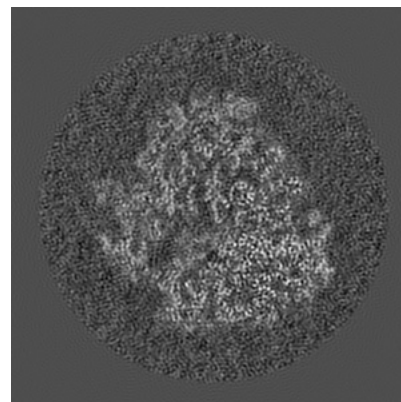
6.3.1 Primary map



X Index: 277

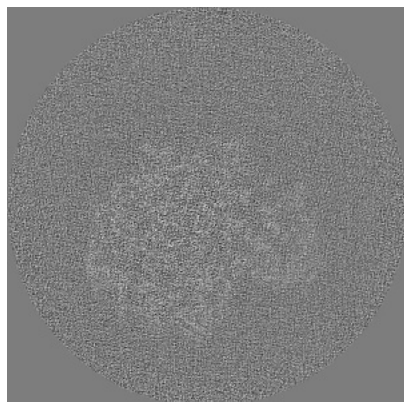


Y Index: 253

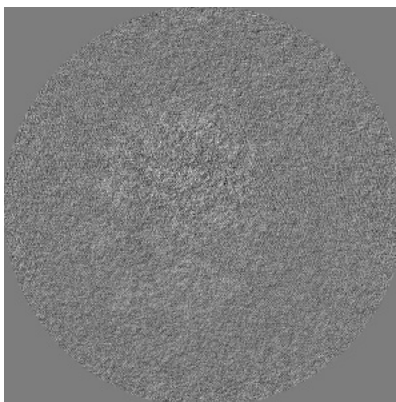


Z Index: 208

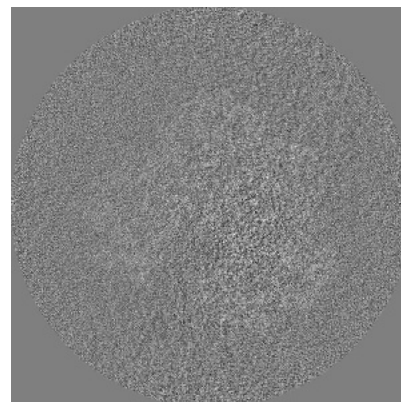
6.3.2 Raw map



X Index: 281



Y Index: 243

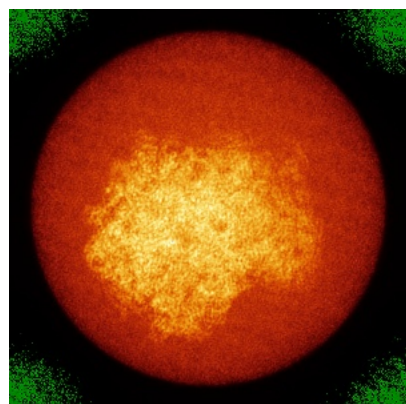


Z Index: 233

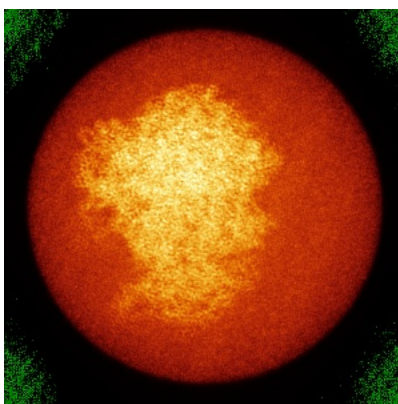
The images above show the largest variance slices of the map in three orthogonal directions.

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

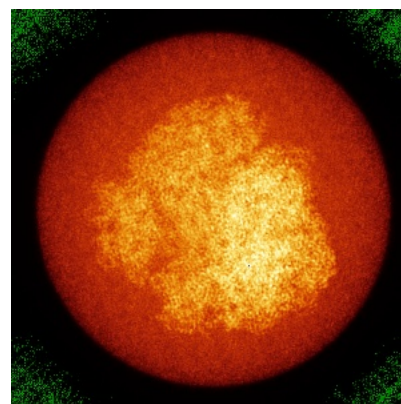
6.4.1 Primary map



X

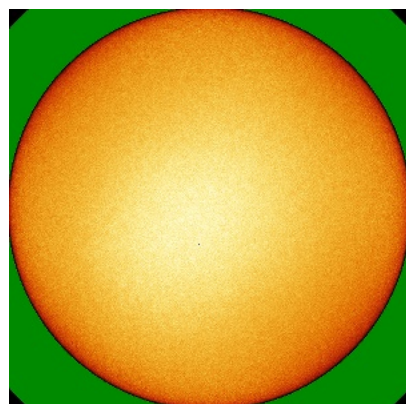


Y

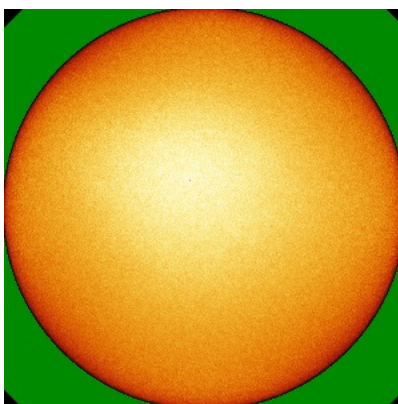


Z

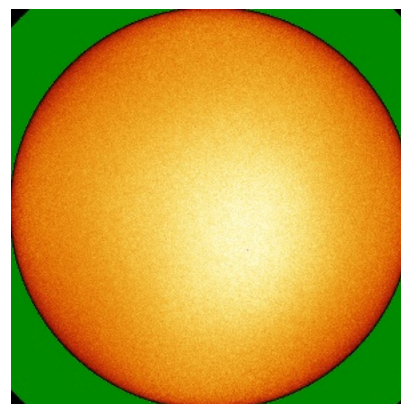
6.4.2 Raw map



X



Y

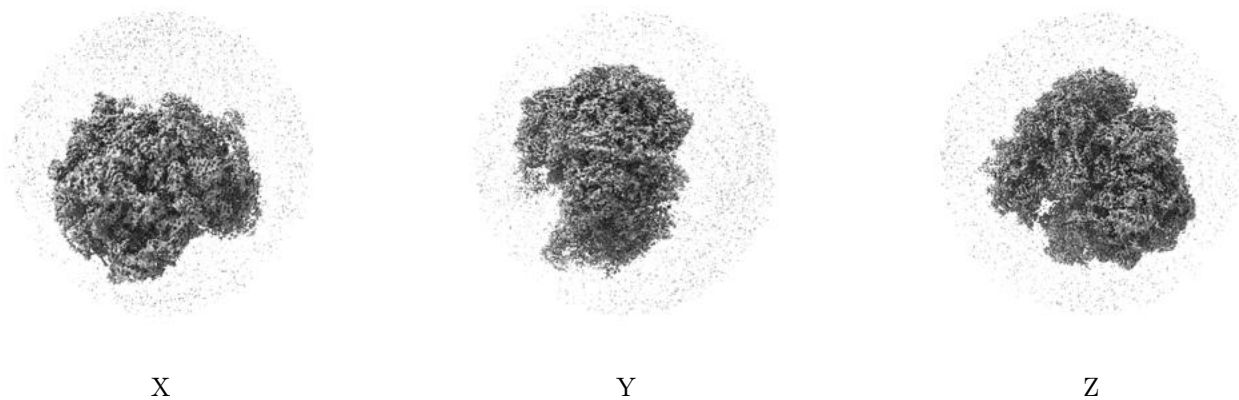


Z

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.

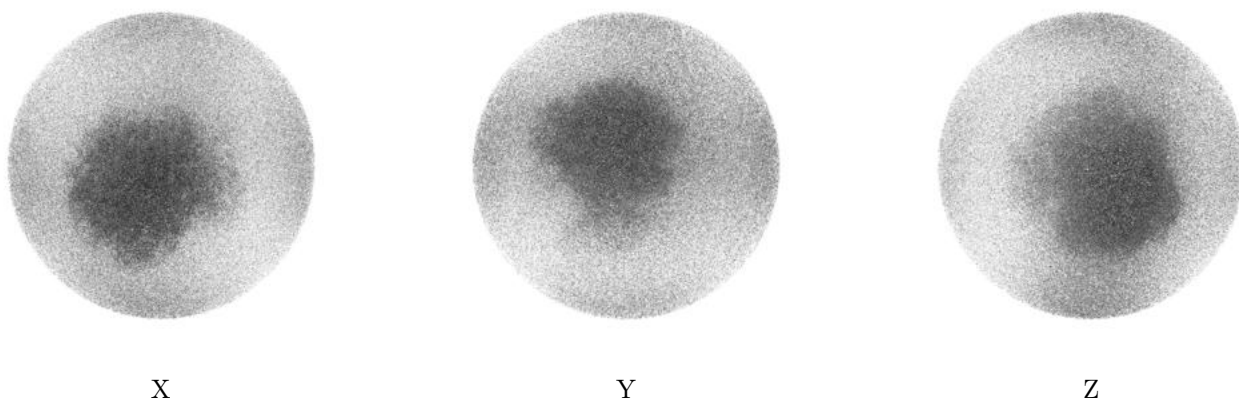
6.5 Orthogonal surface views [i](#)

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.

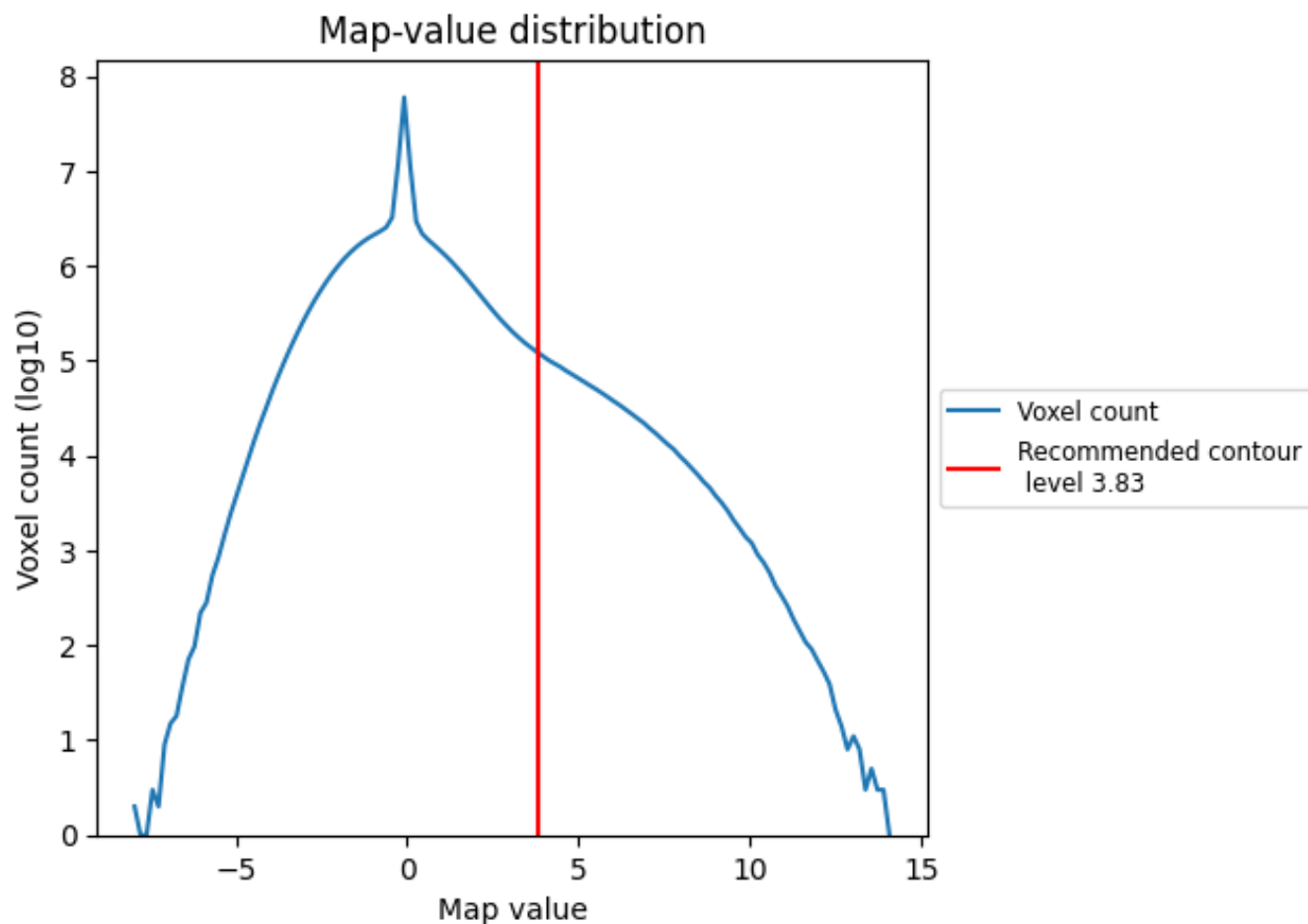
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

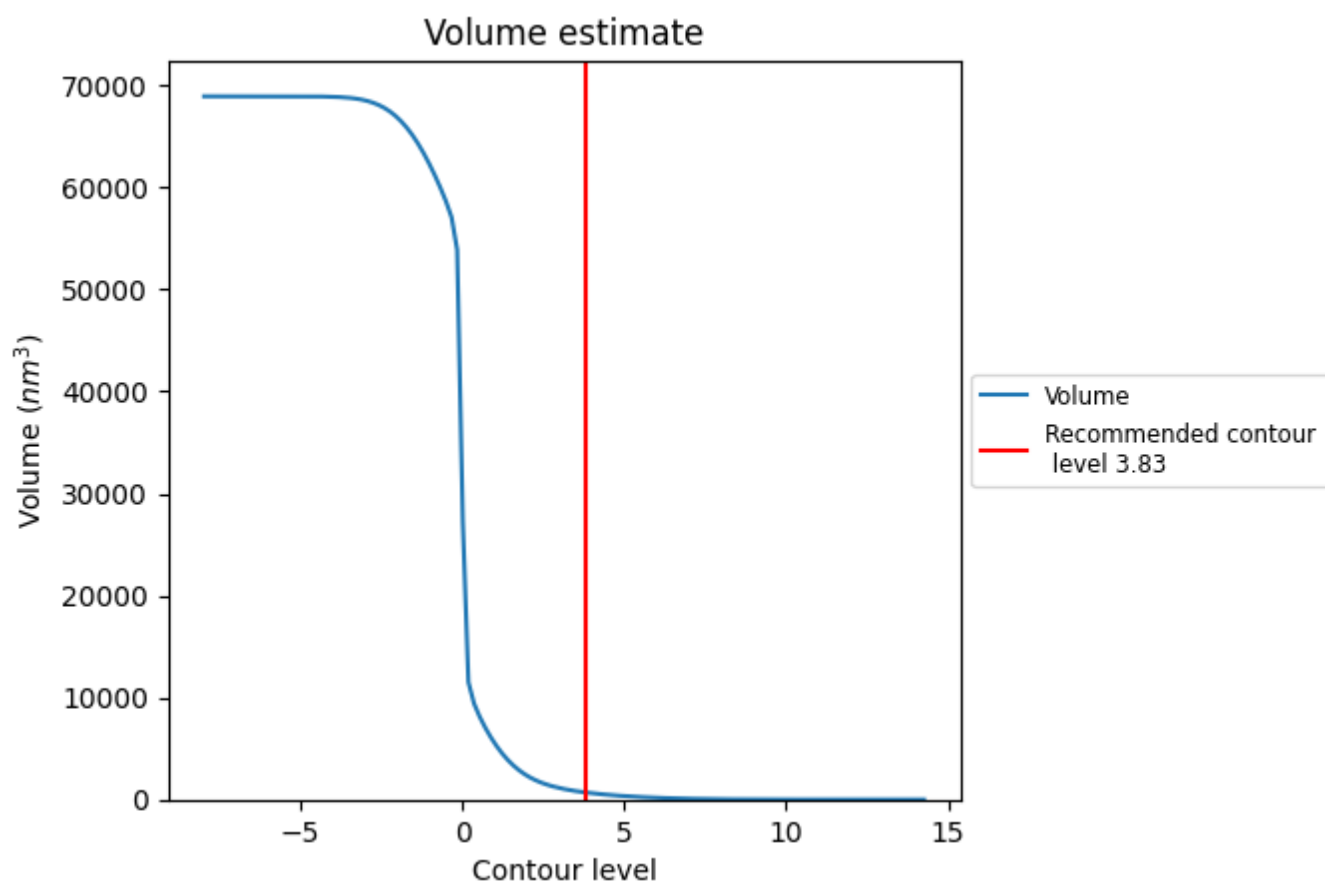
This section contains the results of statistical analysis of the map.

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.

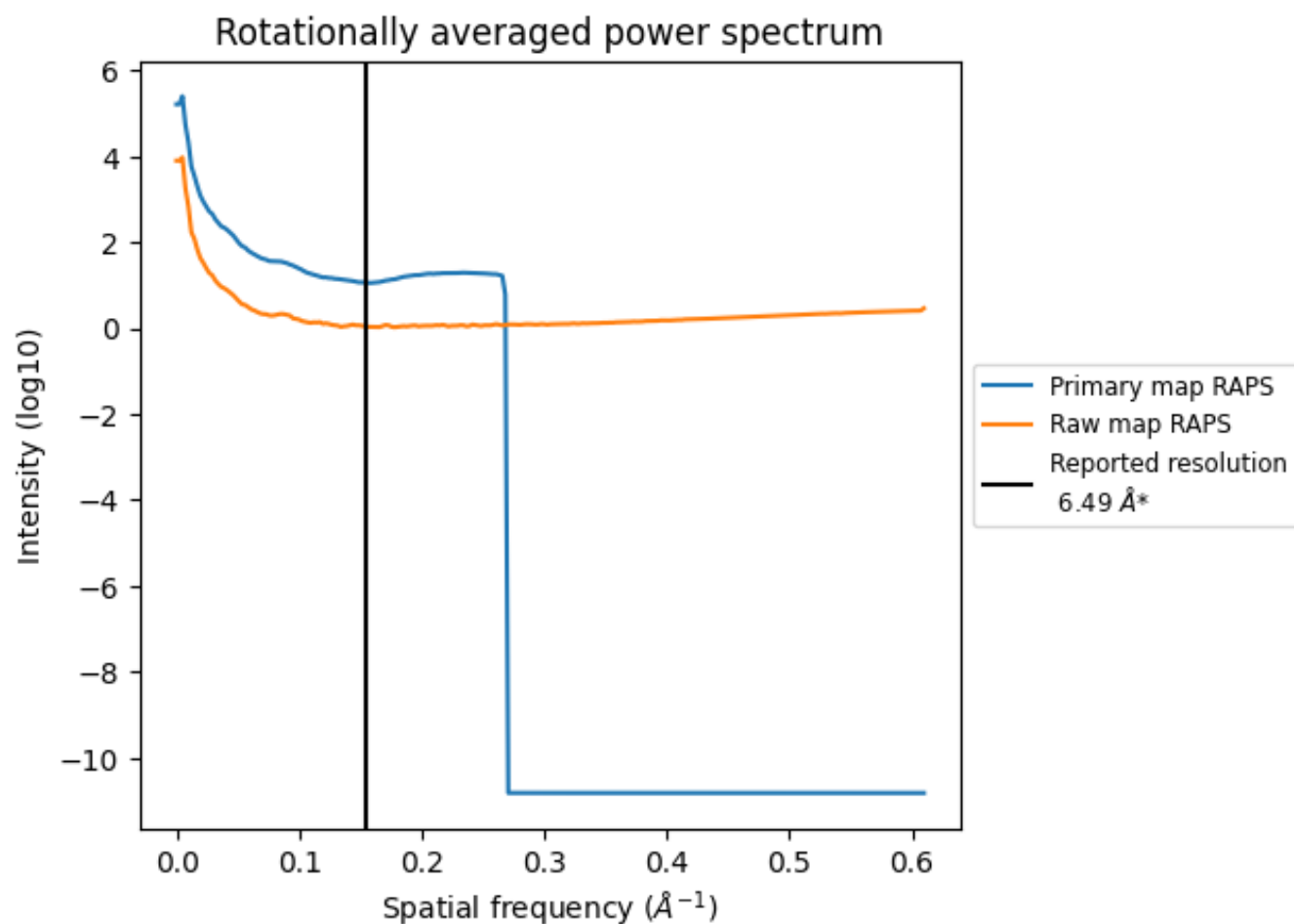
7.2 Volume estimate [i](#)



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 ⓘ

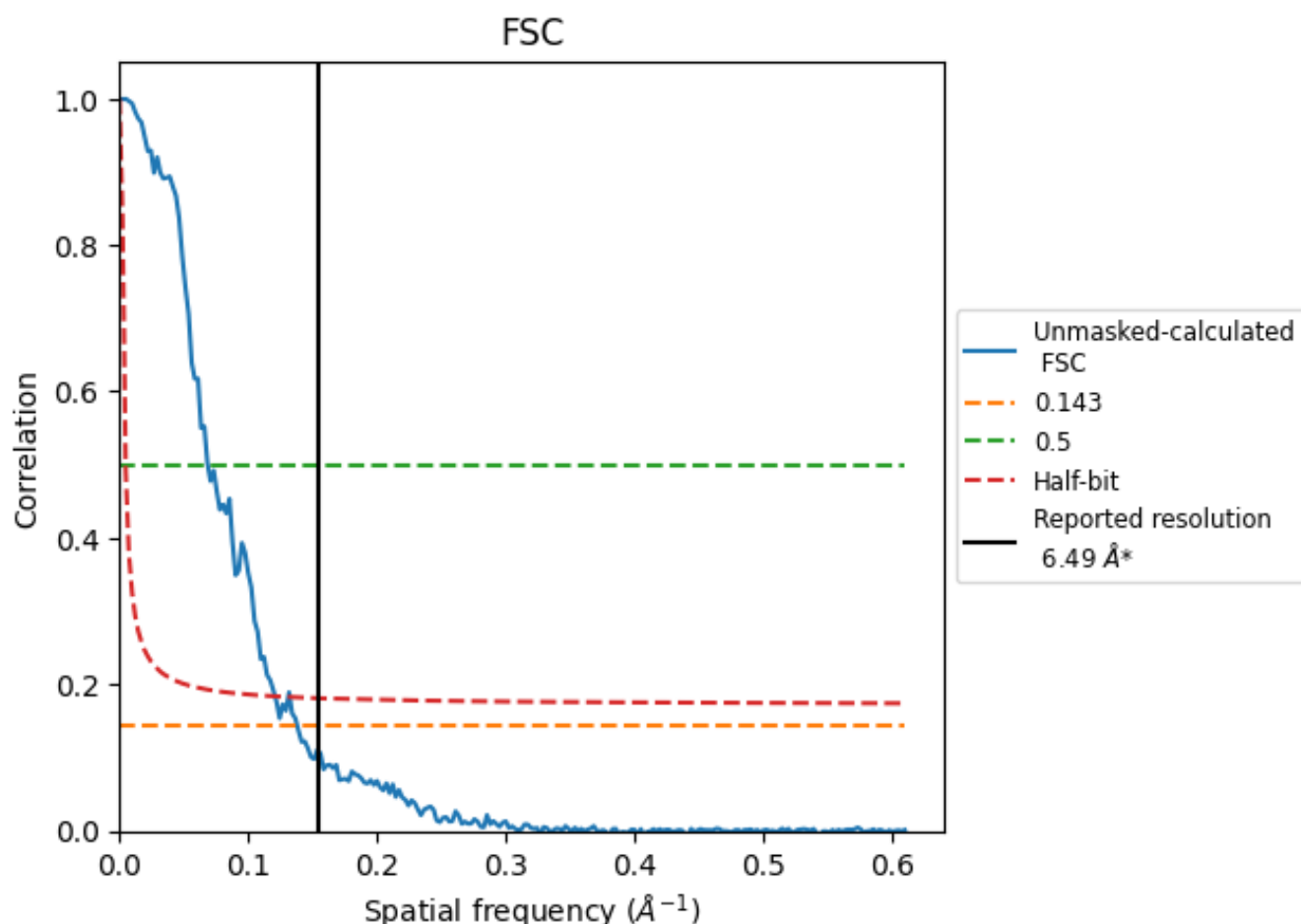


*Reported resolution corresponds to spatial frequency of 0.154 Å⁻¹

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](#)

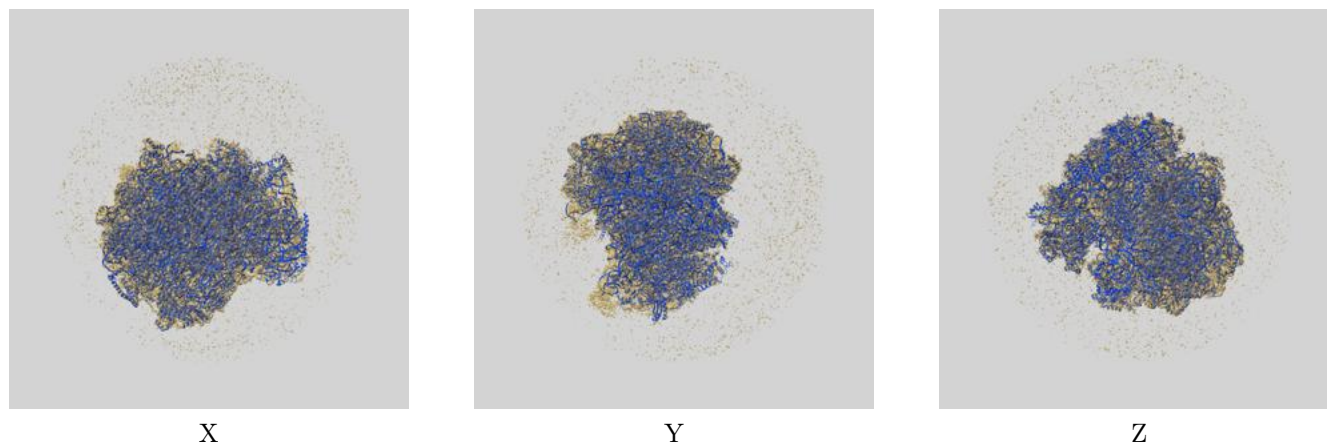
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.49	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.24	14.60	8.28

*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](#)

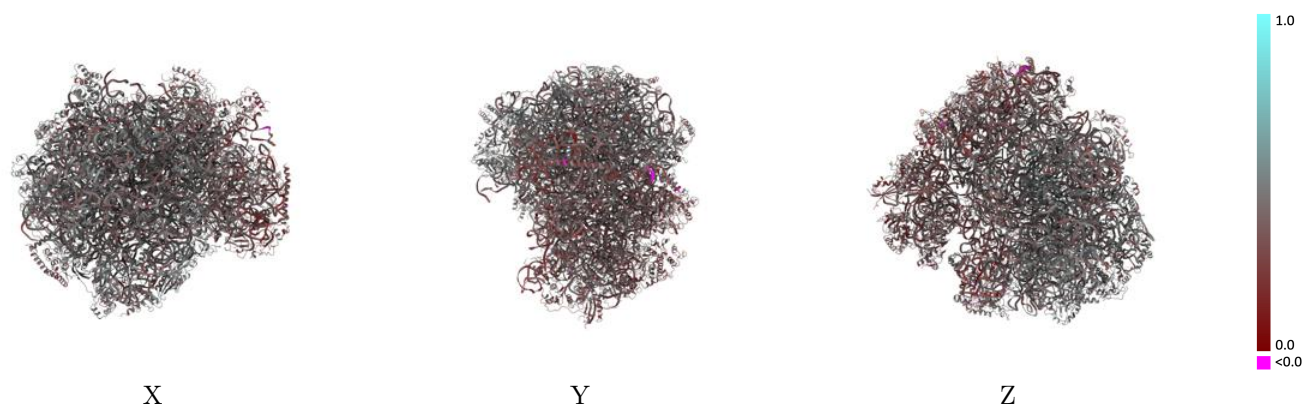
This section contains information regarding the fit between EMDB map EMD-16226 and PDB model 8BSJ. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



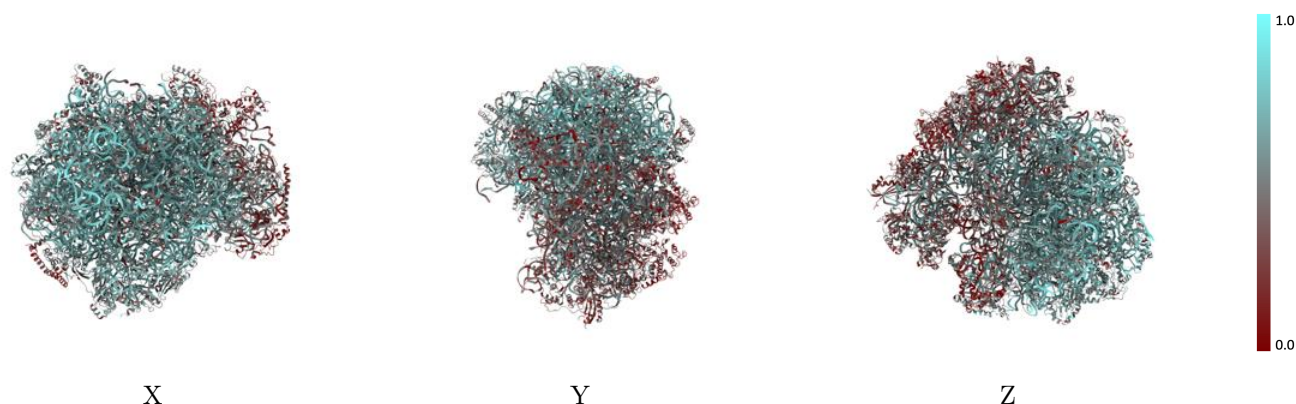
The images above show the 3D surface view of the map at the recommended contour level 3.83 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



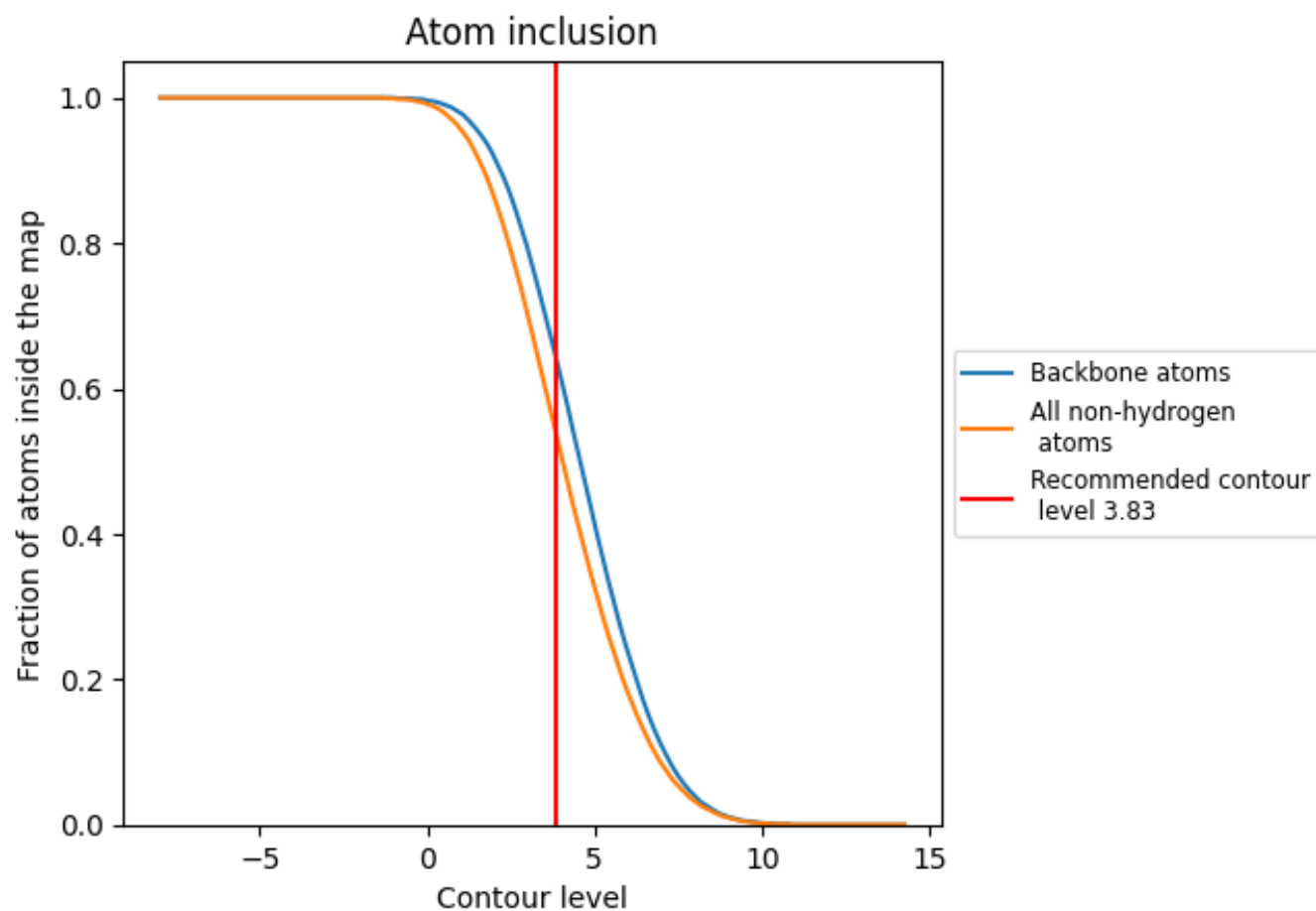
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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