



## wwPDB EM Validation Summary Report ⓘ

Apr 24, 2023 – 11:42 am BST

PDB ID : 8BR8  
EMDB ID : EMD-16211  
Title : Giardia ribosome in POST-T state (A1)  
Authors : Majumdar, S.; Emmerich, A.G.; Sanyal, S.  
Deposited on : 2022-11-22  
Resolution : 3.35 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](mailto: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>.

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

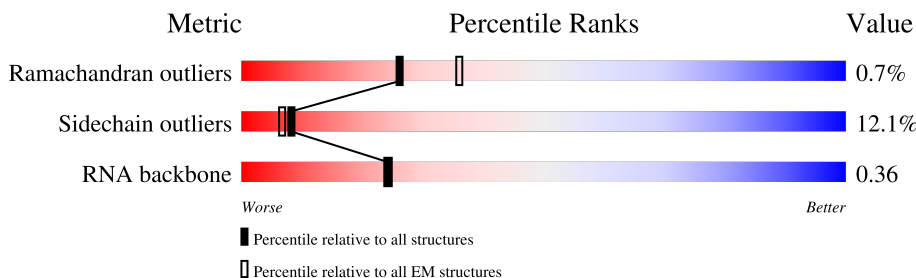
EMDB validation analysis : 0.0.1.dev50  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.32.2

# 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 3.35 Å.

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



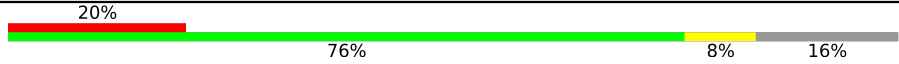
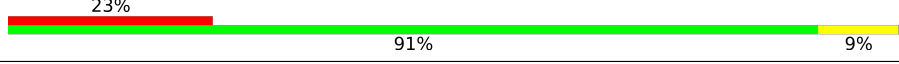
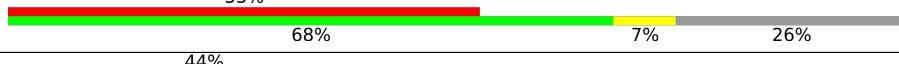


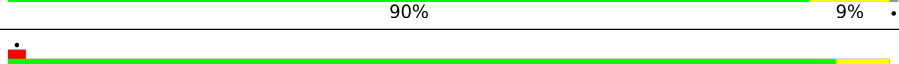
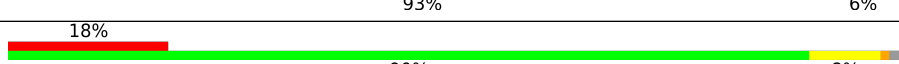
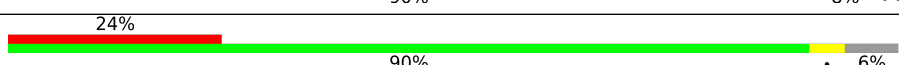
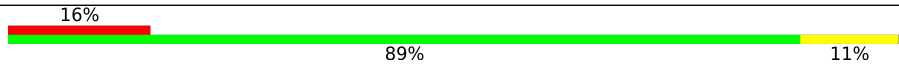

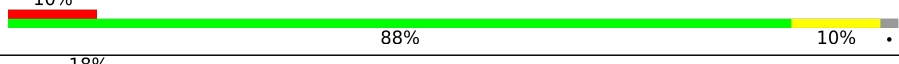
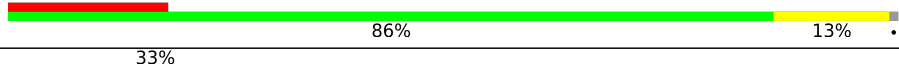
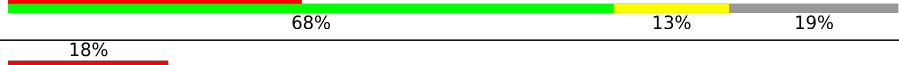

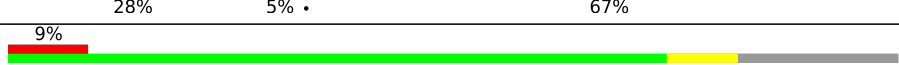


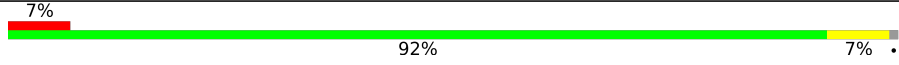


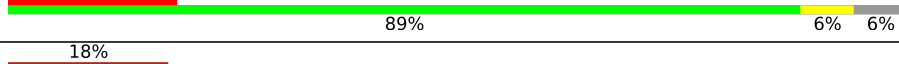




Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	
2	LB	379	
3	LC	316	
4	LD	142	
5	LE	121	
6	LF	297	
7	LG	51	
8	LH	235	

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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	Lu	75	
46	SA	245	
47	SB	242	
48	SC	217	
49	SD	248	
50	SE	268	
51	SF	190	
52	SG	248	
53	SH	190	
54	SI	174	
55	SJ	130	
56	SK	189	
57	SL	134	
58	SM	154	

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Mol	Chain	Length	Quality of chain
59	SO	143	49% 88% 9%
60	SP	154	36% 90% 7%
61	SQ	145	17% 79% 8% 13%
62	SR	145	68% 58% 12% 30%
63	ST	158	77% 83% 13%
64	SU	137	75% 69% 11% 20%
65	SV	154	86% 73% 18% 9%
66	SW	139	86% 89% 9%
67	SX	126	69% 71% 9% 21%
68	SY	89	67% 80% 17%
69	Sb	132	70% 77% 14% 10%
70	Sc	88	78% 68% 17% 15%
71	Sd	109	28% 80% 10% 10%
72	Se	81	64% 89% 10%
73	Sg	64	86% 84% 14%
74	Sh	51	80% 73% 24%
75	Sj	69	70% 78% 12% 10%
76	St	1454	22% 65% 34%

## 2 Entry composition [i](#)

There are 76 unique types of molecules in this entry. The entry contains 174771 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
			Total	C	N	O	S		
1	LA	248	1864	1151	381	320	12	0	0

- Molecule 2 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	LB	377	2978	1880	564	513	21	0	0

- Molecule 3 is a protein called Ribosomal protein L4.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	LD	142	3038	1350	563	983	142	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	LE	117	2502	1116	457	812	117	0	0

- Molecule 6 is a protein called Ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	LF	293	2355	1490	439	418	8	0	0

- Molecule 7 is a protein called Ribosomal protein L39.

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

- Molecule 8 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	LH	213	1726	1097	314	310	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	LI	188	1502	956	276	265	5	0	0

- Molecule 10 is a protein called Ribosomal protein L6.

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

- Molecule 11 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	LK	156	1270	798	245	223	4	0	0

- Molecule 12 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LL	167	1340	845	249	241	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LM	201	1605	999	325	274	7	0	0

- Molecule 14 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	LN	130	1024	649	186	183	6	0	0

- Molecule 15 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	LO	203	1708	1080	357	265	6	0	0

- Molecule 16 is a protein called Ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	LP	193	1570	988	305	265	12	0	0

- Molecule 17 is a protein called Ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	LQ	154	1239	784	240	211	4	0	0

- Molecule 18 is a protein called Ribosomal protein L18.

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

- Molecule 19 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	LS	192	1592	983	334	270	5	0	0

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

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

- Molecule 21 is a protein called Ribosomal protein L21.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	LU	157	Total	C	N	O	S	0	0
			1264	789	260	208	7		

- Molecule 22 is a protein called Ribosomal L22e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LV	100	Total	C	N	O	S	0	0
			820	523	140	155	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	63	Total	C	N	O	S	0	0
			538	340	109	82	7		

- Molecule 25 is a protein called Ribosomal protein L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LY	115	Total	C	N	O	S	0	0
			931	598	168	162	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	119	Total	C	N	O	S	0	0
			957	608	181	163	5		

- Molecule 28 is a protein called Ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lb	148	Total	C	N	O	S	0	0
			1201	759	240	199	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lc	52	Total	C	N	O	S	0	0
			434	260	99	73	2		

- Molecule 30 is a protein called Ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ld	107	Total	C	N	O	S	0	0
			804	506	141	153	4		

- Molecule 31 is a protein called Ribosomal protein L31B.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	Le	100	Total	C	N	O	0	0
			818	518	158	142		

- Molecule 32 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lf	127	Total	C	N	O	S	0	0
			1050	667	211	166	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	95	Total	C	N	O	S	0	0
			765	473	159	129	4		

- Molecule 35 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Li	122	Total	C	N	O	S	0	0
			983	623	192	163	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lj	89	Total	C	N	O	S	0	0
			731	462	146	119	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	93	Total	C	N	O	S	0	0
			767	478	159	125	5		

- Molecule 42 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lq	90	Total	C	N	O	S	0	0
			700	432	143	119	6		

- 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 RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lu	57	Total	C	N	O	P	0	0
			1221	546	228	391	56		

- Molecule 46 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SA	196	Total	C	N	O	S	0	0
			1569	1013	274	274	8		

- Molecule 47 is a protein called Ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SB	199	Total	C	N	O	S	0	0
			1529	976	277	272	4		

- Molecule 48 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SC	208	Total	C	N	O	S	0	0
			1648	1038	304	290	16		

- Molecule 49 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD	231	Total	C	N	O	S	0	0
			1868	1180	349	326	13		

- Molecule 50 is a protein called 40S ribosomal protein S4.

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

- Molecule 51 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SF	184	Total	C	N	O	S	0	0
			1429	889	272	259	9		

- Molecule 52 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SG	205	Total	C	N	O	S	0	0
			1617	1017	307	283	10		

- Molecule 53 is a protein called 40S ribosomal protein S7.

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

- Molecule 54 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SI	173	Total	C	N	O	S	0	0
			1357	850	260	244	3		

- Molecule 55 is a protein called Ribosomal protein S15A.

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

- Molecule 56 is a protein called Ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	SK	176	1423	889	281	247	6	0	0

- Molecule 57 is a protein called Ribosomal protein S10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	SL	98	802	519	134	146	3	0	0

- Molecule 58 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	SM	151	1251	794	246	205	6	0	0

- Molecule 59 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	SO	139	1080	683	213	181	3	0	0

- Molecule 60 is a protein called Ribosomal protein S13.

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

- Molecule 61 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	SQ	126	925	569	190	163	3	0	0

- Molecule 62 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	SR	101	831	530	161	132	8	0	0

- Molecule 63 is a protein called Ribosomal protein S16.

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

- Molecule 64 is a protein called Ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	SU	110	886	550	171	160	5	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SU	104	THR	ALA	conflict	UNP A8BRG5

- Molecule 65 is a protein called Ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	SV	140	1113	685	226	196	6	0	0

- Molecule 66 is a protein called Ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	SW	137	1071	680	202	186	3	0	0

- Molecule 67 is a protein called Ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	SX	100	794	507	145	137	5	0	0

- Molecule 68 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	SY	86	651	403	120	122	6	0	0

- Molecule 69 is a protein called Ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	Sb	119	945	600	178	161	6	0	0

- Molecule 70 is a protein called 40S ribosomal protein S25.

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

- Molecule 71 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	Sd	98	796	491	164	134	7	0	0

- Molecule 72 is a protein called Ribosomal protein S27.

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

- Molecule 73 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	Sg	63	505	311	100	92	2	0	0

- Molecule 74 is a protein called Ribosomal protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	Sh	50	417	264	80	67	6	0	0

- Molecule 75 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	Sj	62	502	315	104	82	1	0	0

- Molecule 76 is a RNA chain called Small Subunit rRNA.

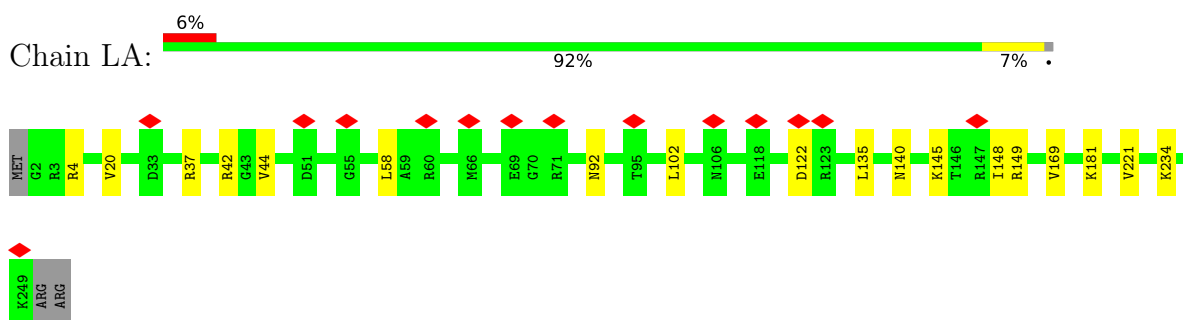


Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
76	St	1454	31176	13861	5772	10090	1453	0	0

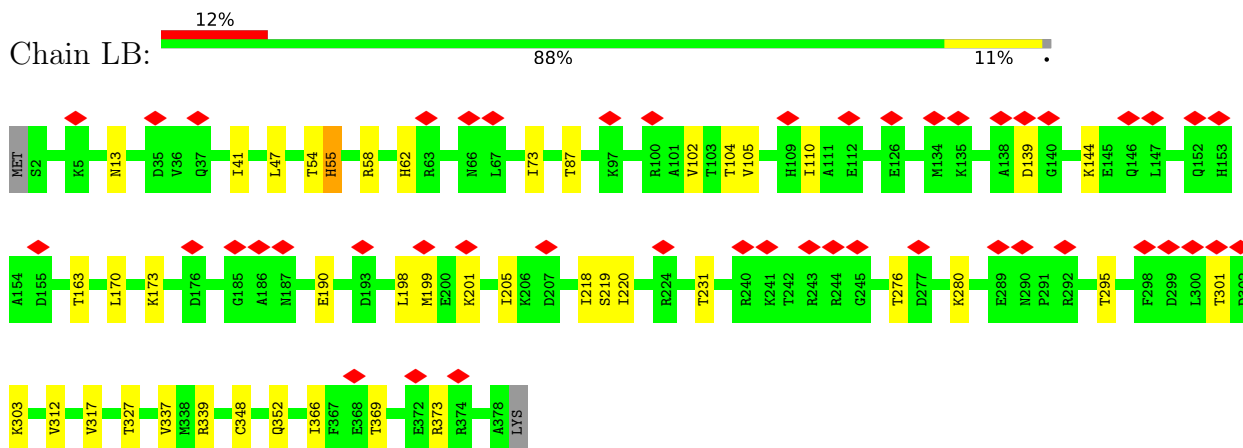
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

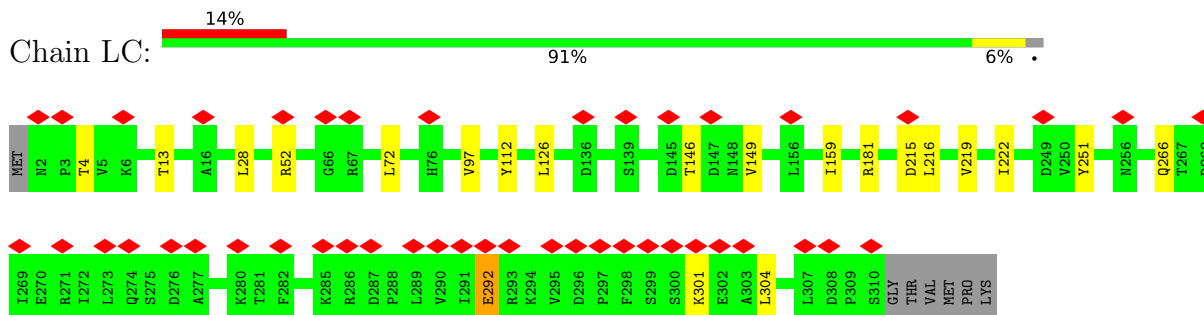
- Molecule 1: Ribosomal protein L2



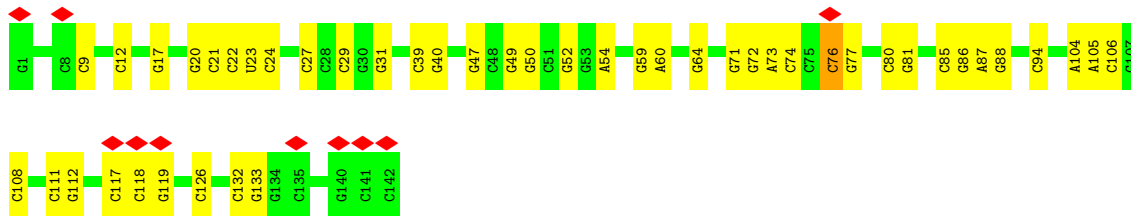
- Molecule 2: Ribosomal protein L3



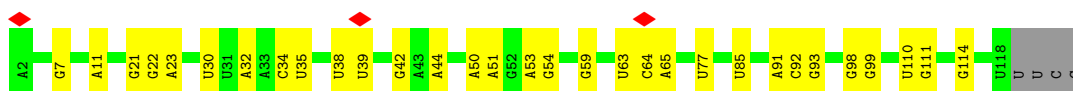
- Molecule 3: Ribosomal protein L4



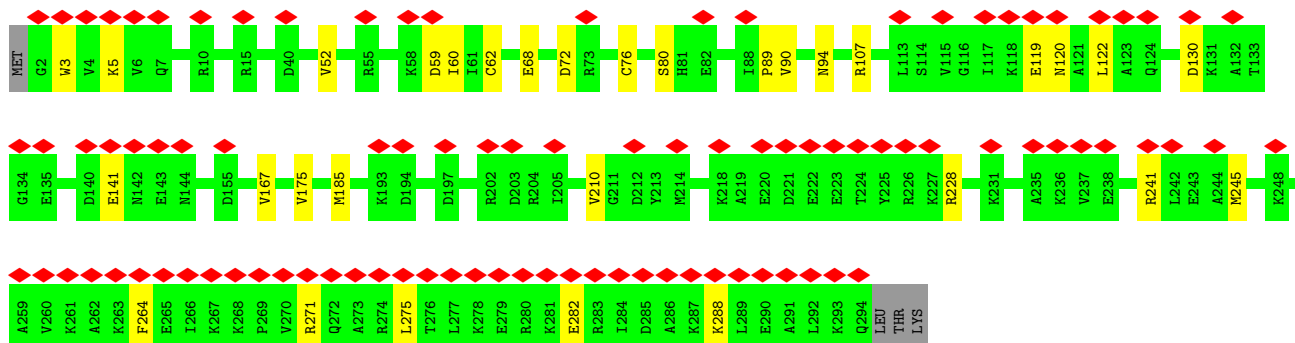
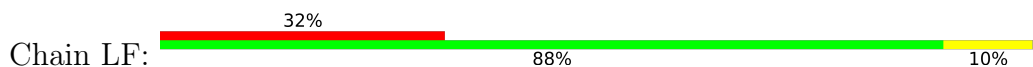
• Molecule 4: 5.8S rRNA



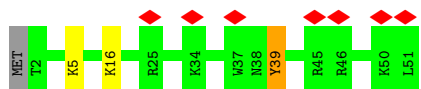
• Molecule 5: 5S rRNA



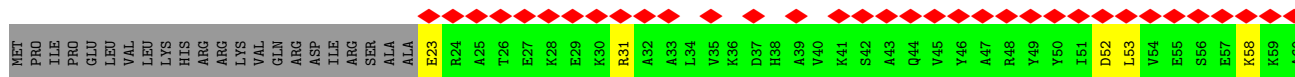
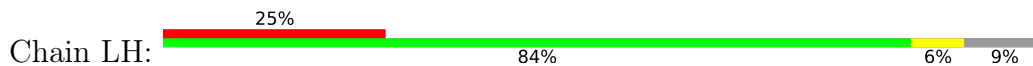
• Molecule 6: Ribosomal protein L5

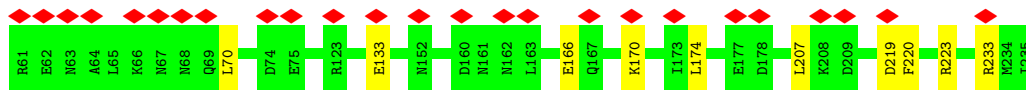


• Molecule 7: Ribosomal protein L39

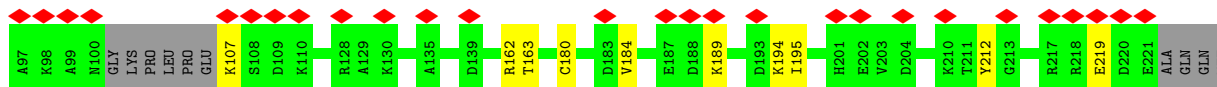
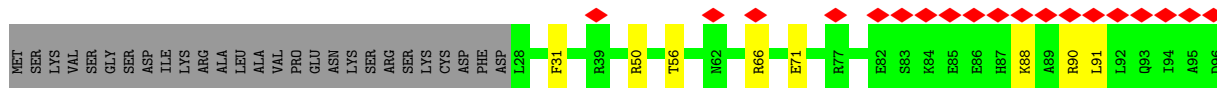
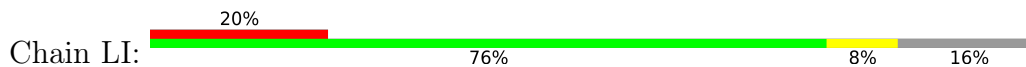


• Molecule 8: Ribosomal protein L7

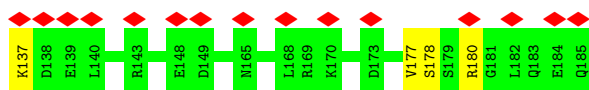
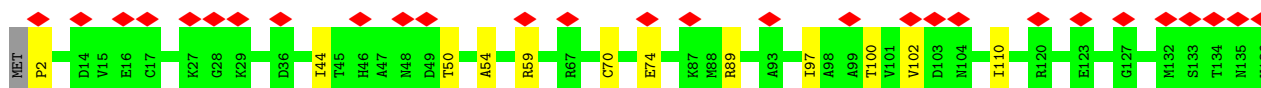
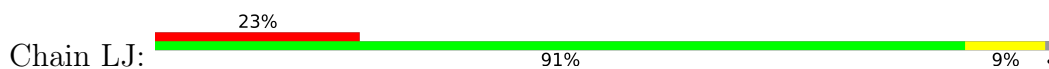




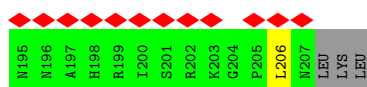
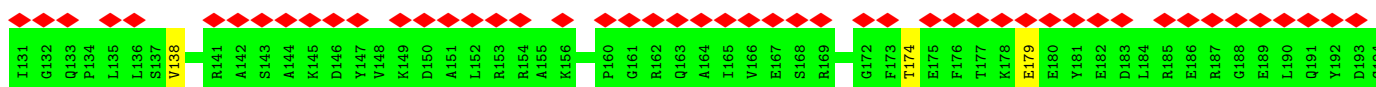
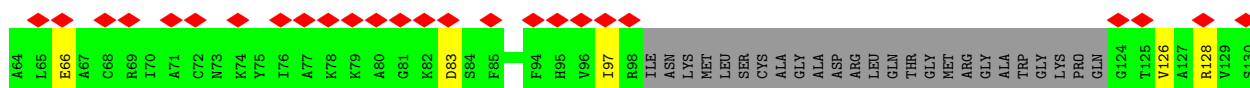
• Molecule 9: 60S ribosomal protein L7a



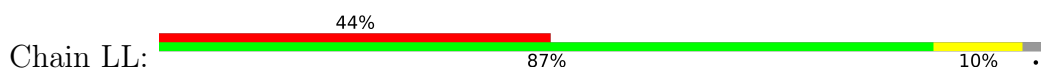
• Molecule 10: Ribosomal protein L6

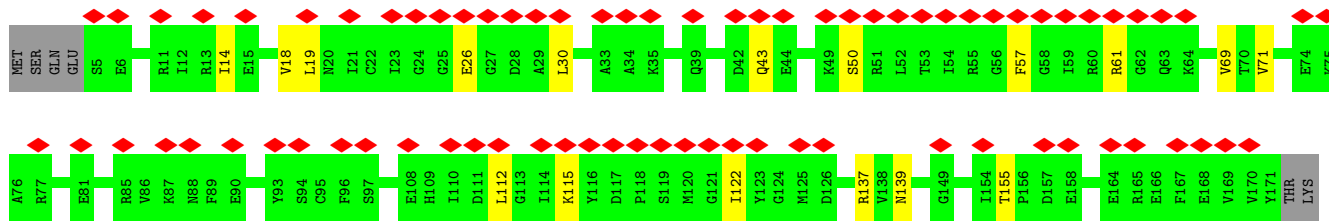


• Molecule 11: Ribosomal protein L10

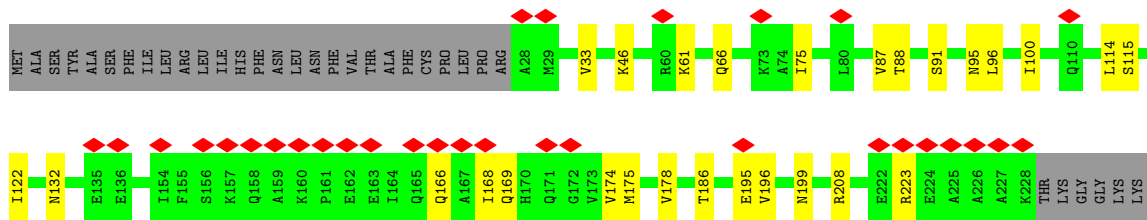
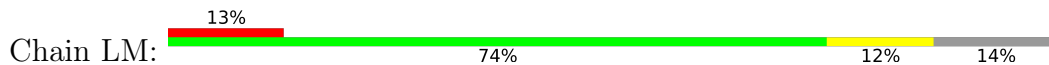


• Molecule 12: Ribosomal protein L11





• Molecule 13: 60S ribosomal protein L13



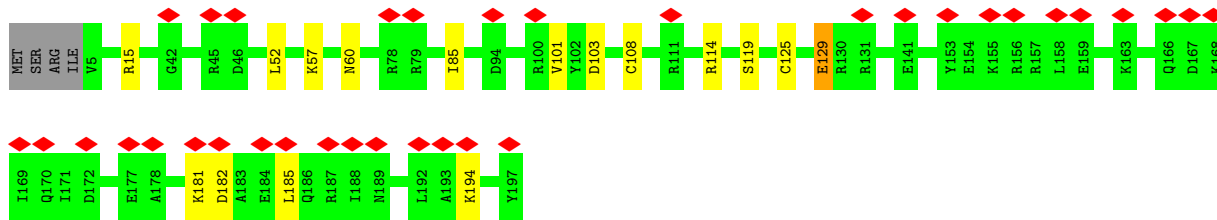
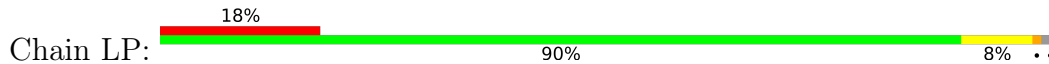
• Molecule 14: Ribosomal protein L14



• Molecule 15: Ribosomal protein L15

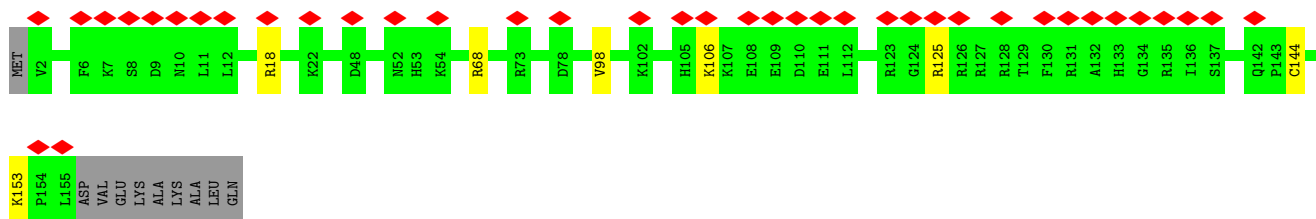


• Molecule 16: Ribosomal protein L13a

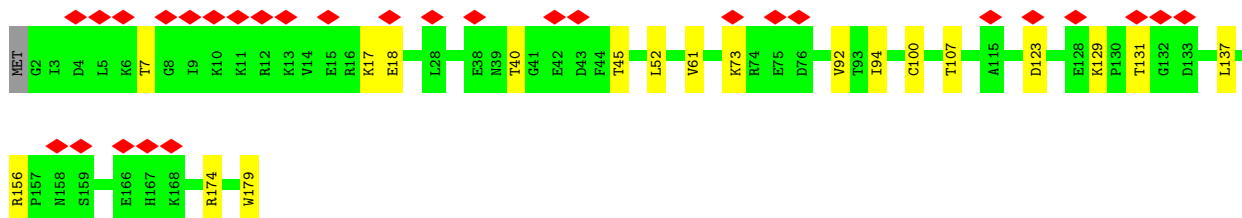
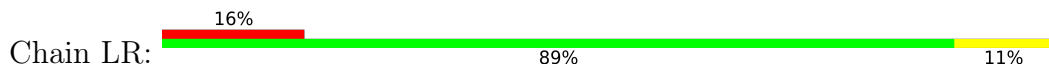


• Molecule 17: Ribosomal protein L17

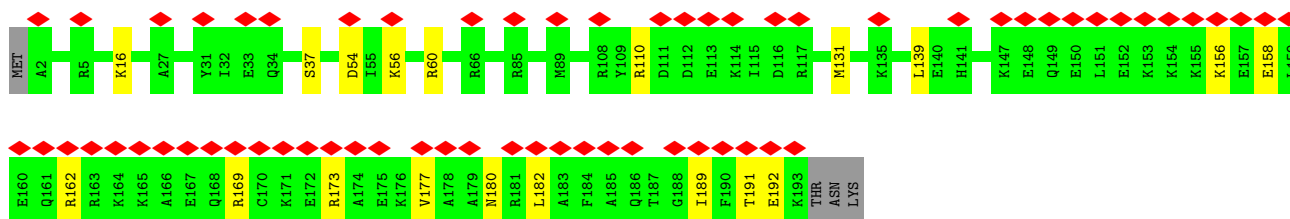
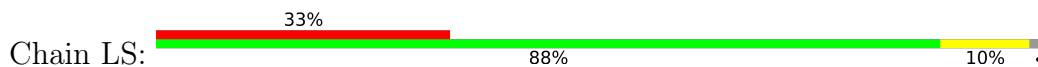




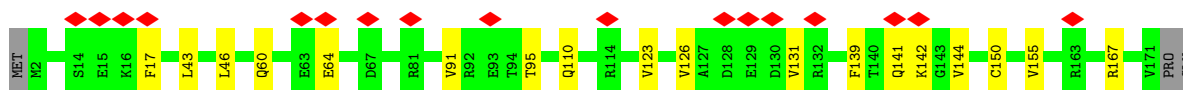
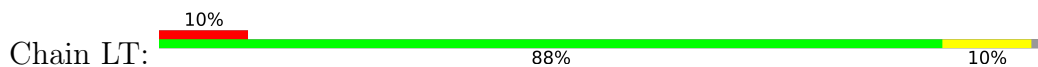
• Molecule 18: Ribosomal protein L18



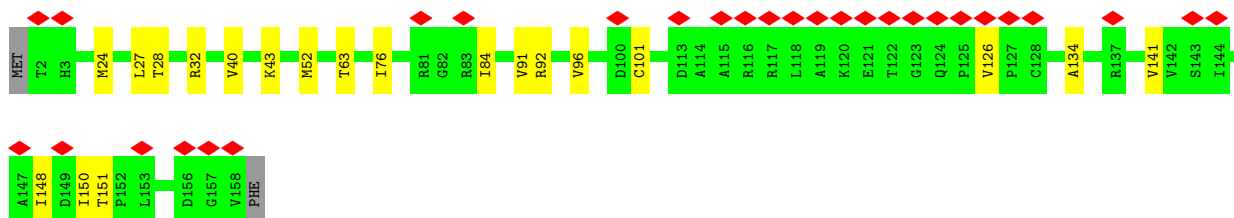
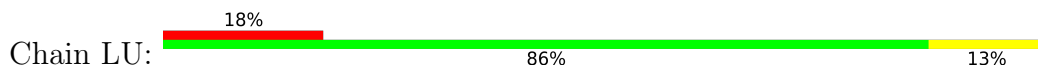
• Molecule 19: Ribosomal protein L19



• Molecule 20: 60S ribosomal protein L18a



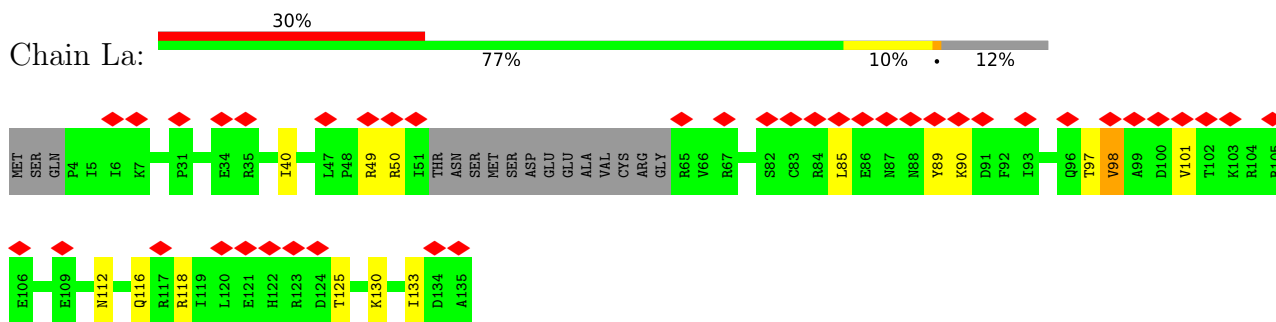
• Molecule 21: Ribosomal protein L21



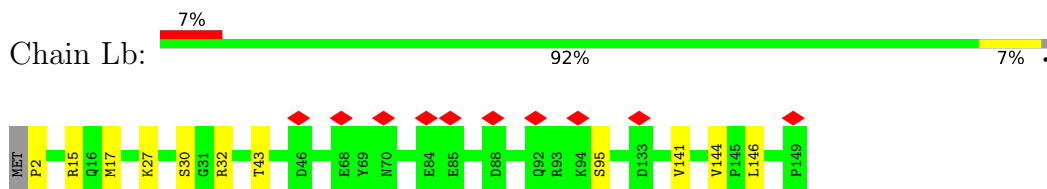
• Molecule 22: Ribosomal L22e



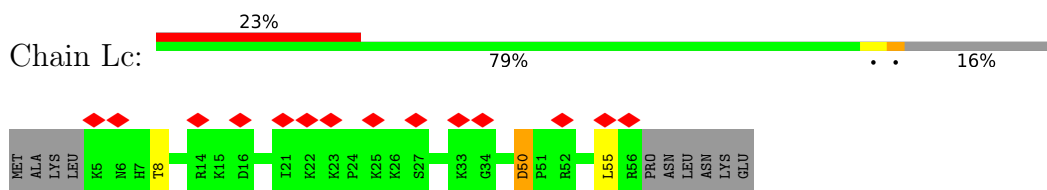
- Molecule 27: 60S ribosomal protein L27



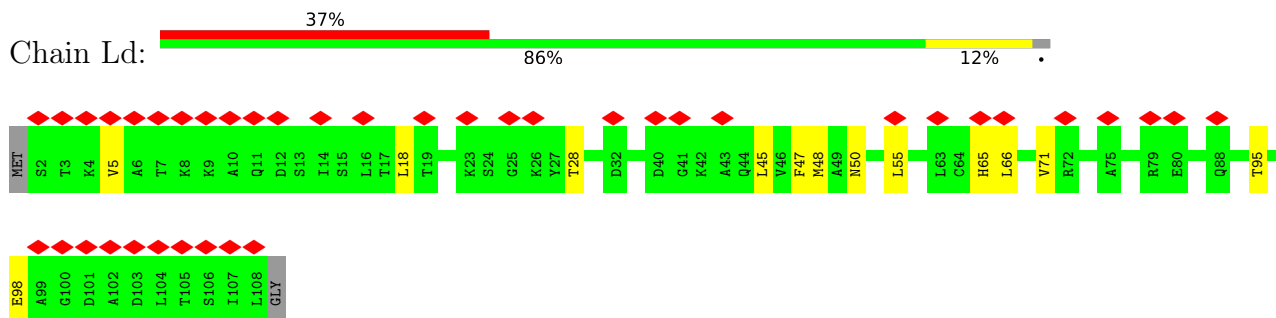
- Molecule 28: Ribosomal protein L27a



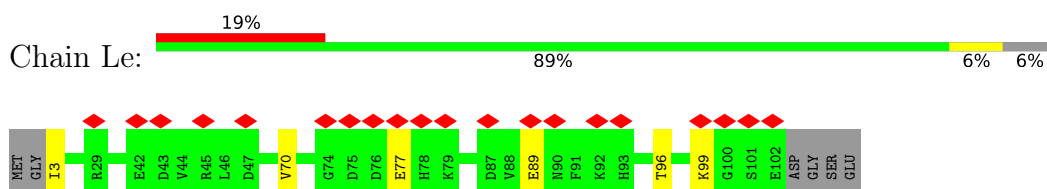
- Molecule 29: 60S ribosomal protein L29



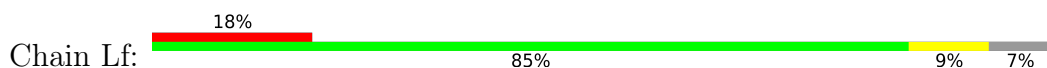
- Molecule 30: Ribosomal protein L30



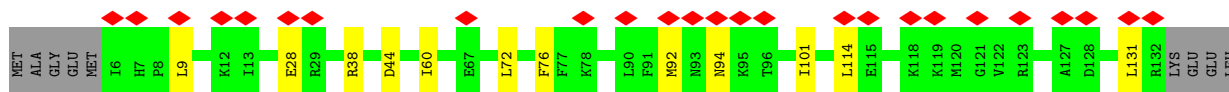
- Molecule 31: Ribosomal protein L31B



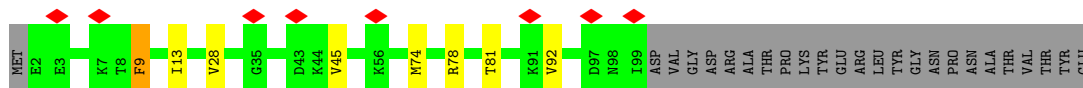
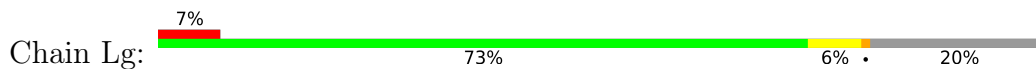
- Molecule 32: Ribosomal protein L32



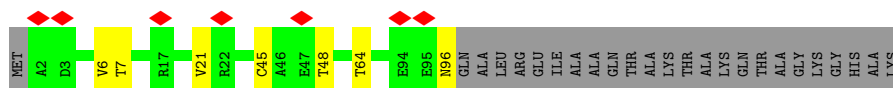
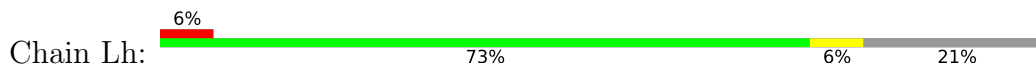




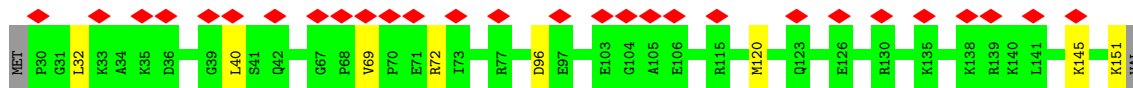
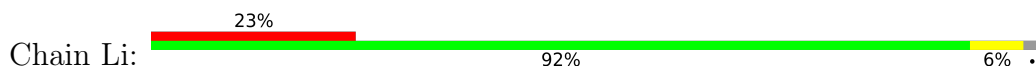
- Molecule 33: Ribosomal protein L35a



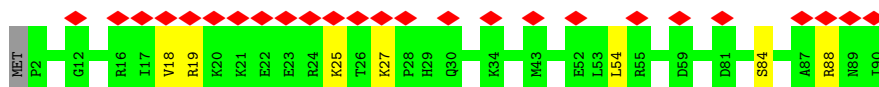
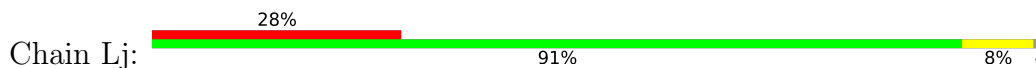
- Molecule 34: Ribosomal protein L34



- Molecule 35: Ribosomal protein L29



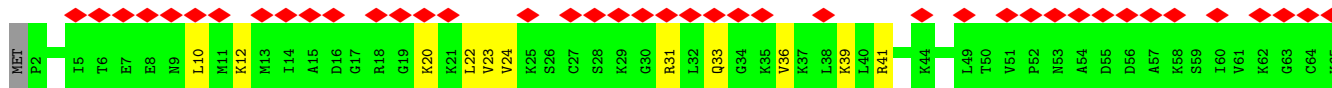
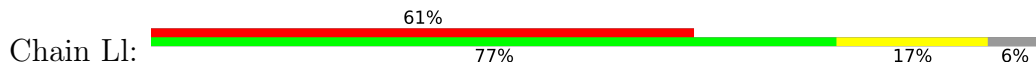
- Molecule 36: Ribosomal protein L36-1

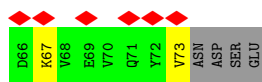


- Molecule 37: Ribosomal protein L37

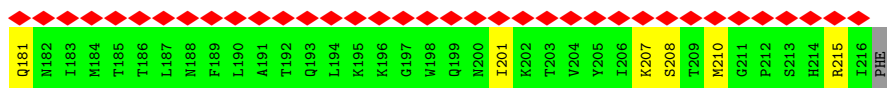
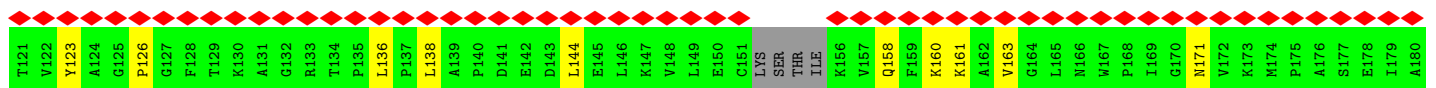
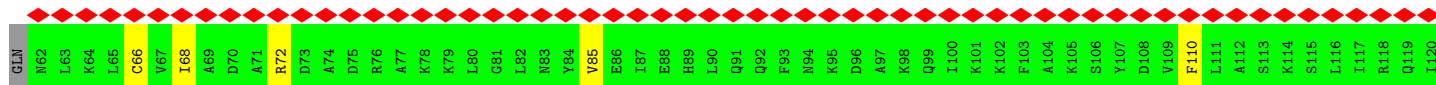
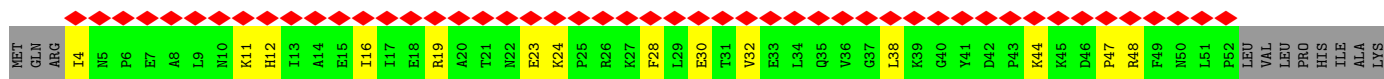
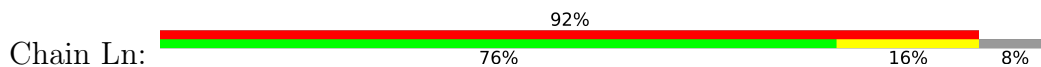


- Molecule 38: Ribosomal protein L38e

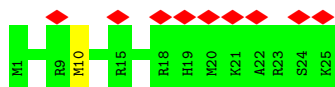




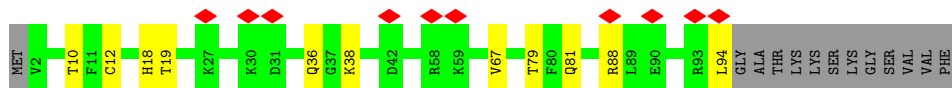
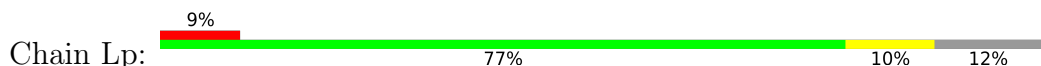
• Molecule 39: Ribosomal protein L10a



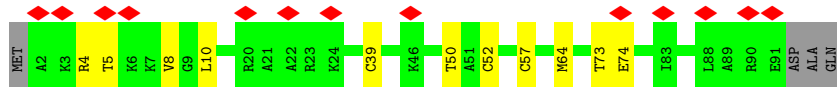
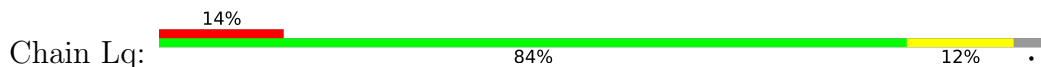
• Molecule 40: 60S ribosomal protein L41



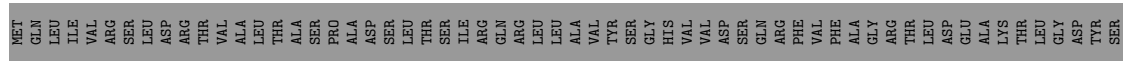
• Molecule 41: Ribosomal protein L44

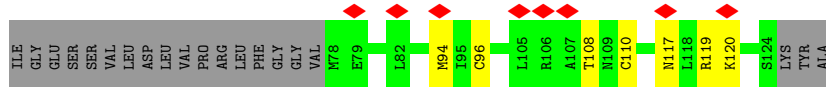


• Molecule 42: Ribosomal protein L37a

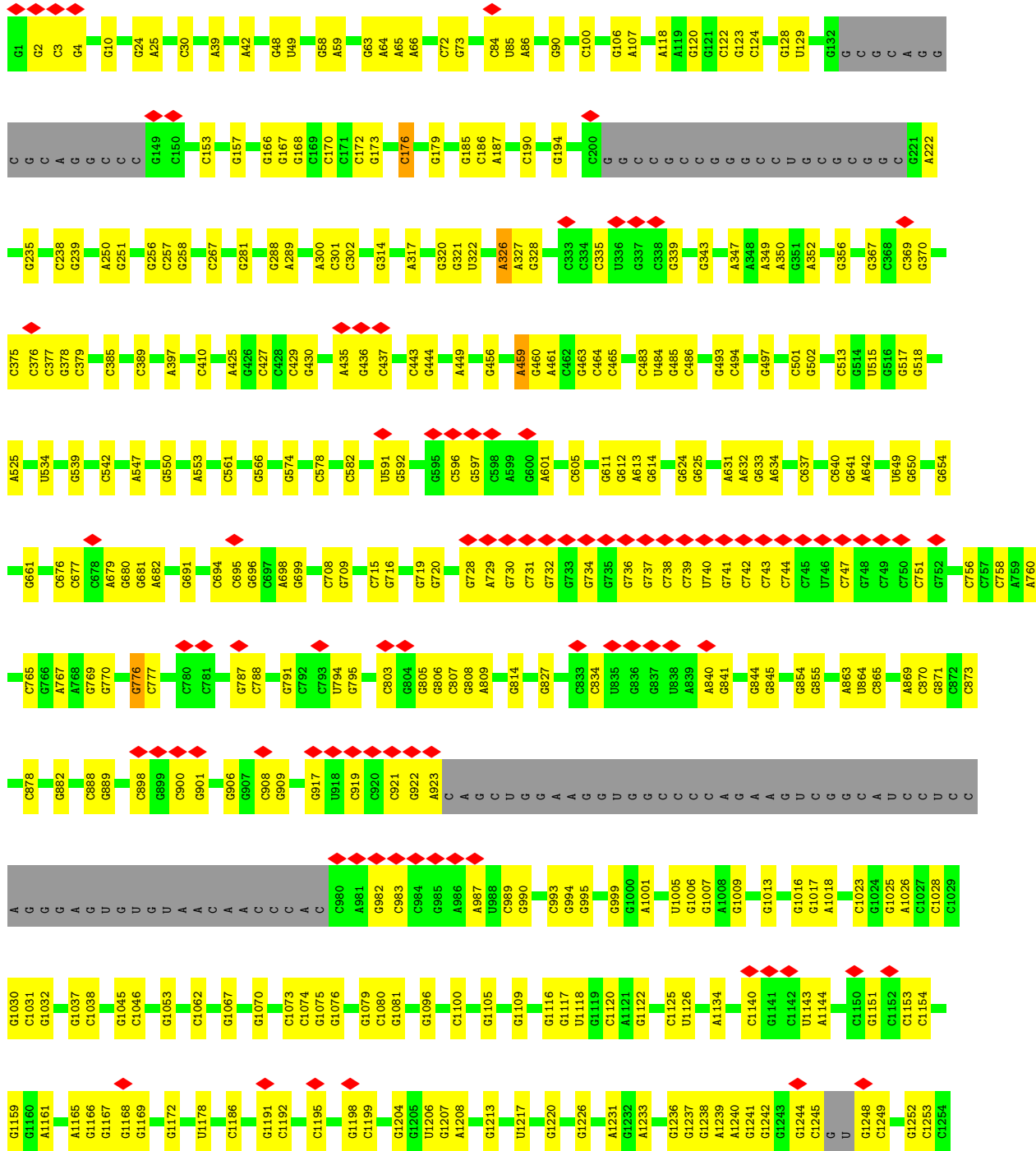


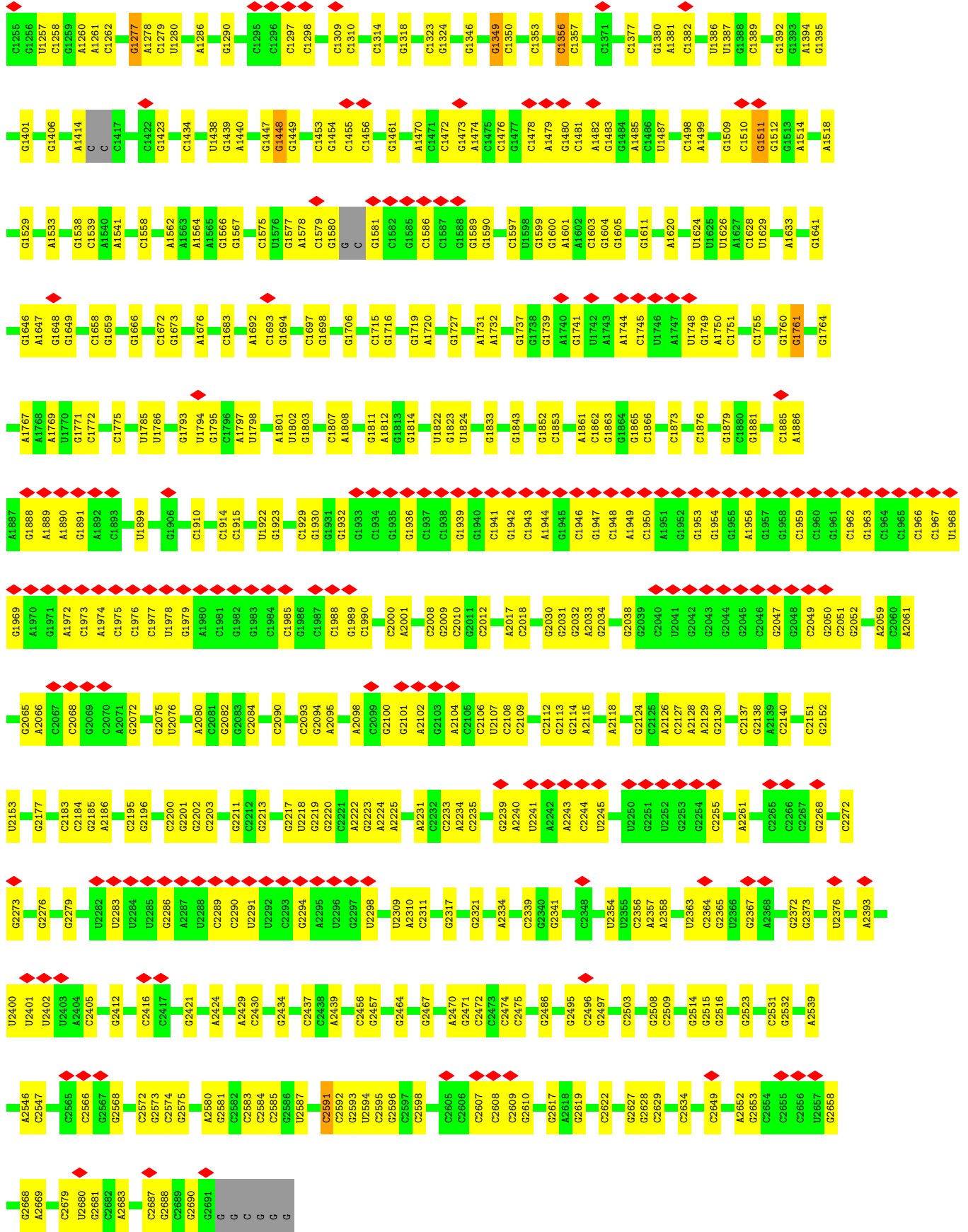
• Molecule 43: Ubiquitin/Ribosomal protein L40e



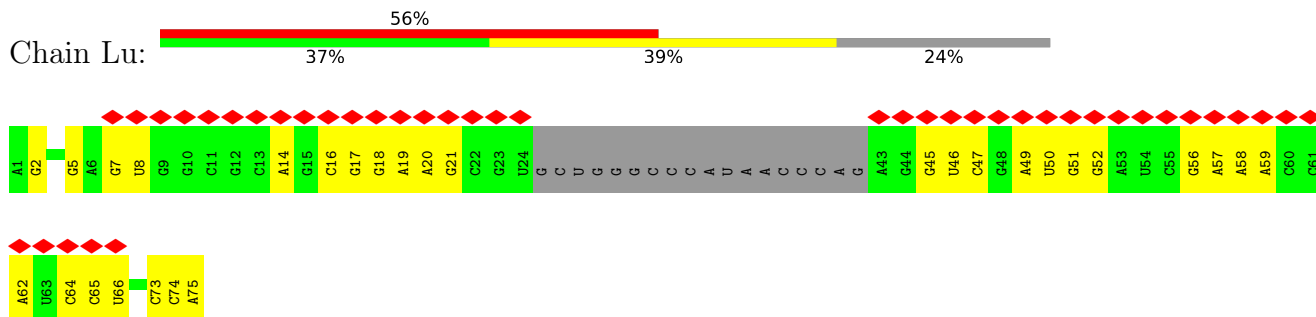


• Molecule 44: Large Subunit rRNA

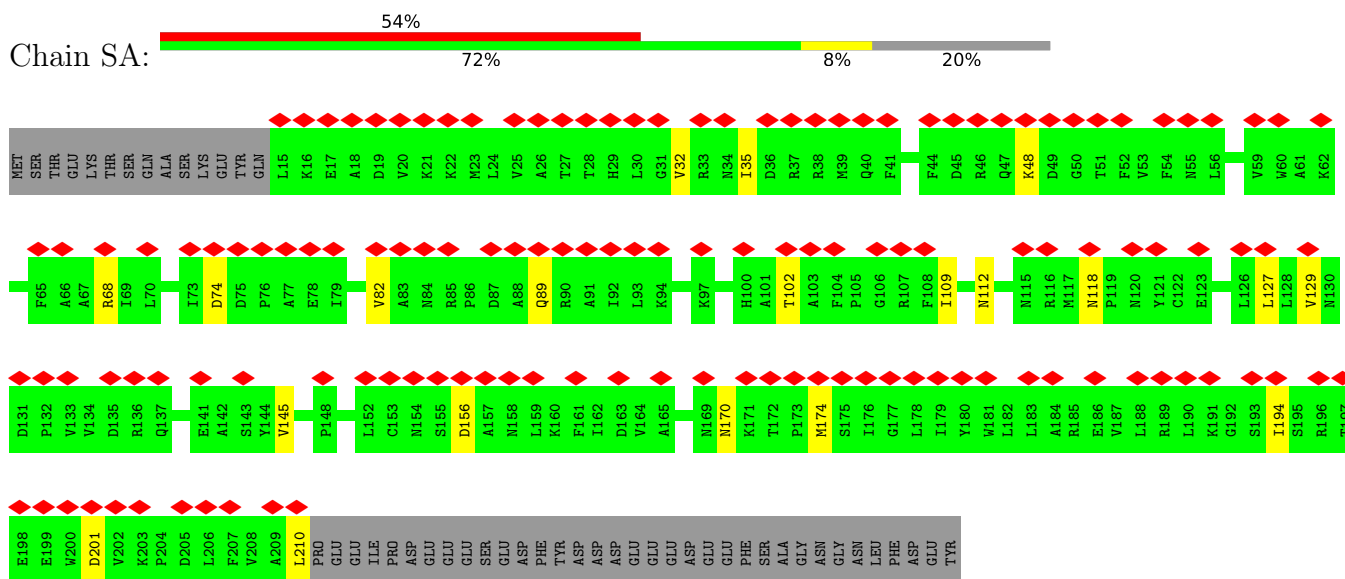




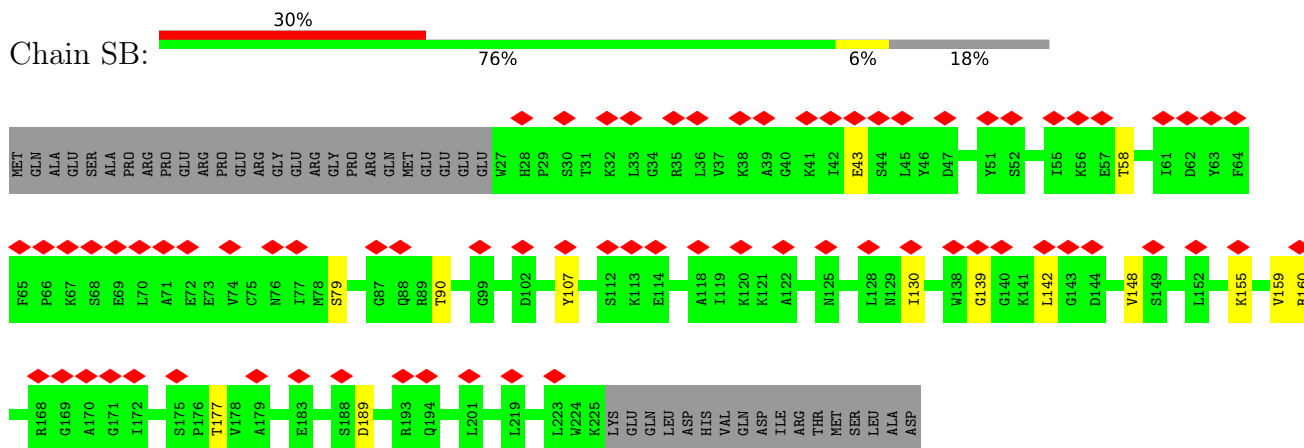
• Molecule 45: E-site tRNA



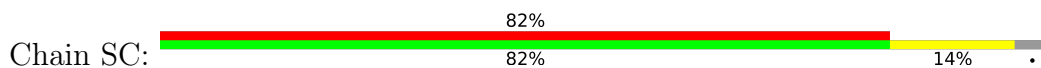
• Molecule 46: 40S ribosomal protein SA

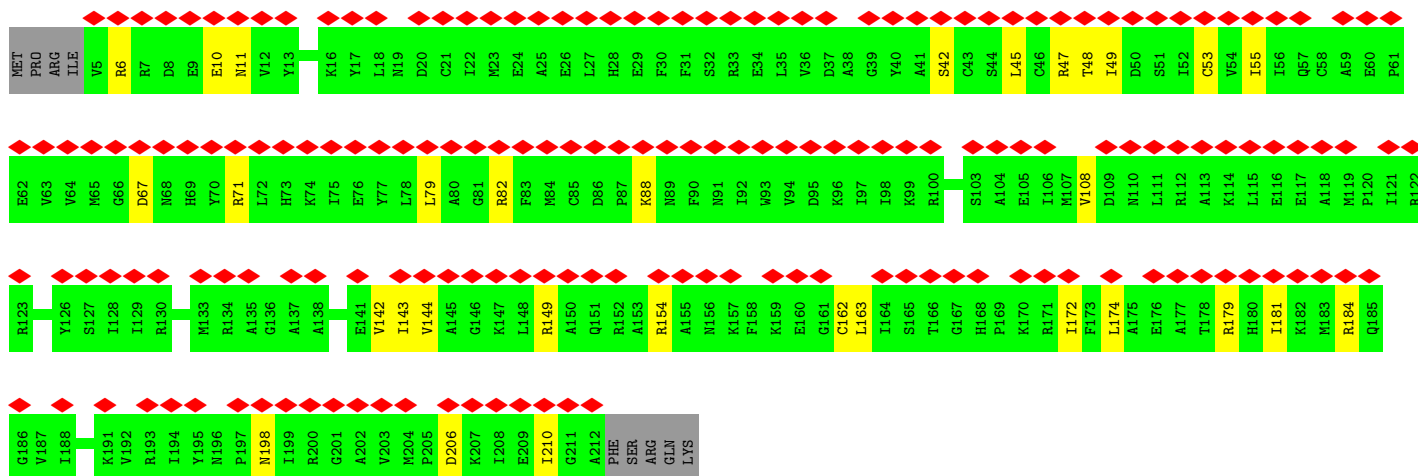


• Molecule 47: Ribosomal protein S2

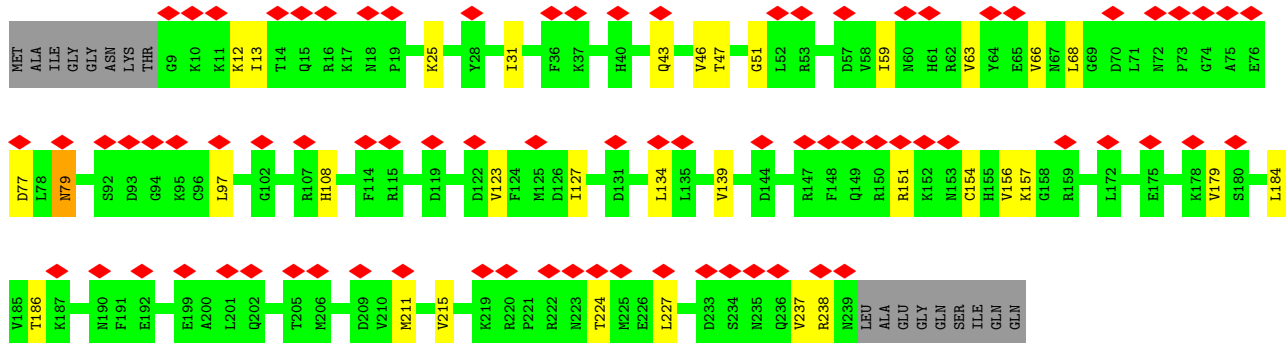
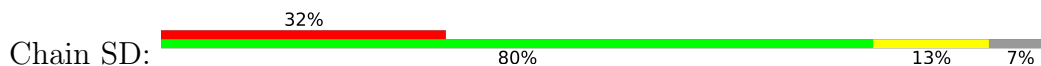


• Molecule 48: Ribosomal protein S3

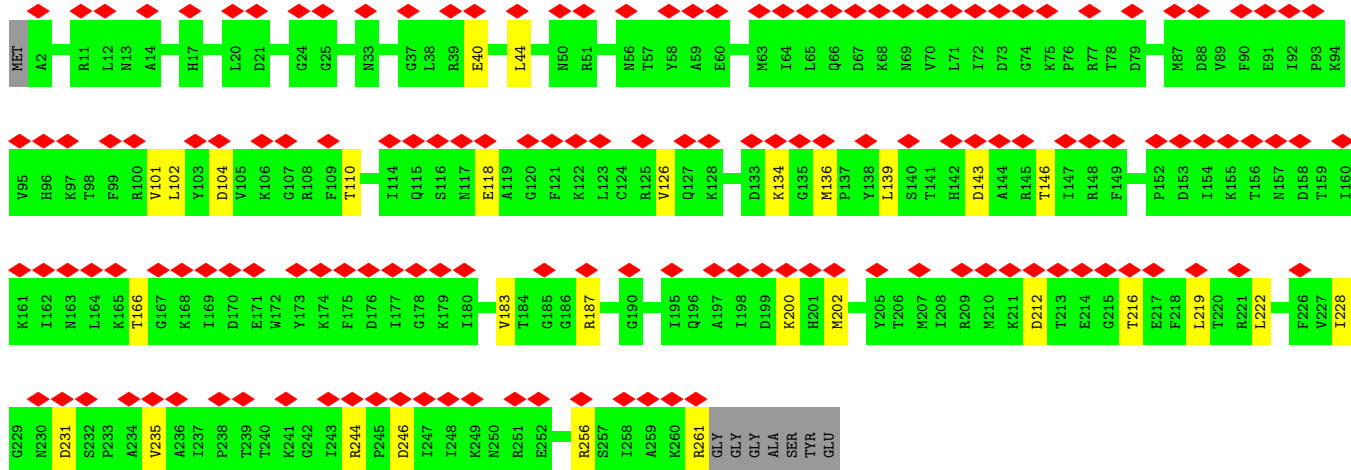
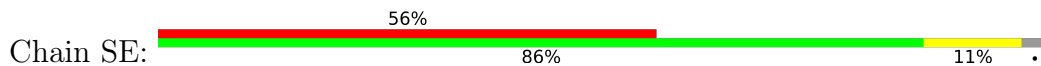




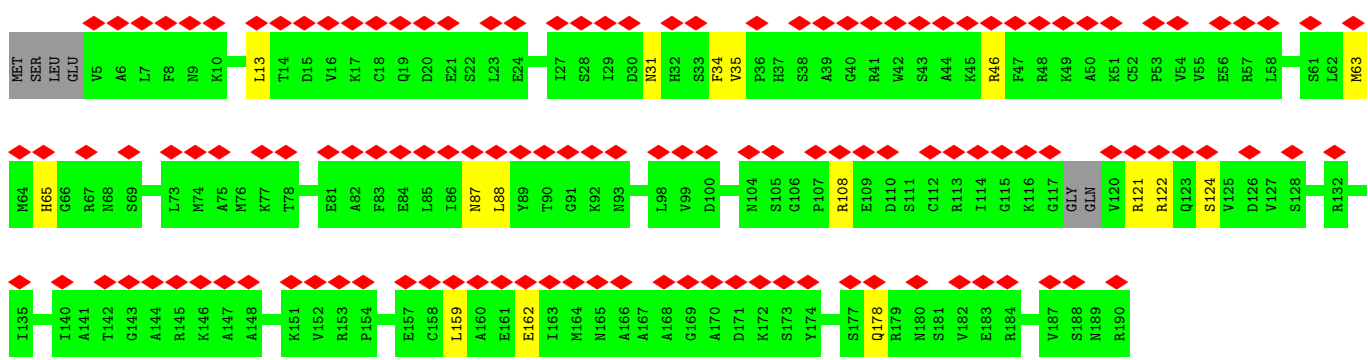
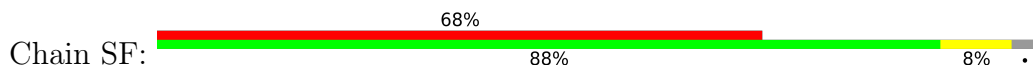
• Molecule 49: 40S ribosomal protein S3a



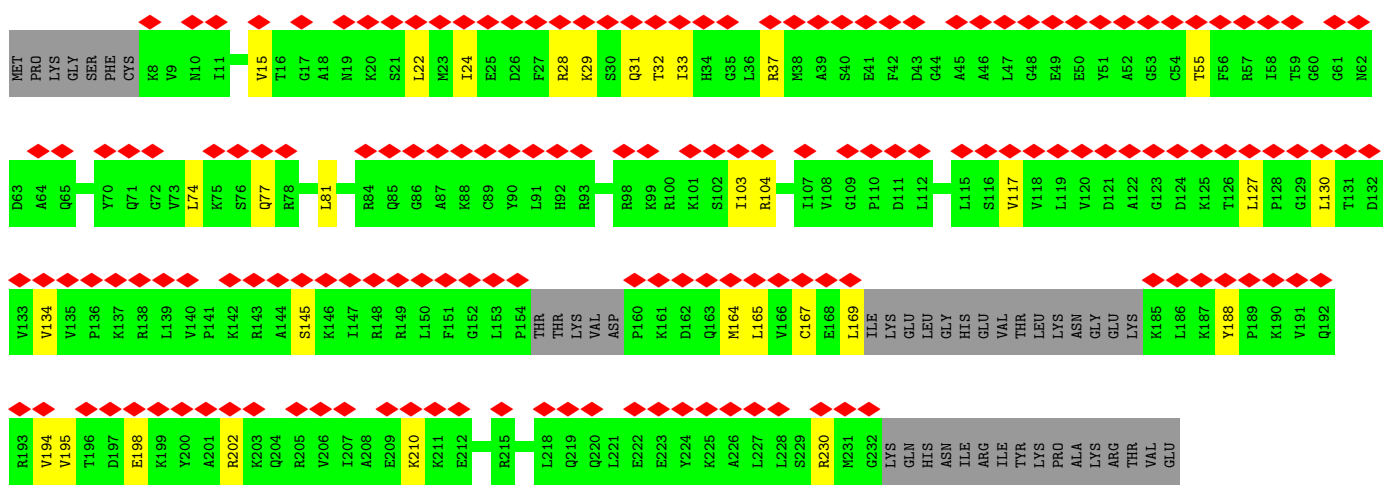
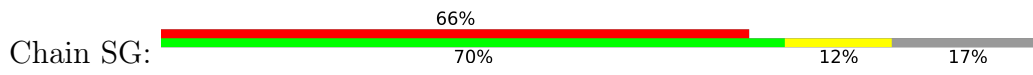
• Molecule 50: 40S ribosomal protein S4



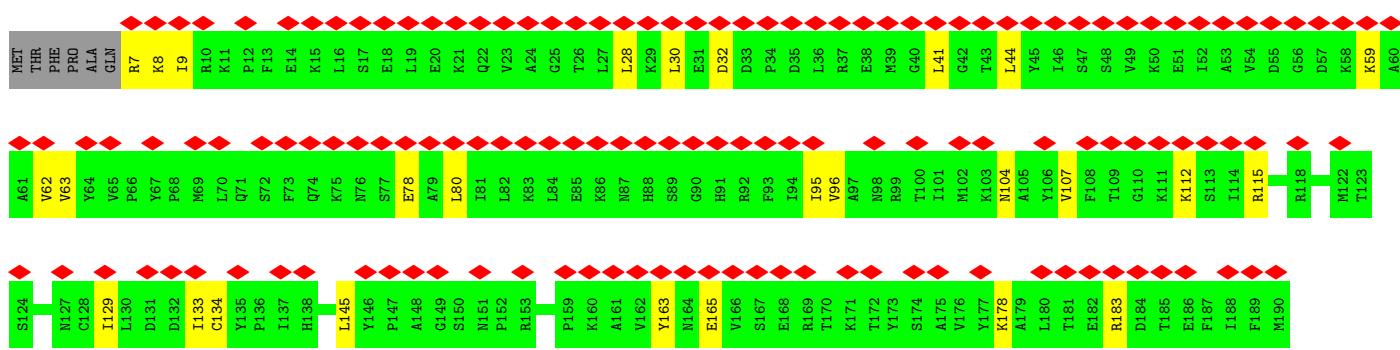
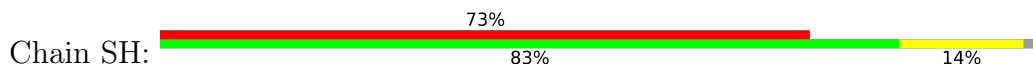
• Molecule 51: Ribosomal protein S5



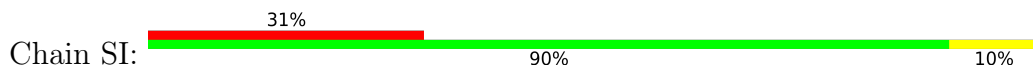
• Molecule 52: 40S ribosomal protein S6

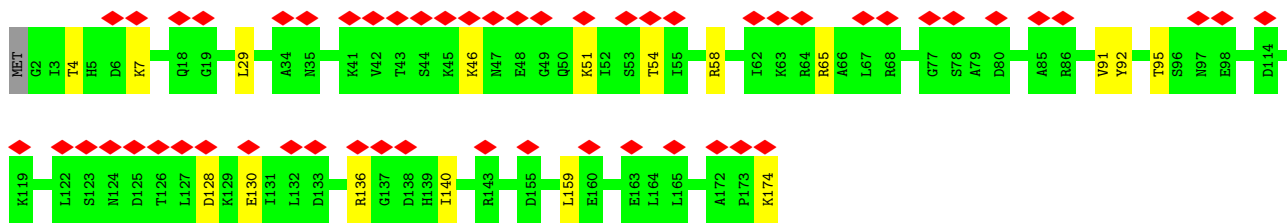


• Molecule 53: 40S ribosomal protein S7

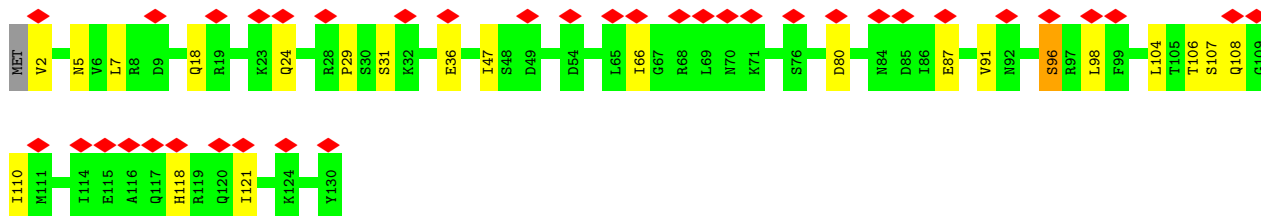
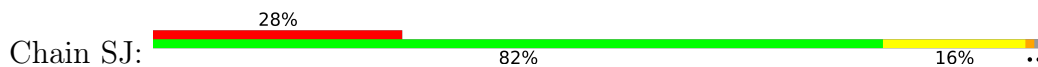


• Molecule 54: 40S ribosomal protein S8

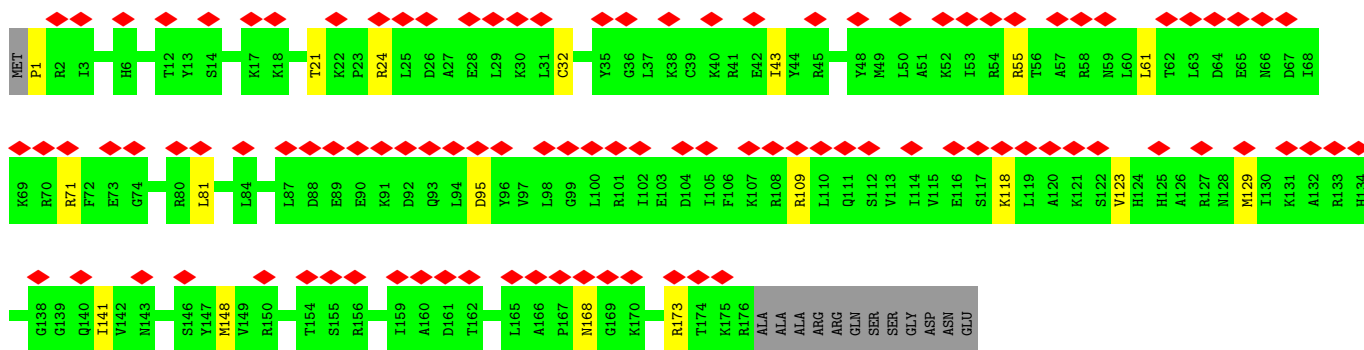
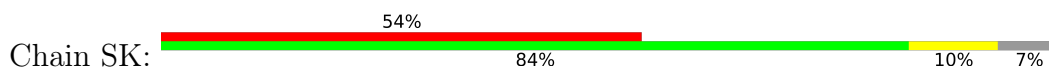




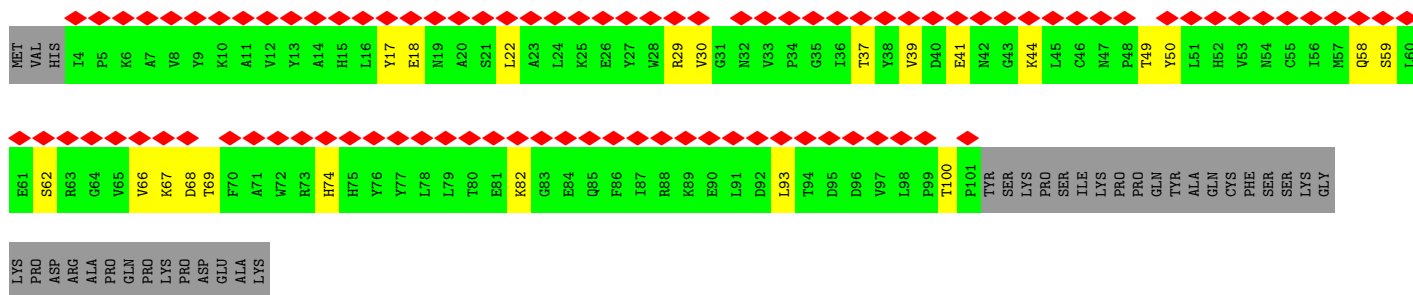
• Molecule 55: Ribosomal protein S15A



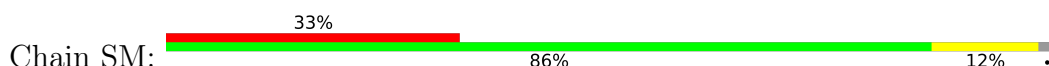
• Molecule 56: Ribosomal protein S9



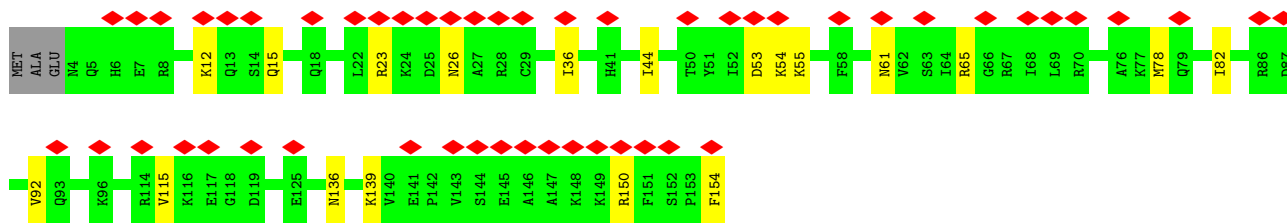
• Molecule 57: Ribosomal protein S10B



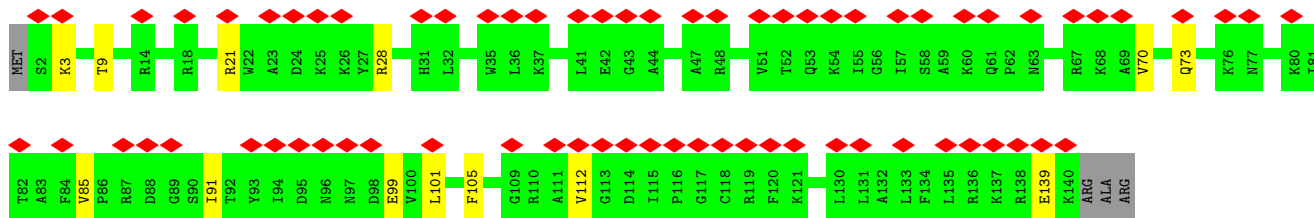
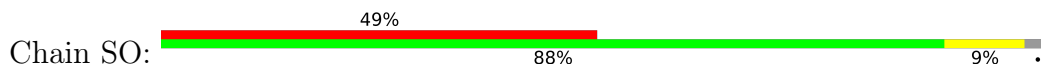
• Molecule 58: Ribosomal protein S11



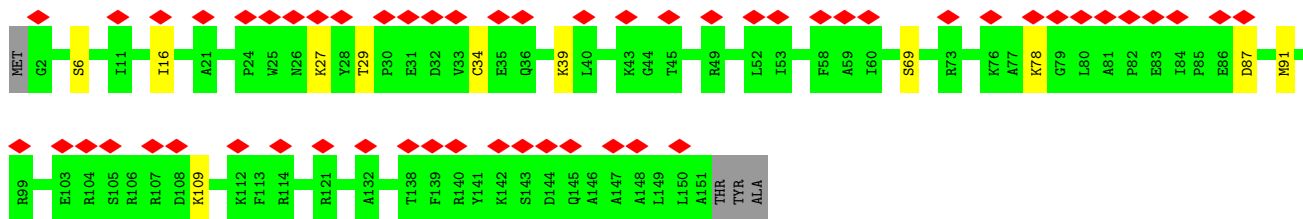
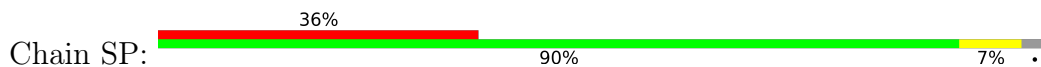




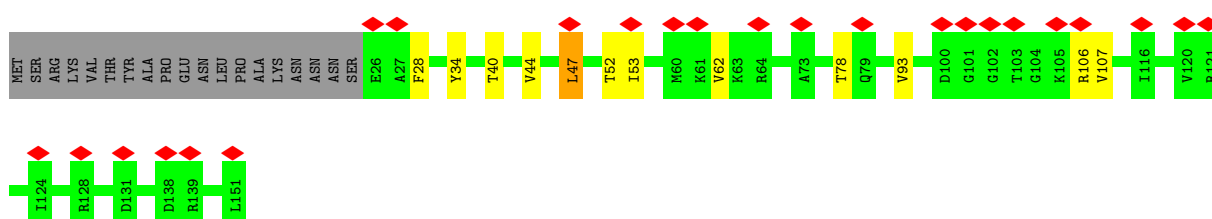
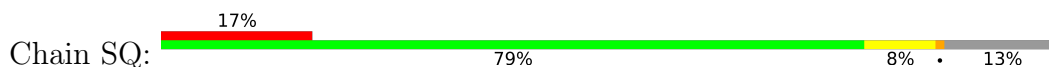
• Molecule 59: Ribosomal protein S23



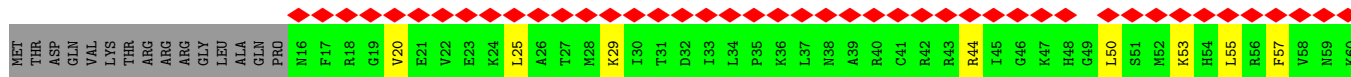
• Molecule 60: Ribosomal protein S13

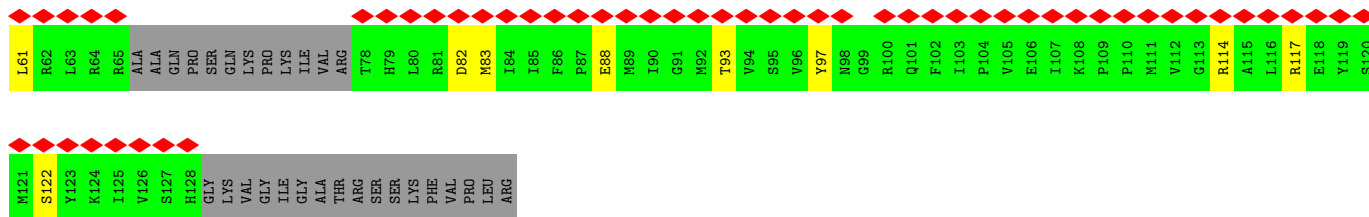


• Molecule 61: Ribosomal protein S14

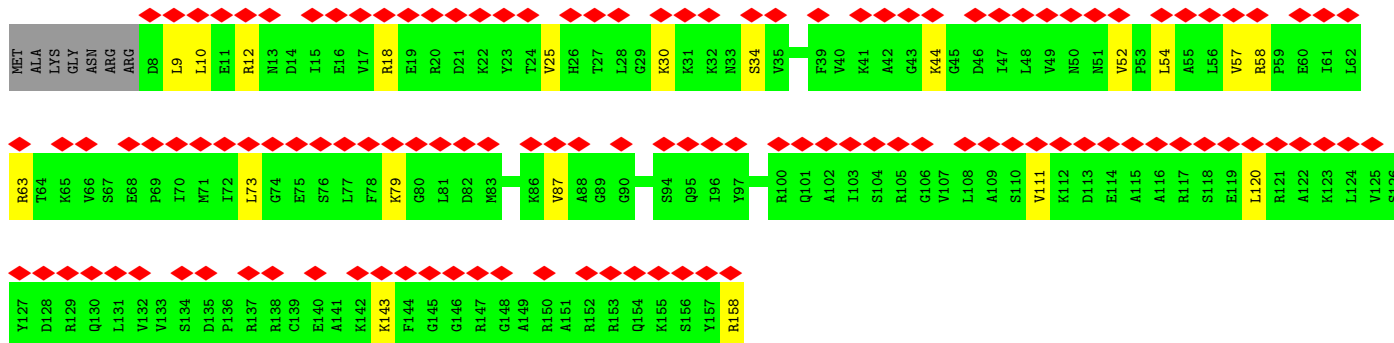
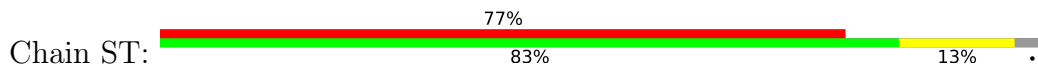


• Molecule 62: Ribosomal protein S15

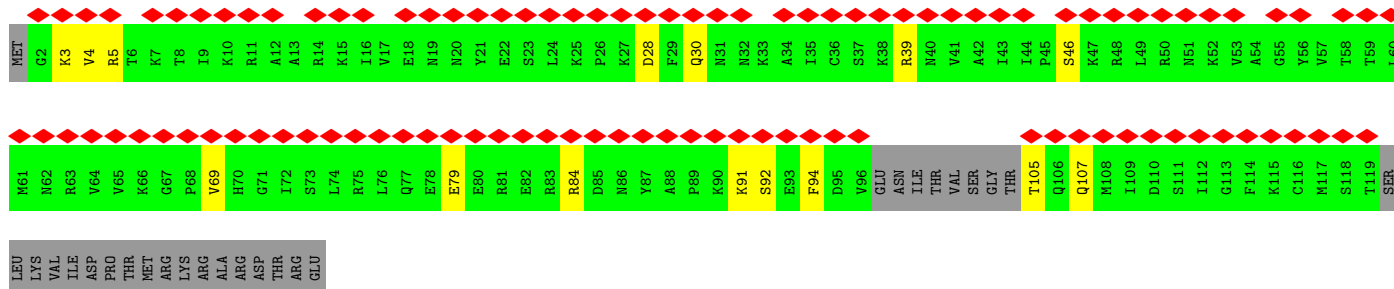
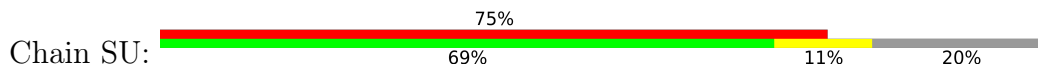




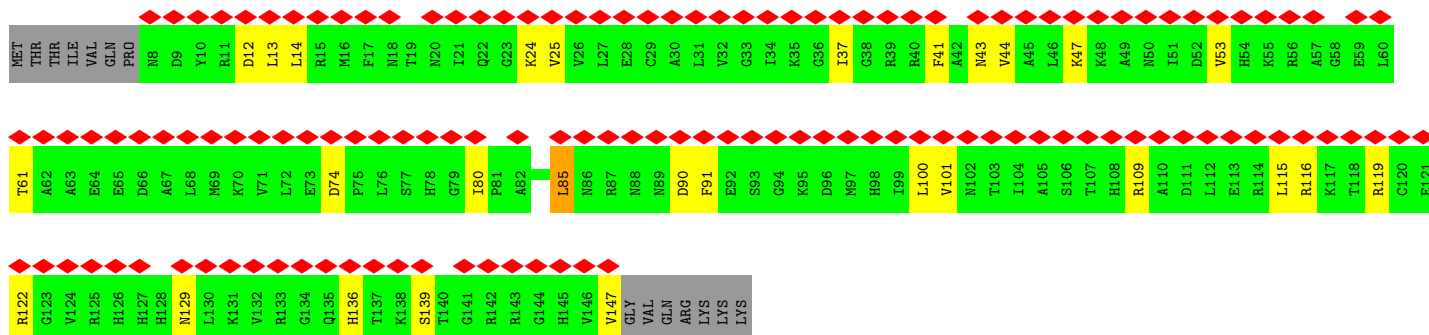
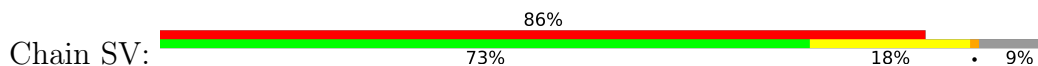
• Molecule 63: Ribosomal protein S16



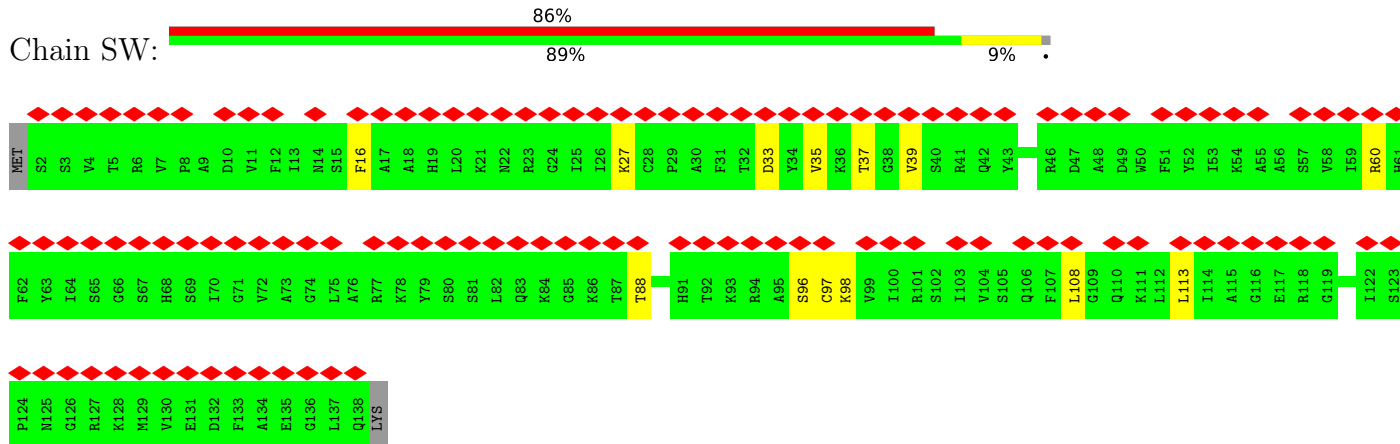
• Molecule 64: Ribosomal protein S17



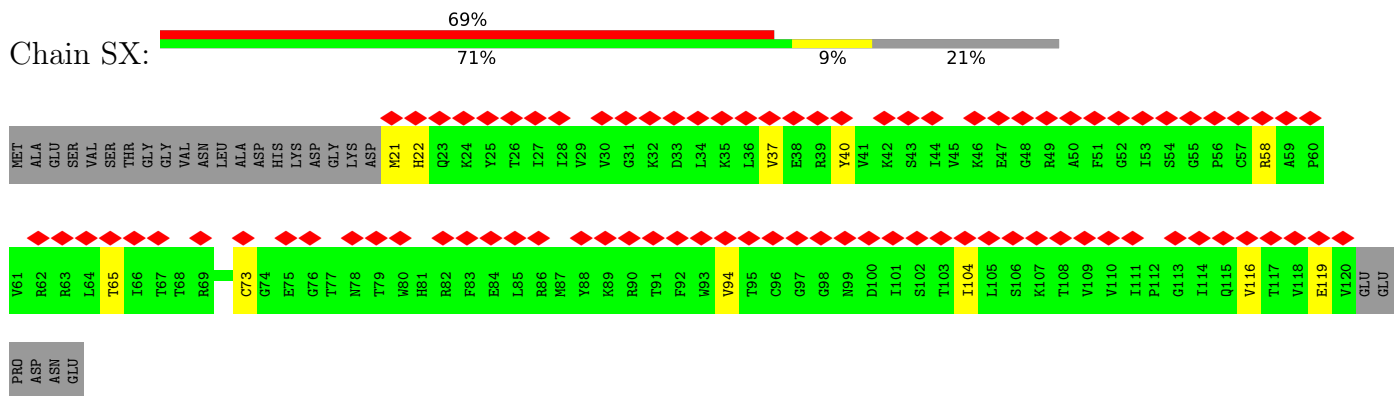
• Molecule 65: Ribosomal protein S18



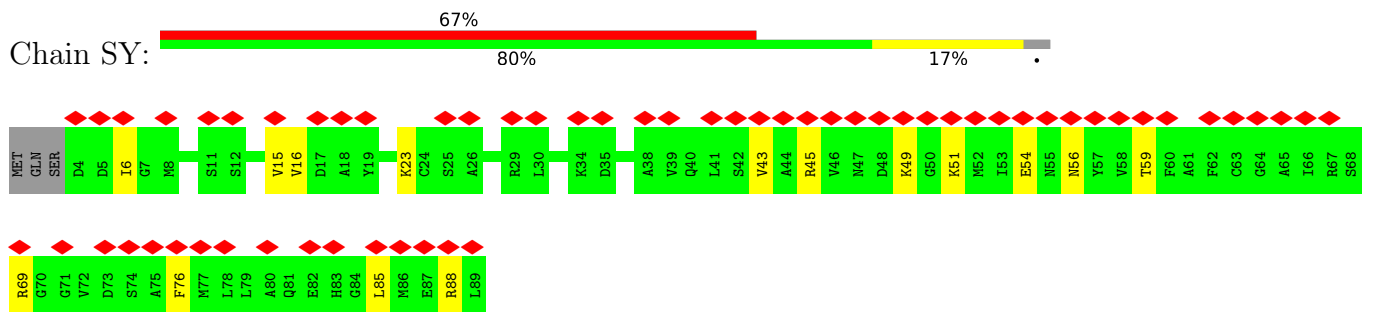
• Molecule 66: Ribosomal protein S19e



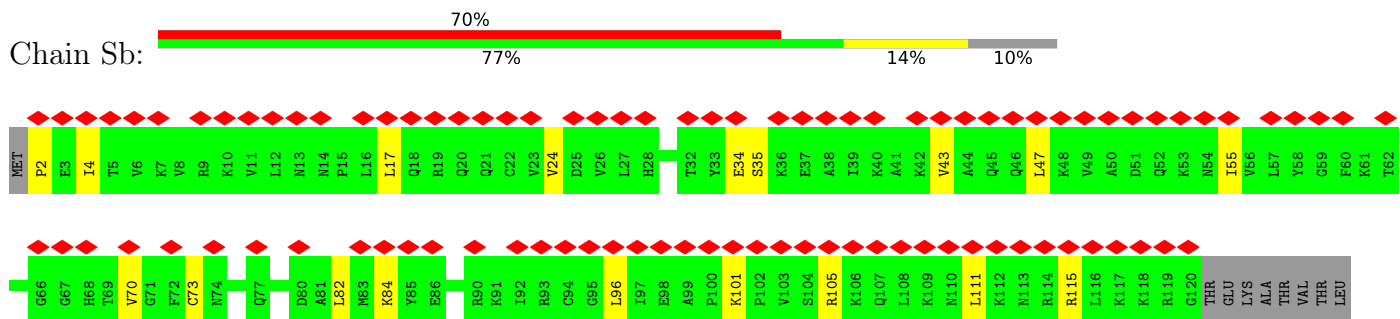
• Molecule 67: Ribosomal protein S20



• Molecule 68: 40S ribosomal protein S21

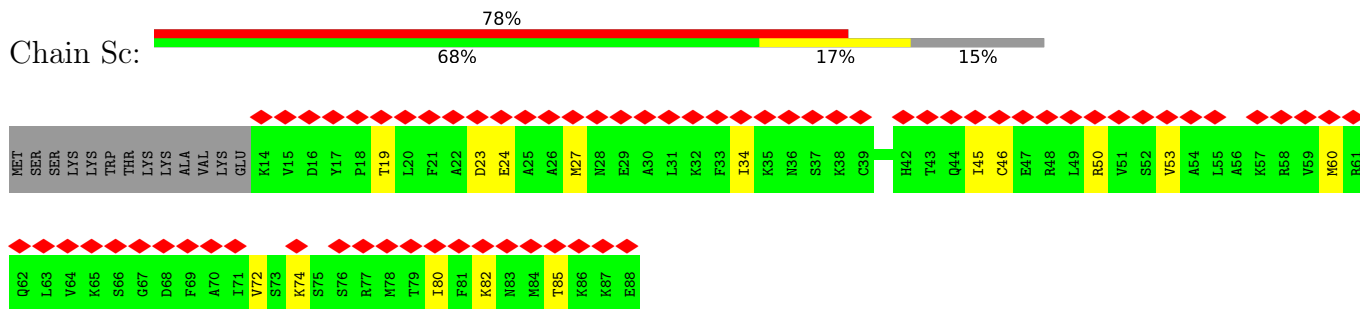


• Molecule 69: Ribosomal protein S24

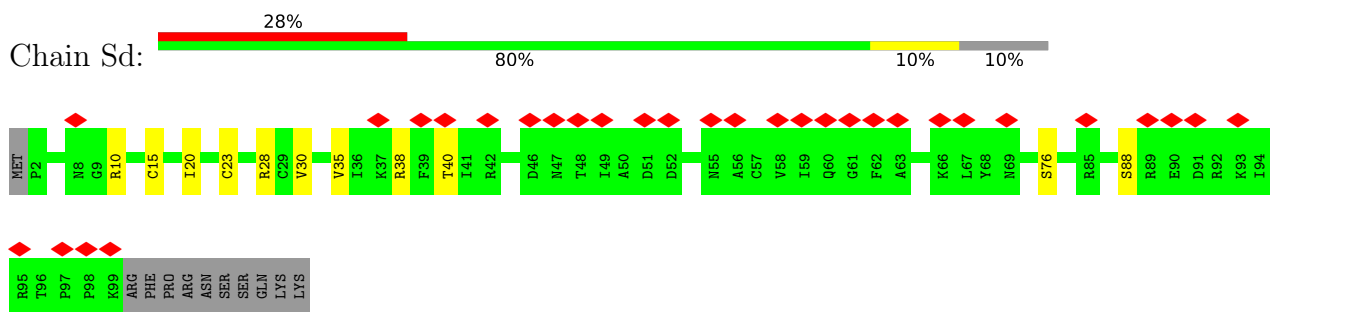


GLY  
ALA  
LYS  
LYS

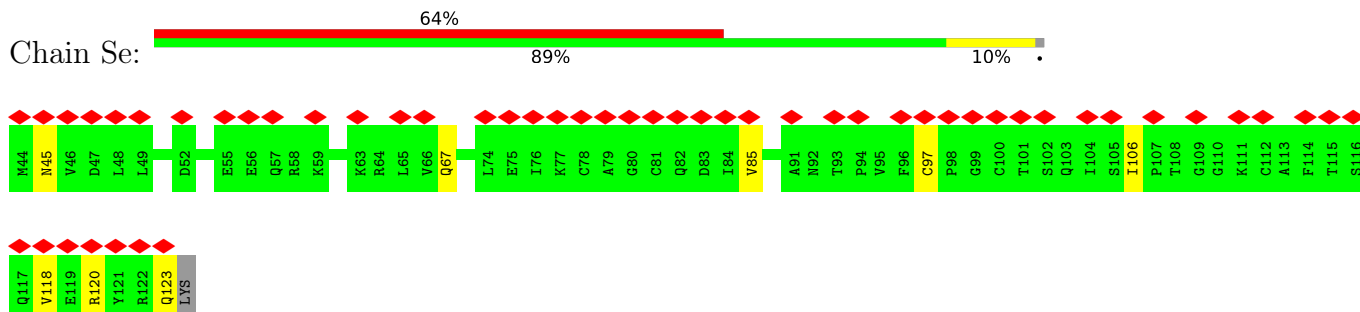
• Molecule 70: 40S ribosomal protein S25



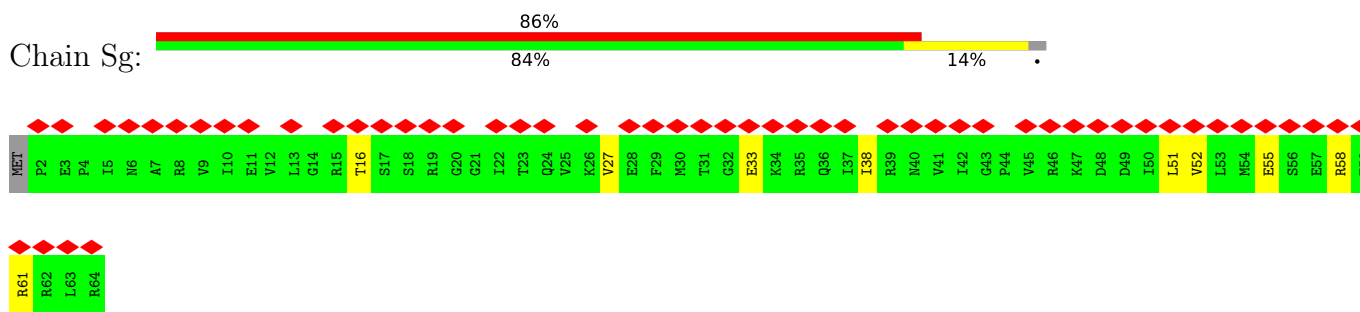
• Molecule 71: 40S ribosomal protein S26



• Molecule 72: Ribosomal protein S27



• Molecule 73: Ribosomal protein S28

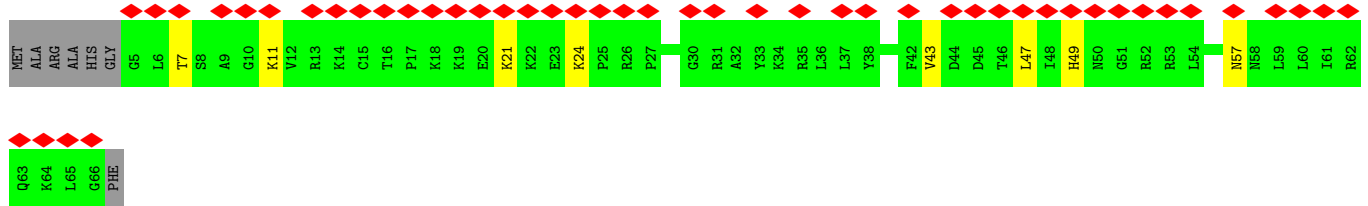
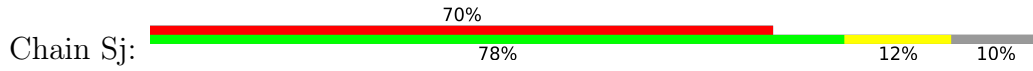


• Molecule 74: Ribosomal protein S29A

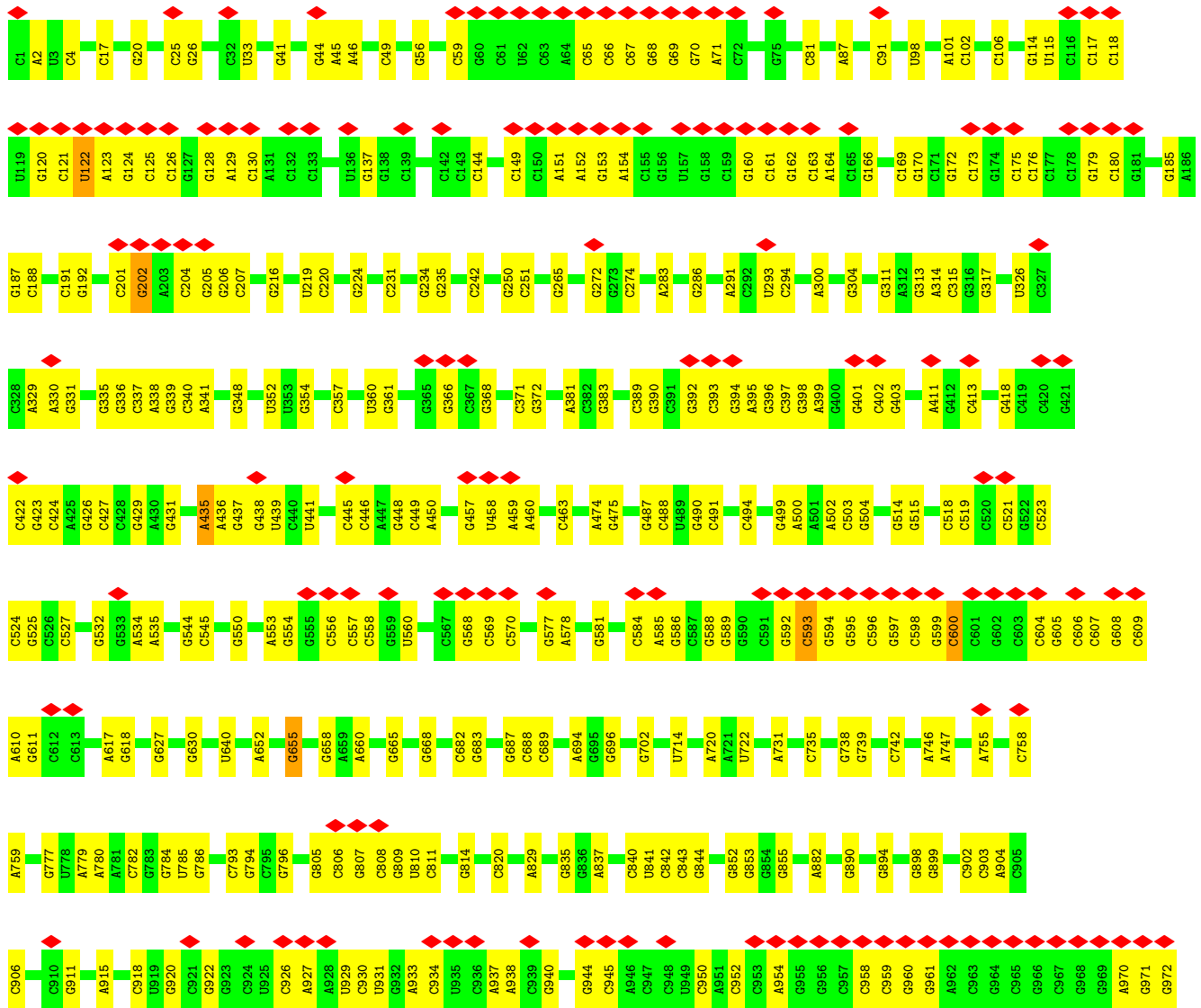


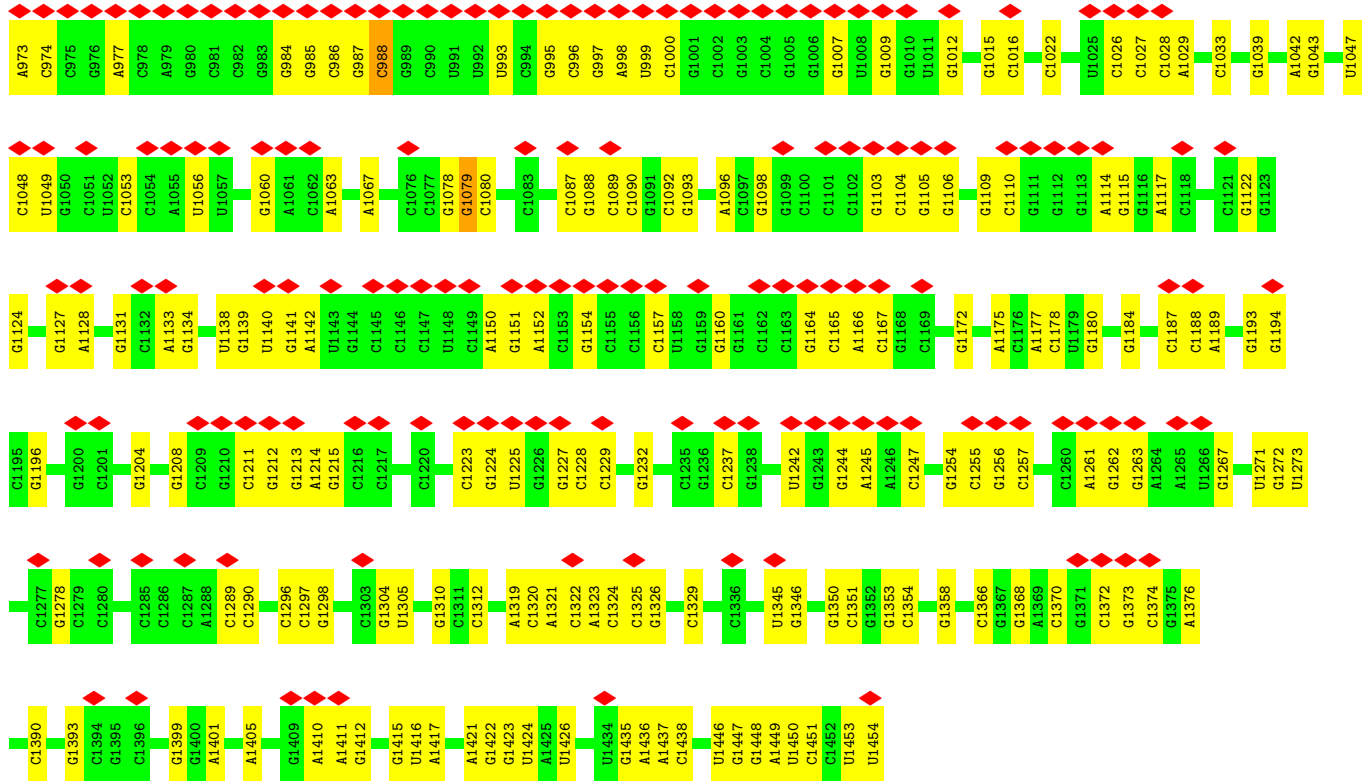


• Molecule 75: 40S ribosomal protein S30



• Molecule 76: Small Subunit rRNA





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29181	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	19.404	Depositor
Minimum map value	-10.312	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	4.7	Depositor
Map size ( $\text{\AA}$ )	410.0, 410.0, 410.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	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	0.60	0/1897	0.81	0/2549
2	LB	0.58	0/3049	0.78	0/4118
3	LC	0.60	0/2463	0.76	1/3342 (0.0%)
4	LD	0.65	0/3393	0.85	1/5292 (0.0%)
5	LE	0.59	0/2798	0.80	0/4361
6	LF	0.58	0/2398	0.76	0/3216
7	LG	0.56	0/450	0.76	1/601 (0.2%)
8	LH	0.58	0/1756	0.74	0/2367
9	LI	0.59	0/1528	0.75	0/2063
10	LJ	0.60	0/1479	0.77	0/1997
11	LK	0.59	0/1296	0.72	0/1736
12	LL	0.60	0/1365	0.72	0/1833
13	LM	0.58	0/1628	0.78	0/2180
14	LN	0.58	0/1037	0.77	0/1390
15	LO	0.57	0/1751	0.76	0/2346
16	LP	0.57	0/1602	0.80	0/2149
17	LQ	0.59	0/1265	0.74	0/1692
18	LR	0.60	0/1425	0.75	0/1907
19	LS	0.56	0/1609	0.69	0/2129
20	LT	0.56	0/1457	0.73	0/1957
21	LU	0.58	0/1290	0.76	0/1735
22	LV	0.56	0/836	0.79	0/1126
23	LW	0.57	0/1035	0.76	0/1396
24	LX	0.57	0/553	0.92	2/736 (0.3%)
25	LY	0.57	0/951	0.74	0/1286
26	LZ	0.58	0/1091	0.74	0/1454
27	La	0.59	0/974	0.79	1/1313 (0.1%)
28	Lb	0.59	0/1231	0.78	1/1647 (0.1%)
29	Lc	0.58	0/441	0.88	1/583 (0.2%)
30	Ld	0.60	0/812	0.82	0/1097
31	Le	0.58	0/832	0.75	0/1118
32	Lf	0.58	0/1074	0.75	1/1432 (0.1%)
33	Lg	0.59	0/793	0.81	0/1062
34	Lh	0.60	0/780	0.81	0/1048



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	Li	0.56	0/996	0.73	0/1328
36	Lj	0.57	0/741	0.76	0/982
37	Lk	0.61	0/705	0.77	0/934
38	Ll	0.59	0/562	0.77	0/749
39	Ln	0.62	0/1621	0.76	0/2183
40	Lo	0.51	0/229	0.72	0/291
41	Lp	0.57	0/778	0.73	0/1029
42	Lq	0.57	0/709	0.80	0/945
43	Ls	0.56	0/392	0.87	0/522
44	Lt	0.62	0/62214	0.84	24/97098 (0.0%)
45	Lu	0.62	0/1366	0.80	0/2127
46	SA	0.59	0/1603	0.76	0/2178
47	SB	0.61	0/1561	0.77	0/2107
48	SC	0.61	0/1674	0.76	0/2248
49	SD	0.57	0/1903	0.74	1/2562 (0.0%)
50	SE	0.60	0/2131	0.76	0/2874
51	SF	0.63	0/1451	0.74	0/1950
52	SG	0.60	0/1637	0.74	0/2185
53	SH	0.61	0/1508	0.74	0/2032
54	SI	0.60	0/1378	0.76	0/1848
55	SJ	0.61	0/1048	0.78	0/1412
56	SK	0.60	0/1443	0.73	1/1930 (0.1%)
57	SL	0.58	0/824	0.75	0/1122
58	SM	0.60	0/1280	0.74	0/1712
59	SO	0.59	0/1095	0.79	0/1467
60	SP	0.57	0/1215	0.74	0/1632
61	SQ	0.60	0/937	0.84	0/1258
62	SR	0.61	0/845	0.79	0/1127
63	ST	0.62	0/1192	0.77	0/1594
64	SU	0.61	0/895	0.81	0/1193
65	SV	0.60	0/1129	0.87	0/1514
66	SW	0.63	0/1095	0.77	0/1473
67	SX	0.59	0/809	0.77	0/1092
68	SY	0.63	0/659	0.80	0/883
69	Sb	0.59	0/960	0.76	0/1284
70	Sc	0.62	0/603	0.78	0/802
71	Sd	0.59	0/809	0.78	0/1088
72	Se	0.62	0/643	0.77	0/871
73	Sg	0.62	0/508	0.79	0/677
74	Sh	0.58	0/425	0.92	2/563 (0.4%)
75	Sj	0.58	0/510	0.76	0/679
76	St	0.63	0/34858	0.85	14/54401 (0.0%)
All	All	0.61	0/187280	0.81	51/274204 (0.0%)

There are no bond length outliers.

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	St	1079	G	C2'-C3'-O3'	8.74	128.72	109.50
74	Sh	120	CYS	CB-CA-C	-7.80	94.79	110.40
29	Lc	50	ASP	CB-CA-C	7.77	125.94	110.40
44	Lt	1448	G	C2'-C3'-O3'	7.65	126.33	109.50
44	Lt	1349	G	C2'-C3'-O3'	7.37	125.72	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	246/251 (98%)	235 (96%)	11 (4%)	0	100	100
2	LB	375/379 (99%)	355 (95%)	16 (4%)	4 (1%)	14	46
3	LC	307/316 (97%)	298 (97%)	8 (3%)	1 (0%)	41	73
6	LF	291/297 (98%)	280 (96%)	10 (3%)	1 (0%)	41	73
7	LG	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
8	LH	211/235 (90%)	205 (97%)	5 (2%)	1 (0%)	29	63
9	LI	184/225 (82%)	171 (93%)	11 (6%)	2 (1%)	14	46
10	LJ	182/185 (98%)	163 (90%)	15 (8%)	4 (2%)	6	32
11	LK	152/210 (72%)	146 (96%)	5 (3%)	1 (1%)	22	56
12	LL	165/173 (95%)	157 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	LM	199/234 (85%)	187 (94%)	10 (5%)	2 (1%)	15	49
14	LN	128/131 (98%)	123 (96%)	5 (4%)	0	100	100
15	LO	201/204 (98%)	192 (96%)	8 (4%)	1 (0%)	29	63
16	LP	191/197 (97%)	185 (97%)	4 (2%)	2 (1%)	15	49
17	LQ	152/164 (93%)	146 (96%)	5 (3%)	1 (1%)	22	56
18	LR	176/179 (98%)	168 (96%)	7 (4%)	1 (1%)	25	59
19	LS	190/196 (97%)	186 (98%)	4 (2%)	0	100	100
20	LT	168/173 (97%)	164 (98%)	4 (2%)	0	100	100
21	LU	155/159 (98%)	145 (94%)	8 (5%)	2 (1%)	12	42
22	LV	98/124 (79%)	86 (88%)	9 (9%)	3 (3%)	4	25
23	LW	130/142 (92%)	126 (97%)	4 (3%)	0	100	100
24	LX	61/189 (32%)	57 (93%)	4 (7%)	0	100	100
25	LY	113/141 (80%)	108 (96%)	4 (4%)	1 (1%)	17	51
26	LZ	131/135 (97%)	127 (97%)	4 (3%)	0	100	100
27	La	115/135 (85%)	104 (90%)	9 (8%)	2 (2%)	9	36
28	Lb	146/149 (98%)	136 (93%)	8 (6%)	2 (1%)	11	40
29	Lc	50/62 (81%)	46 (92%)	3 (6%)	1 (2%)	7	33
30	Ld	105/109 (96%)	102 (97%)	3 (3%)	0	100	100
31	Le	98/106 (92%)	94 (96%)	4 (4%)	0	100	100
32	Lf	125/136 (92%)	121 (97%)	4 (3%)	0	100	100
33	Lg	96/123 (78%)	94 (98%)	1 (1%)	1 (1%)	15	49
34	Lh	93/120 (78%)	89 (96%)	1 (1%)	3 (3%)	4	24
35	Li	120/124 (97%)	112 (93%)	8 (7%)	0	100	100
36	Lj	87/90 (97%)	81 (93%)	5 (6%)	1 (1%)	14	46
37	Lk	83/89 (93%)	78 (94%)	5 (6%)	0	100	100
38	Ll	70/77 (91%)	68 (97%)	2 (3%)	0	100	100
39	Ln	194/217 (89%)	180 (93%)	12 (6%)	2 (1%)	15	49
40	Lo	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
41	Lp	91/106 (86%)	88 (97%)	3 (3%)	0	100	100
42	Lq	88/94 (94%)	87 (99%)	1 (1%)	0	100	100
43	Ls	45/127 (35%)	44 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	SA	194/245 (79%)	188 (97%)	5 (3%)	1 (0%)	29	63
47	SB	197/242 (81%)	186 (94%)	10 (5%)	1 (0%)	29	63
48	SC	206/217 (95%)	193 (94%)	12 (6%)	1 (0%)	29	63
49	SD	229/248 (92%)	217 (95%)	10 (4%)	2 (1%)	17	51
50	SE	258/268 (96%)	241 (93%)	15 (6%)	2 (1%)	19	53
51	SF	180/190 (95%)	174 (97%)	5 (3%)	1 (1%)	25	59
52	SG	199/248 (80%)	189 (95%)	10 (5%)	0	100	100
53	SH	182/190 (96%)	169 (93%)	12 (7%)	1 (0%)	29	63
54	SI	171/174 (98%)	165 (96%)	4 (2%)	2 (1%)	13	44
55	SJ	127/130 (98%)	121 (95%)	4 (3%)	2 (2%)	9	38
56	SK	174/189 (92%)	167 (96%)	6 (3%)	1 (1%)	25	59
57	SL	96/134 (72%)	94 (98%)	2 (2%)	0	100	100
58	SM	149/154 (97%)	135 (91%)	12 (8%)	2 (1%)	12	42
59	SO	137/143 (96%)	132 (96%)	3 (2%)	2 (2%)	10	39
60	SP	148/154 (96%)	142 (96%)	6 (4%)	0	100	100
61	SQ	124/145 (86%)	116 (94%)	7 (6%)	1 (1%)	19	53
62	SR	97/145 (67%)	94 (97%)	3 (3%)	0	100	100
63	ST	149/158 (94%)	143 (96%)	6 (4%)	0	100	100
64	SU	106/137 (77%)	100 (94%)	4 (4%)	2 (2%)	8	34
65	SV	138/154 (90%)	120 (87%)	14 (10%)	4 (3%)	4	26
66	SW	135/139 (97%)	126 (93%)	8 (6%)	1 (1%)	22	56
67	SX	98/126 (78%)	95 (97%)	3 (3%)	0	100	100
68	SY	84/89 (94%)	78 (93%)	5 (6%)	1 (1%)	13	44
69	Sb	117/132 (89%)	110 (94%)	6 (5%)	1 (1%)	17	51
70	Sc	73/88 (83%)	65 (89%)	7 (10%)	1 (1%)	11	40
71	Sd	96/109 (88%)	92 (96%)	4 (4%)	0	100	100
72	Se	78/81 (96%)	72 (92%)	6 (8%)	0	100	100
73	Sg	61/64 (95%)	56 (92%)	5 (8%)	0	100	100
74	Sh	48/51 (94%)	44 (92%)	3 (6%)	1 (2%)	7	32
75	Sj	60/69 (87%)	56 (93%)	4 (7%)	0	100	100
All	All	9994/11192 (89%)	9480 (95%)	445 (4%)	69 (1%)	26	56

5 of 69 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	LV	45	ILE
27	La	89	TYR
27	La	98	VAL
29	Lc	50	ASP
48	SC	210	ILE

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	LA	189/192 (98%)	171 (90%)	18 (10%)	8 31
2	LB	311/313 (99%)	272 (88%)	39 (12%)	4 18
3	LC	257/263 (98%)	237 (92%)	20 (8%)	12 40
6	LF	238/242 (98%)	208 (87%)	30 (13%)	4 18
7	LG	47/48 (98%)	44 (94%)	3 (6%)	17 48
8	LH	184/204 (90%)	170 (92%)	14 (8%)	13 41
9	LI	166/198 (84%)	150 (90%)	16 (10%)	8 30
10	LJ	163/164 (99%)	151 (93%)	12 (7%)	13 42
11	LK	133/177 (75%)	120 (90%)	13 (10%)	8 30
12	LL	143/149 (96%)	126 (88%)	17 (12%)	5 20
13	LM	169/197 (86%)	144 (85%)	25 (15%)	3 13
14	LN	110/111 (99%)	98 (89%)	12 (11%)	6 25
15	LO	174/175 (99%)	161 (92%)	13 (8%)	13 42
16	LP	161/165 (98%)	146 (91%)	15 (9%)	9 32
17	LQ	131/139 (94%)	125 (95%)	6 (5%)	27 59
18	LR	154/155 (99%)	136 (88%)	18 (12%)	5 21
19	LS	163/167 (98%)	144 (88%)	19 (12%)	5 21
20	LT	151/154 (98%)	133 (88%)	18 (12%)	5 20
21	LU	131/133 (98%)	113 (86%)	18 (14%)	3 15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	LV	88/110 (80%)	75 (85%)	13 (15%)	3	13
23	LW	108/114 (95%)	98 (91%)	10 (9%)	9	32
24	LX	61/174 (35%)	51 (84%)	10 (16%)	2	10
25	LY	104/123 (85%)	94 (90%)	10 (10%)	8	30
26	LZ	114/115 (99%)	102 (90%)	12 (10%)	7	26
27	La	105/119 (88%)	92 (88%)	13 (12%)	4	19
28	Lb	126/127 (99%)	118 (94%)	8 (6%)	18	49
29	Lc	48/57 (84%)	46 (96%)	2 (4%)	30	60
30	Ld	91/92 (99%)	78 (86%)	13 (14%)	3	14
31	Le	88/92 (96%)	82 (93%)	6 (7%)	16	46
32	Lf	113/120 (94%)	102 (90%)	11 (10%)	8	30
33	Lg	82/103 (80%)	74 (90%)	8 (10%)	8	30
34	Lh	84/100 (84%)	80 (95%)	4 (5%)	25	57
35	Li	105/107 (98%)	97 (92%)	8 (8%)	13	41
36	Lj	77/78 (99%)	71 (92%)	6 (8%)	12	40
37	Lk	71/74 (96%)	66 (93%)	5 (7%)	15	45
38	Ll	63/68 (93%)	50 (79%)	13 (21%)	1	4
39	Ln	173/189 (92%)	140 (81%)	33 (19%)	1	5
40	Lo	22/22 (100%)	21 (96%)	1 (4%)	27	59
41	Lp	83/93 (89%)	72 (87%)	11 (13%)	4	16
42	Lq	70/73 (96%)	59 (84%)	11 (16%)	2	11
43	Ls	43/110 (39%)	36 (84%)	7 (16%)	2	10
46	SA	171/217 (79%)	152 (89%)	19 (11%)	6	24
47	SB	163/201 (81%)	150 (92%)	13 (8%)	12	39
48	SC	173/182 (95%)	143 (83%)	30 (17%)	2	8
49	SD	208/220 (94%)	177 (85%)	31 (15%)	3	13
50	SE	228/232 (98%)	201 (88%)	27 (12%)	5	21
51	SF	152/157 (97%)	137 (90%)	15 (10%)	8	29
52	SG	174/213 (82%)	143 (82%)	31 (18%)	2	7
53	SH	165/170 (97%)	139 (84%)	26 (16%)	2	11
54	SI	147/148 (99%)	132 (90%)	15 (10%)	7	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	SJ	114/115 (99%)	93 (82%)	21 (18%)	1	6
56	SK	155/164 (94%)	139 (90%)	16 (10%)	7	27
57	SL	87/119 (73%)	65 (75%)	22 (25%)	0	2
58	SM	134/136 (98%)	117 (87%)	17 (13%)	4	18
59	SO	111/114 (97%)	100 (90%)	11 (10%)	8	29
60	SP	125/130 (96%)	114 (91%)	11 (9%)	10	34
61	SQ	87/113 (77%)	75 (86%)	12 (14%)	3	15
62	SR	92/128 (72%)	75 (82%)	17 (18%)	1	6
63	ST	125/130 (96%)	105 (84%)	20 (16%)	2	10
64	SU	99/124 (80%)	86 (87%)	13 (13%)	4	17
65	SV	118/131 (90%)	93 (79%)	25 (21%)	1	3
66	SW	113/115 (98%)	101 (89%)	12 (11%)	6	26
67	SX	89/110 (81%)	78 (88%)	11 (12%)	4	19
68	SY	69/72 (96%)	55 (80%)	14 (20%)	1	4
69	Sb	103/113 (91%)	86 (84%)	17 (16%)	2	10
70	Sc	67/79 (85%)	53 (79%)	14 (21%)	1	4
71	Sd	92/103 (89%)	81 (88%)	11 (12%)	5	20
72	Se	72/73 (99%)	64 (89%)	8 (11%)	6	24
73	Sg	56/57 (98%)	47 (84%)	9 (16%)	2	10
74	Sh	44/45 (98%)	32 (73%)	12 (27%)	0	1
75	Sj	54/58 (93%)	46 (85%)	8 (15%)	3	13
All	All	8681/9575 (91%)	7632 (88%)	1049 (12%)	8	20

5 of 1049 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
65	SV	116	ARG
67	SX	104	ILE
65	SV	115	LEU
74	Sh	122	ARG
27	La	101	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 110 such sidechains are listed below:

Mol	Chain	Res	Type
41	Lp	18	HIS
51	SF	139	ASN
75	Sj	57	ASN
68	SY	81	GLN
43	Ls	98	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	LD	141/142 (99%)	42 (29%)	11 (7%)
44	Lt	2588/2697 (95%)	760 (29%)	0
45	Lu	55/75 (73%)	29 (52%)	0
5	LE	116/121 (95%)	30 (25%)	5 (4%)
76	St	1453/1454 (99%)	496 (34%)	0
All	All	4353/4489 (96%)	1357 (31%)	16 (0%)

5 of 1357 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	LD	9	C
4	LD	12	C
4	LD	17	G
4	LD	20	G
4	LD	21	C

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	LE	85	U
5	LE	63	U
4	LD	88	G
5	LE	50	A
4	LD	87	A

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.



## 5.6 Ligand geometry [i](#)

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.

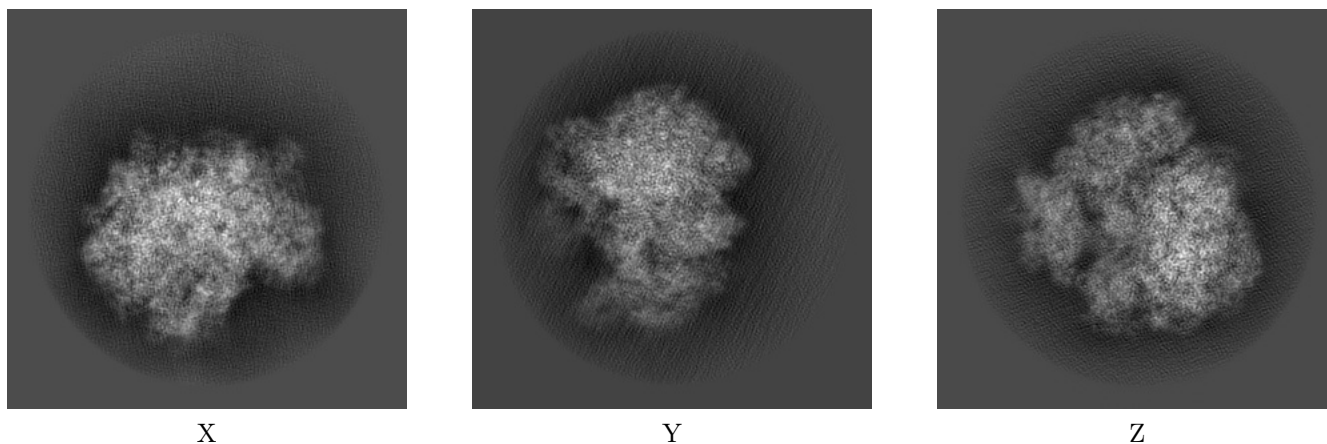
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16211. These allow visual inspection of the internal detail of the map and identification of artifacts.

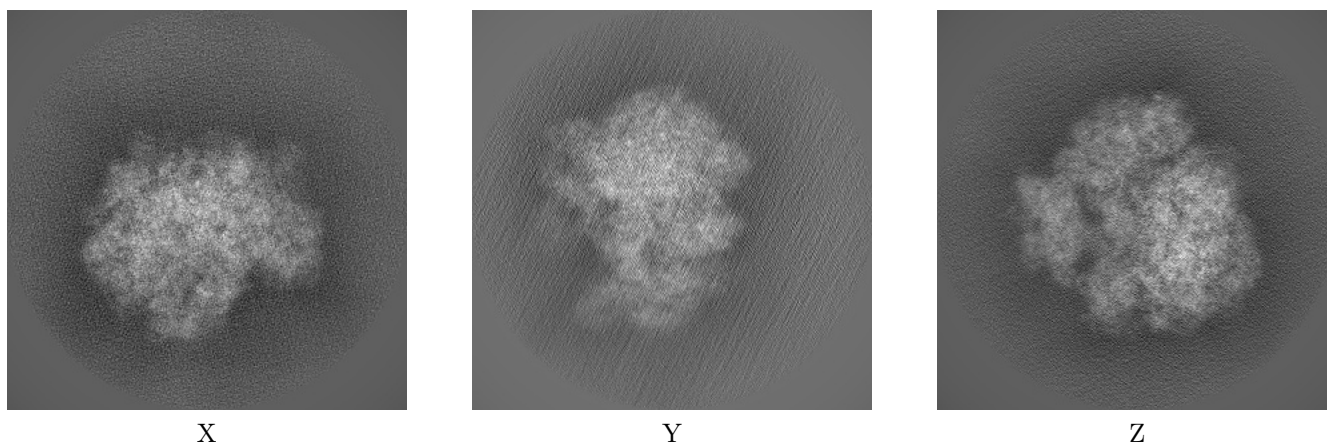
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

#### 6.1.1 Primary map



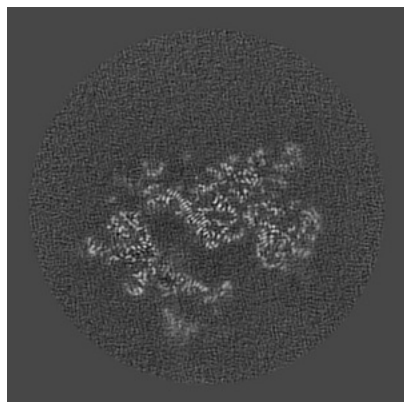
#### 6.1.2 Raw map



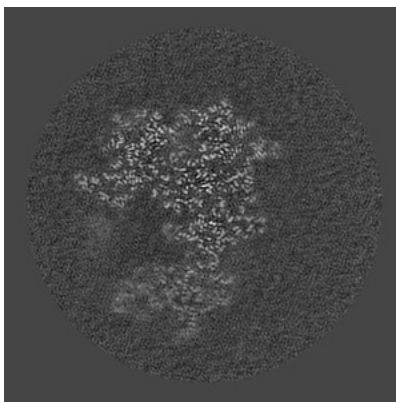
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

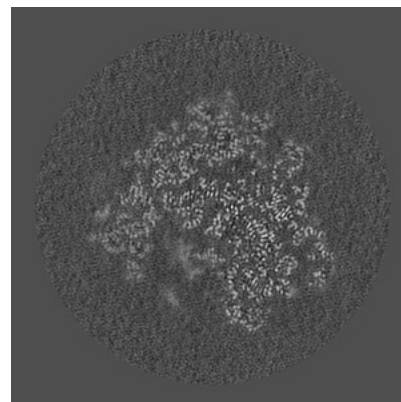
### 6.2.1 Primary map



X Index: 250

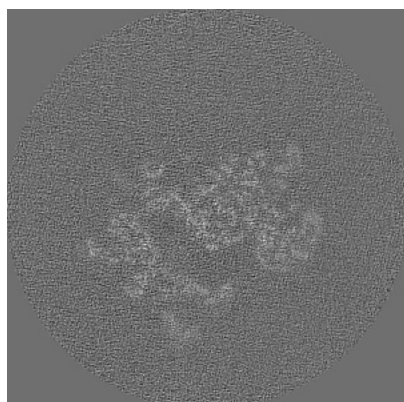


Y Index: 250

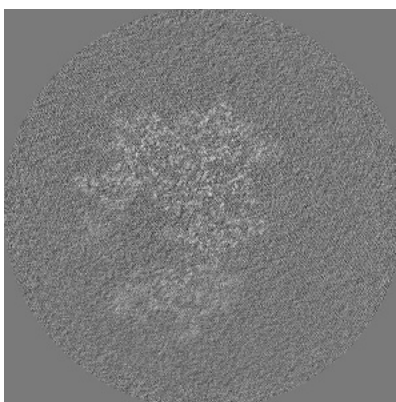


Z Index: 250

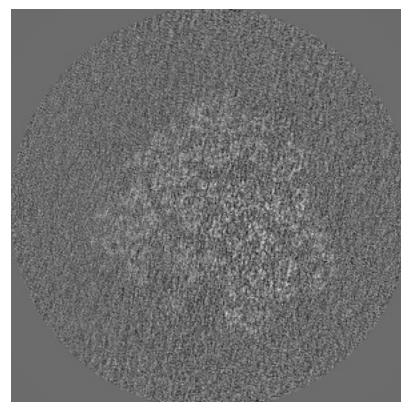
### 6.2.2 Raw map



X Index: 250



Y Index: 250

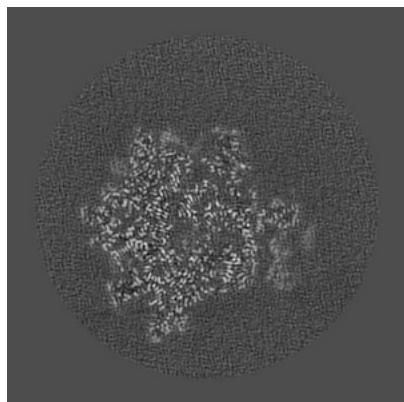


Z Index: 250

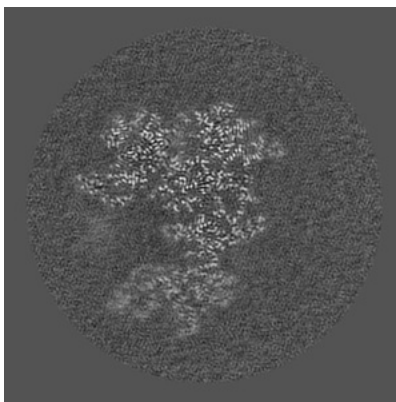
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

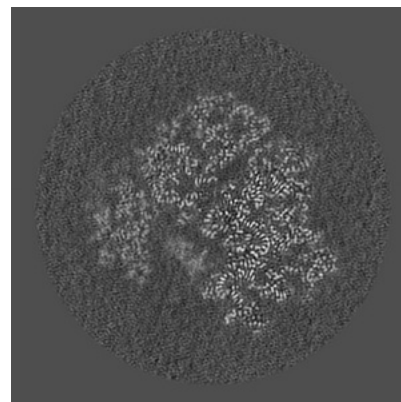
### 6.3.1 Primary map



X Index: 307

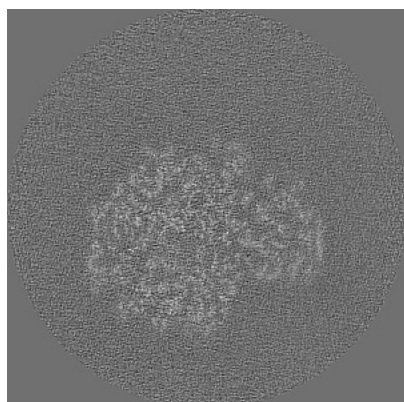


Y Index: 252

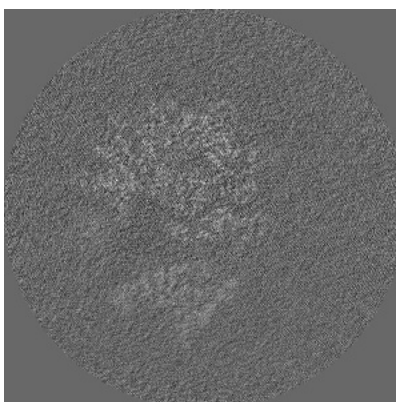


Z Index: 241

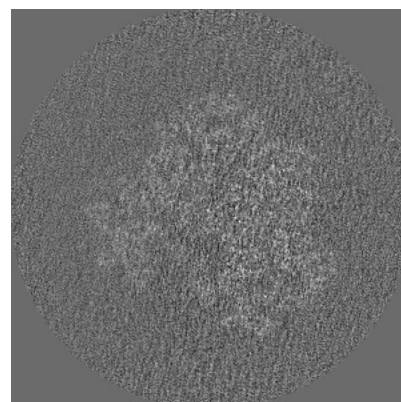
### 6.3.2 Raw map



X Index: 278



Y Index: 242



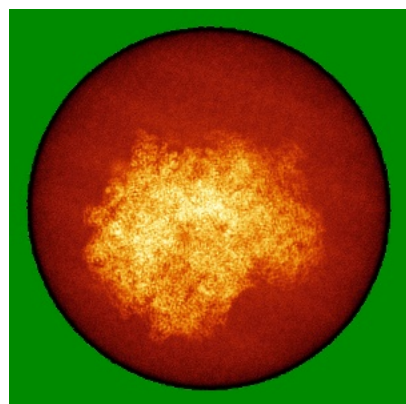
Z Index: 236

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

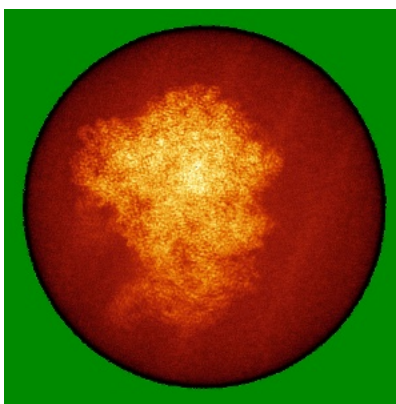


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

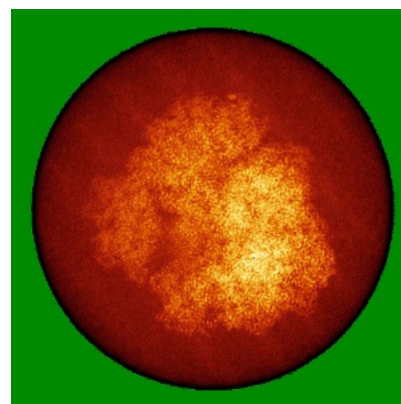
### 6.4.1 Primary map



X

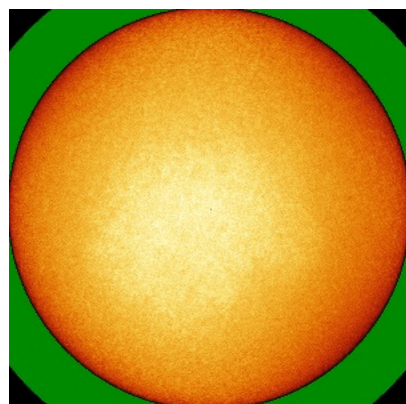


Y

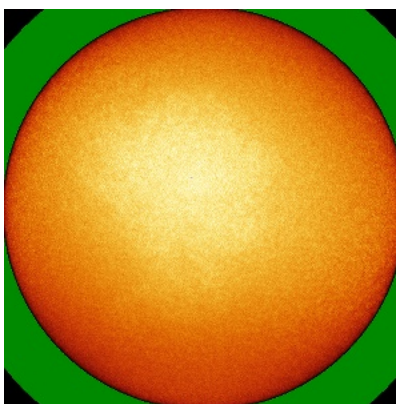


Z

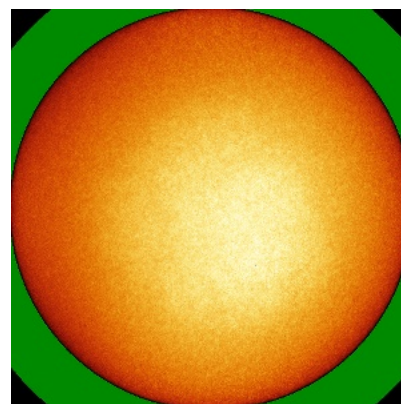
### 6.4.2 Raw map



X



Y

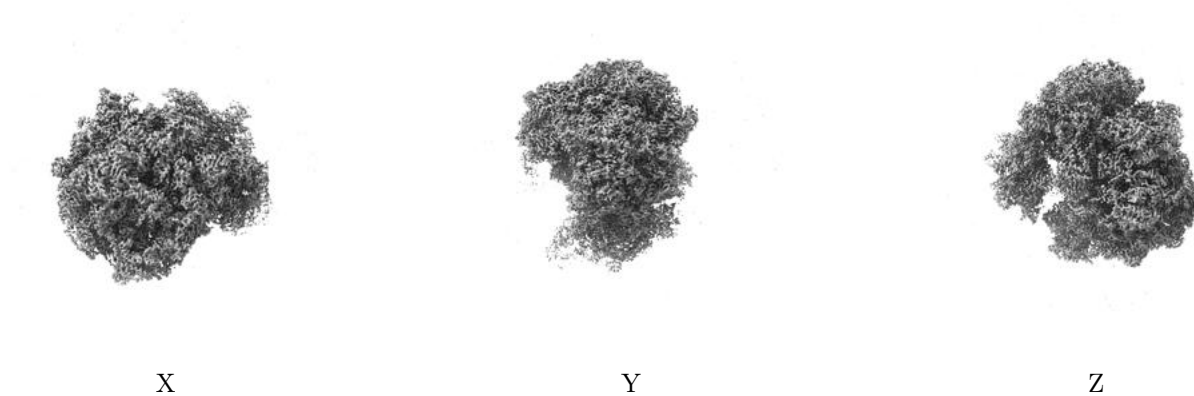


Z

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.

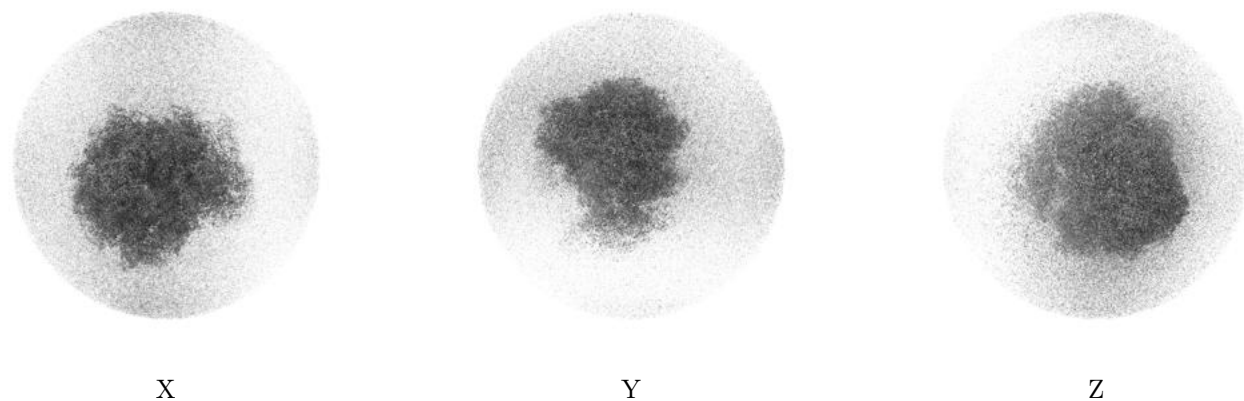
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.7. 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.

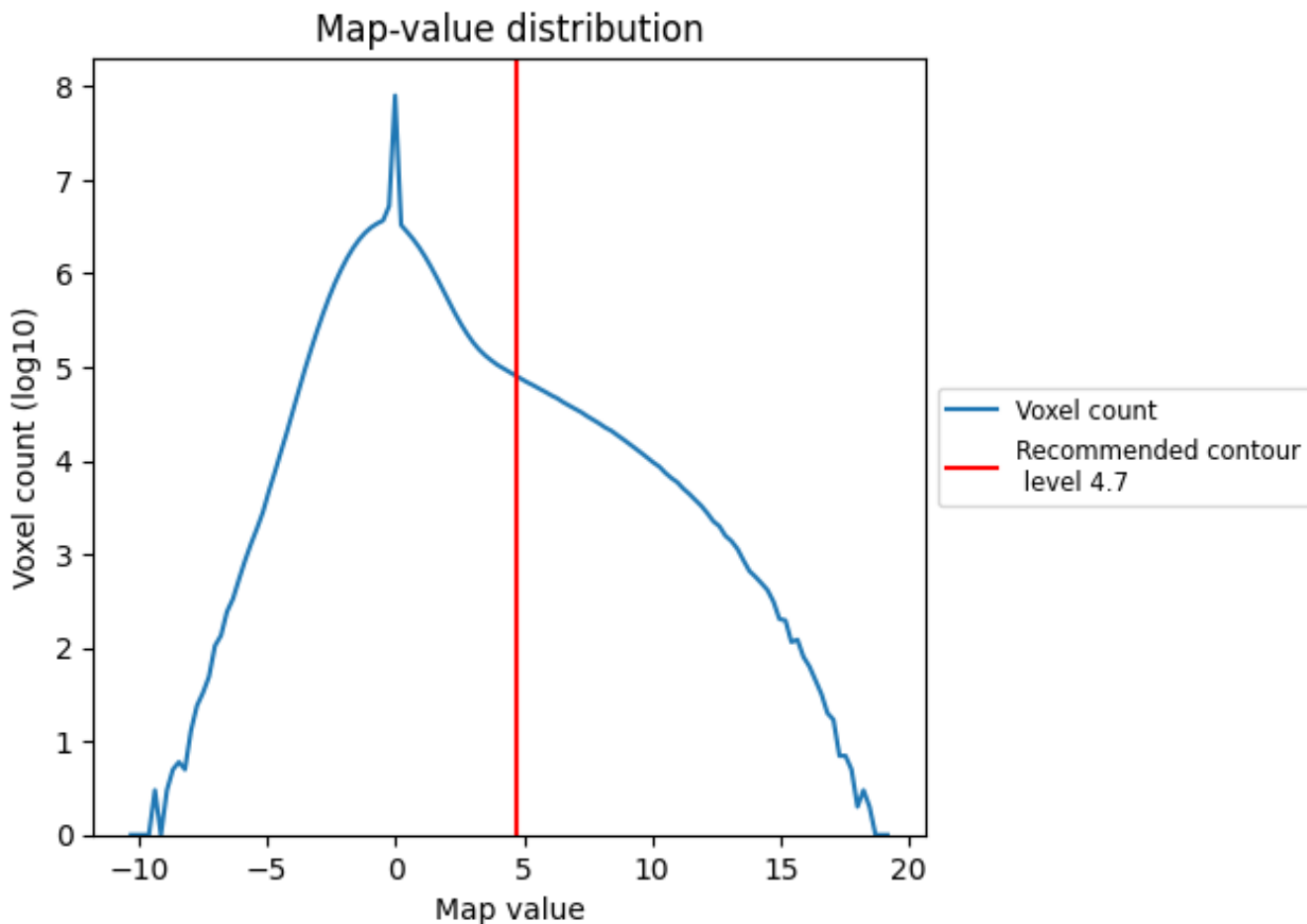
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

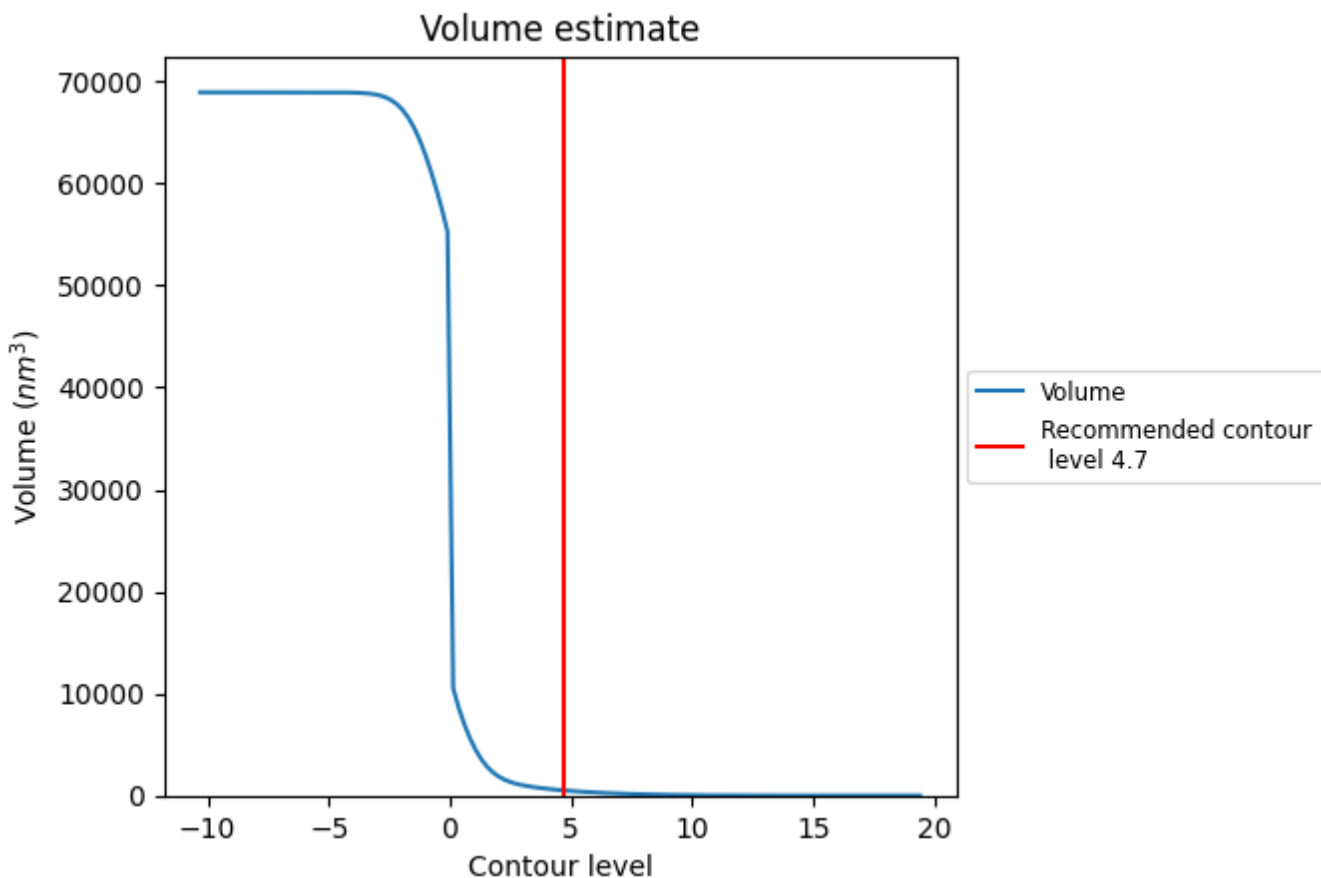
This section contains the results of statistical analysis of the map.

### 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 [\(i\)](#)

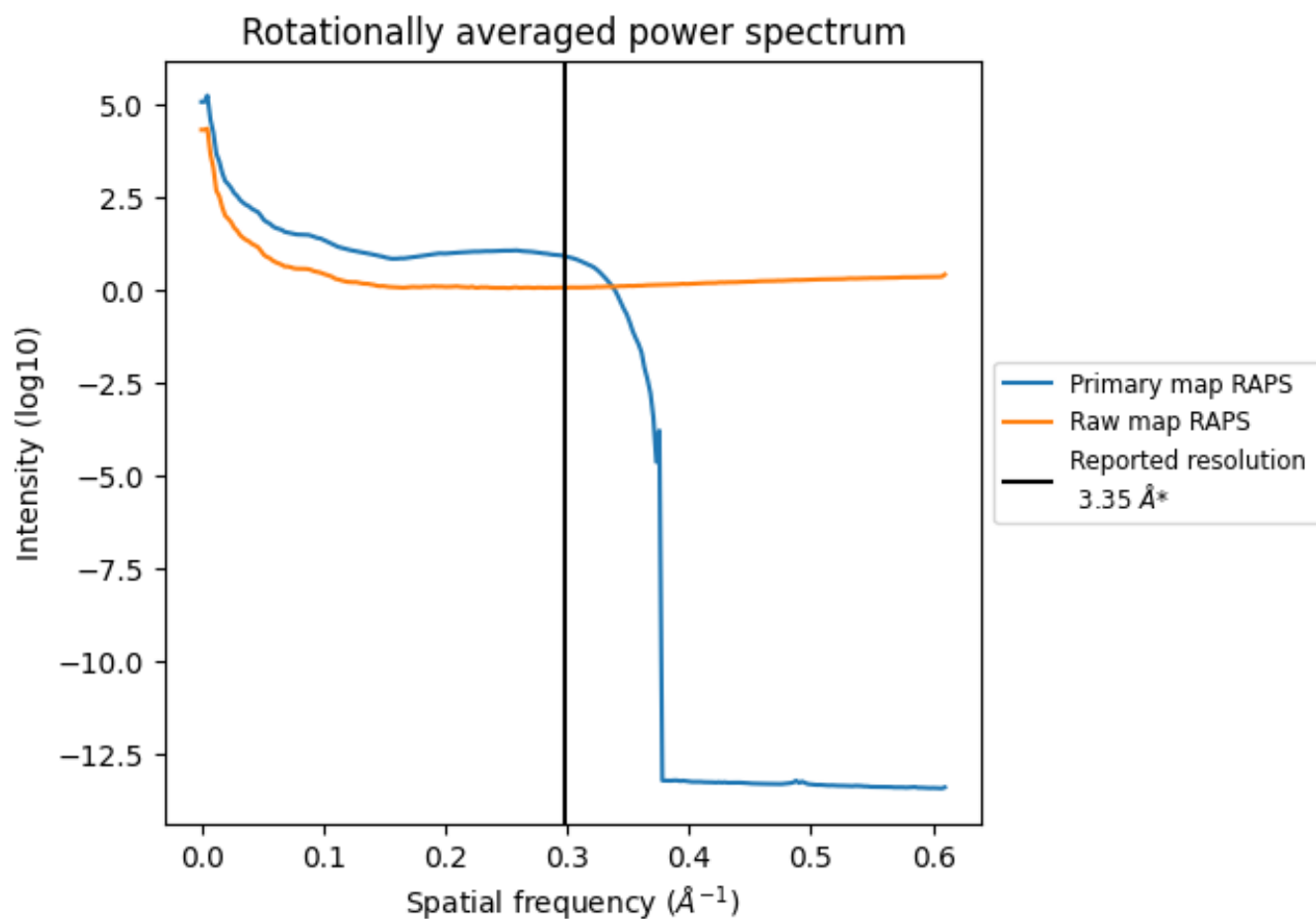


The volume at the recommended contour level is 506 nm<sup>3</sup>; this corresponds to an approximate mass of 457 kDa.

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



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

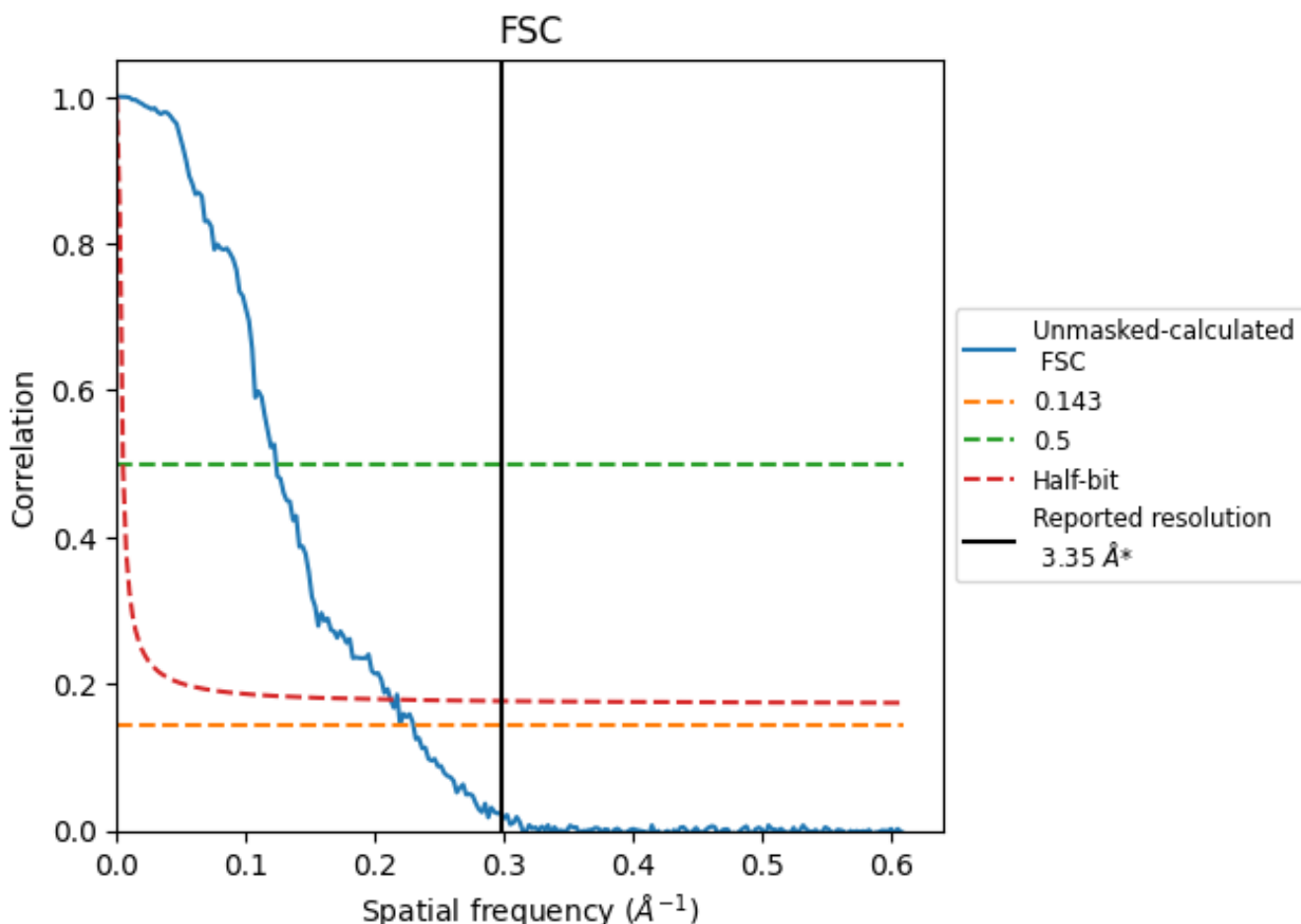


\*Reported resolution corresponds to spatial frequency of 0.299 Å<sup>-1</sup>

## 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 0.299 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

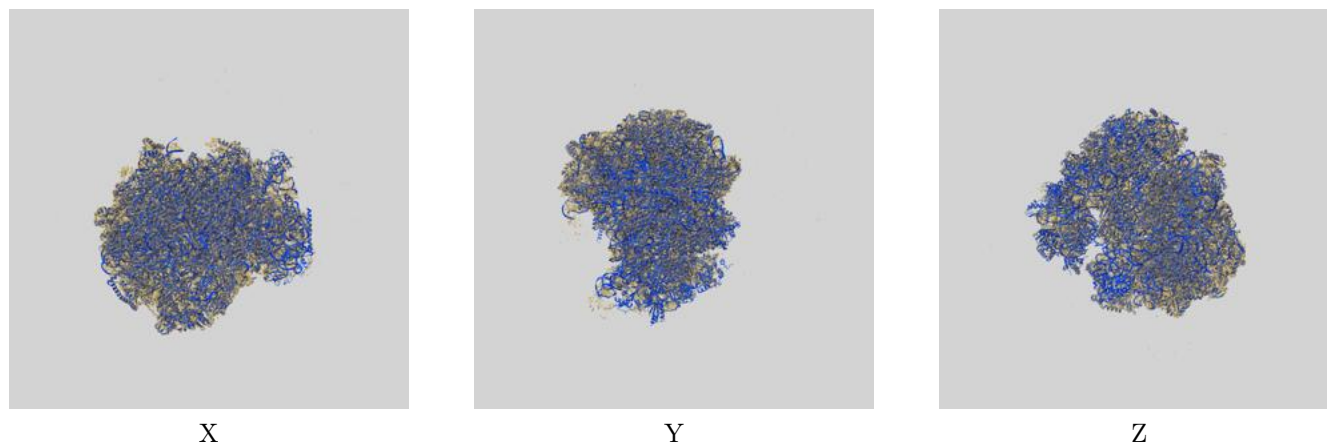
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.35	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.35	8.10	4.71

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.35 differs from the reported value 3.35 by more than 10 %

## 9 Map-model fit [i](#)

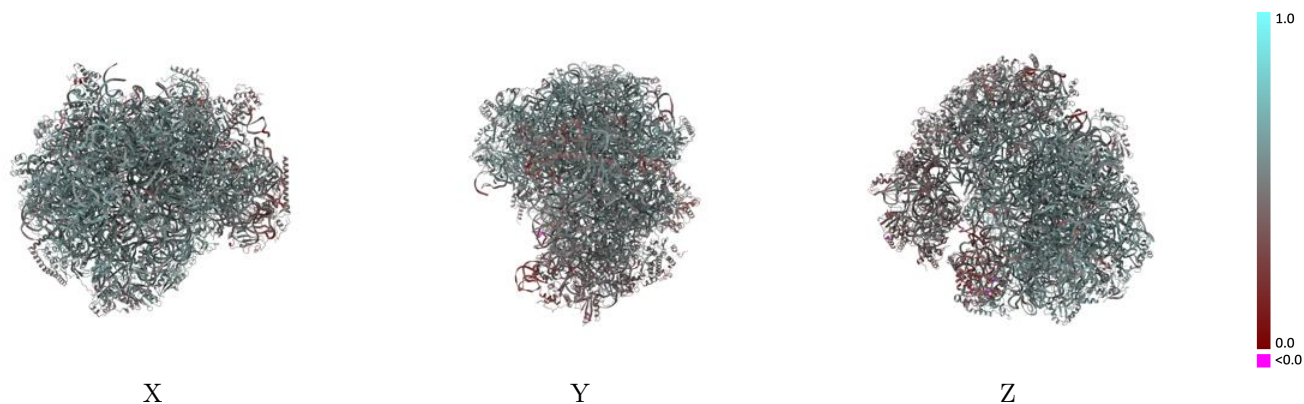
This section contains information regarding the fit between EMDB map EMD-16211 and PDB model 8BR8. Per-residue inclusion information can be found in section 3 on page 18.

### 9.1 Map-model overlay [i](#)



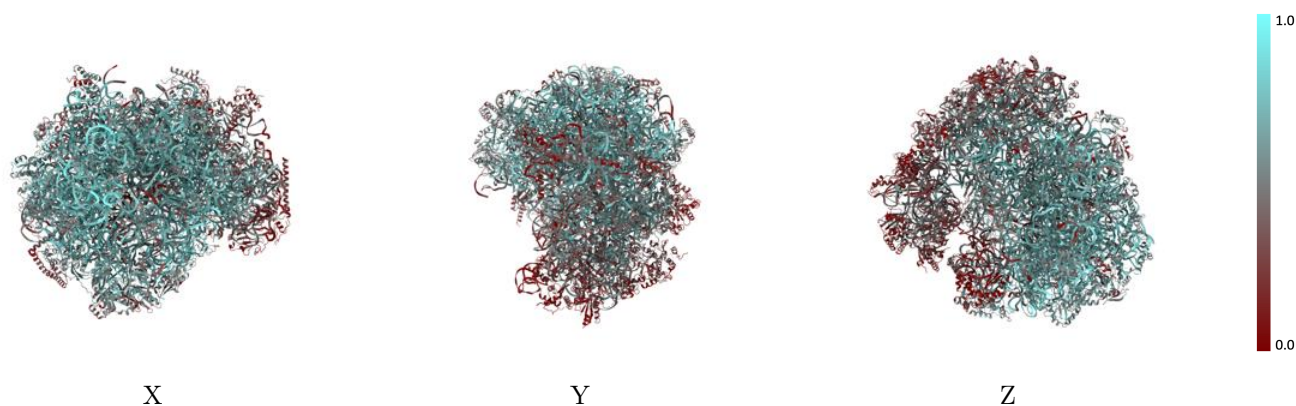
The images above show the 3D surface view of the map at the recommended contour level 4.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



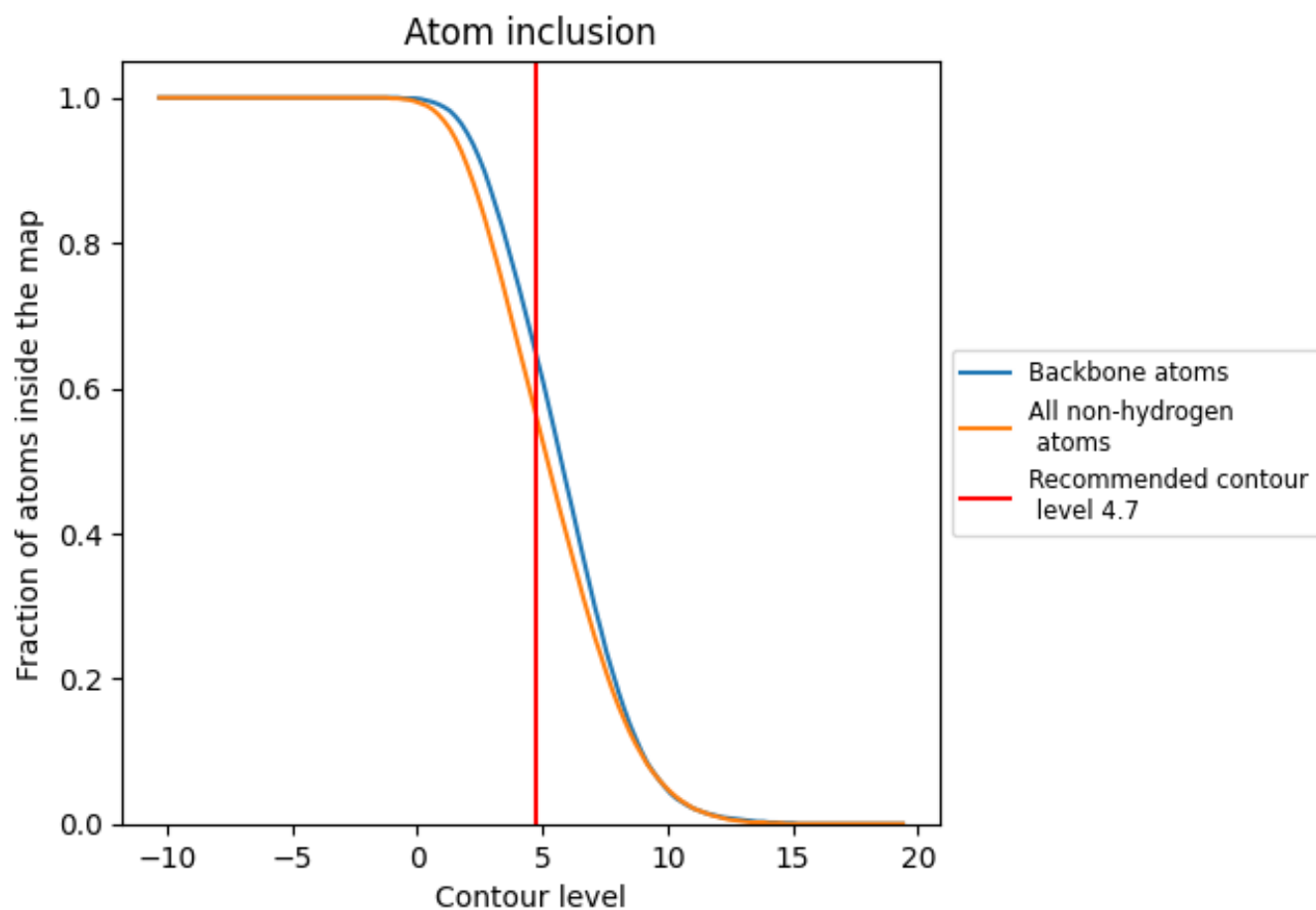
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.7).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 57% 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 (4.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5680	0.5130
LA	0.6440	0.5730
LB	0.6170	0.5550
LC	0.6070	0.5510
LD	0.7530	0.5500
LE	0.7290	0.5400
LF	0.4750	0.5040
LG	0.6220	0.5640
LH	0.5340	0.5310
LI	0.5110	0.5150
LJ	0.5210	0.5210
LK	0.2940	0.4730
LL	0.4260	0.4900
LM	0.5910	0.5350
LN	0.5370	0.5160
LO	0.7030	0.5790
LP	0.5770	0.5390
LQ	0.5540	0.5460
LR	0.5740	0.5550
LS	0.5120	0.5120
LT	0.6140	0.5480
LU	0.5910	0.5450
LV	0.4560	0.4850
LW	0.5750	0.5570
LX	0.5730	0.5170
LY	0.6110	0.5530
LZ	0.6040	0.5420
La	0.4770	0.5070
Lb	0.6710	0.5650
Lc	0.5460	0.5360
Ld	0.4620	0.5030
Le	0.5480	0.5440
Lf	0.5760	0.5570
Lg	0.6190	0.5600
Lh	0.6330	0.5670



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Chain	Atom inclusion	Q-score
Li	0.5480	0.5280
Lj	0.4900	0.5010
Lk	0.6640	0.5630
Ll	0.3460	0.4470
Ln	0.0250	0.2830
Lo	0.4950	0.5270
Lp	0.6170	0.5680
Lq	0.6190	0.5700
Ls	0.5780	0.5400
Lt	0.7180	0.5460
Lu	0.2640	0.3560
SA	0.3410	0.4660
SB	0.4700	0.5030
SC	0.2150	0.4170
SD	0.4700	0.4990
SE	0.3920	0.4930
SF	0.3000	0.4560
SG	0.2270	0.4250
SH	0.2510	0.4350
SI	0.4850	0.5160
SJ	0.4910	0.5170
SK	0.3730	0.4700
SL	0.1050	0.3710
SM	0.4550	0.5200
SO	0.4060	0.5190
SP	0.4800	0.5320
SQ	0.5380	0.5370
SR	0.0900	0.4050
ST	0.2290	0.4220
SU	0.1410	0.3910
SV	0.1610	0.3920
SW	0.2390	0.4060
SX	0.1740	0.4130
SY	0.3120	0.4620
Sb	0.2490	0.4220
Sc	0.1760	0.3890
Sd	0.5120	0.5230
Se	0.3370	0.4540
Sg	0.2250	0.4360
Sh	0.2390	0.4220
Sj	0.2440	0.4490
St	0.5670	0.4860