



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 08:04 AM EST

PDB ID : 4V6I
EMDB ID : EMD-1669
Title : Localization of the small subunit ribosomal proteins into a 6.1 Å cryo-EM map of *Saccharomyces cerevisiae* translating 80S ribosome
Authors : Armache, J.-P.; Jarasch, A.; Anger, A.M.; Villa, E.; Becker, T.; Bhushan, S.; Jossinet, F.; Habeck, M.; Dindar, G.; Franckenberg, S.; Marquez, V.; Mielke, T.; Thomm, M.; Berninghausen, O.; Beatrix, B.; Soeding, J.; Westhof, E.; Wilson, D.N.; Beckmann, R.
Deposited on : 2010-10-12
Resolution : 8.80 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

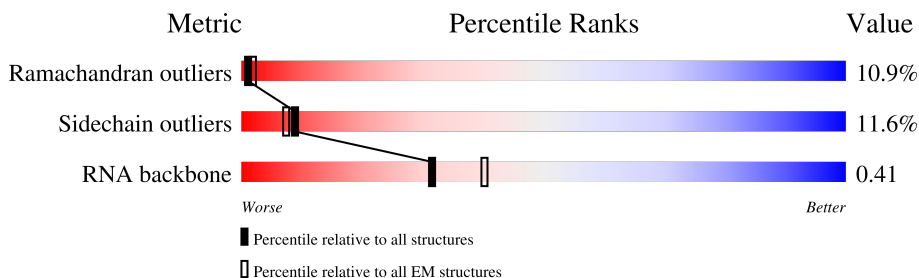
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.80 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	Aa	319	<div> <div>47%</div> <div>72% 19% 8% .</div> </div>
2	AA	252	<div> <div>27%</div> <div>65% 25% 6% 5%</div> </div>
3	AB	240	<div> <div>41%</div> <div>49% 23% 10% . 15%</div> </div>
4	AD	261	<div> <div>24%</div> <div>43% 21% 11% . 23%</div> </div>
5	AC	197	<div> <div>35%</div> <div>49% 31% 14% 6%</div> </div>
6	AE	254	<div> <div>33%</div> <div>64% 19% 13% .</div> </div>
7	AG	144	<div> <div>31%</div> <div>78% 21% .</div> </div>
8	AF	225	<div> <div>38%</div> <div>61% 19% 7% . 12%</div> </div>

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Mol	Chain	Length	Quality of chain
9	AH	130	
10	AI	143	
11	AJ	121	
12	AK	137	
13	AL	145	
14	AM	146	
15	AN	56	
16	AO	151	
17	AQ	136	
18	AP	156	
19	AR	142	
20	AS	144	
21	AT	87	
22	AV	108	
23	AW	93	
24	AX	82	
25	AY	67	
26	AZ	63	
27	Ab	37	
28	Ac	26	
29	AU	135	
30	BA	217	
31	BB	254	
32	BC	388	
33	BD	362	

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Mol	Chain	Length	Quality of chain
34	BE	174	
35	BG	176	
36	BF	191	
37	BH	256	
38	Bs	312	
39	BJ	165	
40	BK	199	
41	BN	138	
42	BM	137	
43	BP	204	
44	BO	149	
45	BR	186	
46	BT	189	
47	BU	160	
48	BW	121	
49	BV	170	
50	BX	142	
51	BZ	155	
52	BY	123	
53	Ba	136	
54	Bd	59	
55	Bc	120	
56	Bf	105	
57	Be	244	
58	Bg	113	

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Mol	Chain	Length	Quality of chain
59	Bh	130	
60	Bi	118	
61	Bj	107	
62	Bk	100	
63	Bm	92	
64	Bl	88	
65	Bn	78	
66	Bo	51	
67	Bp	52	
68	Bq	25	
69	Br	106	
70	Bx	21	
70	By	21	
71	Bz	15	
72	Bt	106	
72	Bu	106	
73	Bv	106	
73	Bw	106	
74	BQ	297	
75	BL	170	
76	BS	167	
77	BI	221	
78	CA	1800	
79	CB	75	
80	CC	11	

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Mol	Chain	Length	Quality of chain
81	DA	3396	<div><div></div><div>10%7%49%43%</div><div></div></div>
82	DB	158	<div><div></div><div>9%9%42%49%</div><div></div></div>
83	DC	118	<div><div></div><div>44%56%</div><div></div></div>

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 191627 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 40S ribosomal protein RACK1 (RACK1).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	319	Total	C	N	O	S	0	0
			2442	1544	420	469	9		

- Molecule 2 is a protein called 40S ribosomal protein rpS0 (S2p).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AA	252	Total	C	N	O	S	0	0
			1922	1204	336	380	2		

- Molecule 3 is a protein called 40S ribosomal protein rpS3 (S3p).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AB	204	Total	C	N	O	S	0	0
			1511	945	282	278	6		

- Molecule 4 is a protein called 40S ribosomal protein rpS4 (S4e).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	200	Total	C	N	O	S	0	0
			1591	1018	288	283	2		

- Molecule 5 is a protein called 40S ribosomal protein rpS9 (S4p).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AC	197	Total	C	N	O	S	0	0
			1521	951	298	270	2		

- Molecule 6 is a protein called 40S ribosomal protein rpS2 (S5p).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AE	254	Total	C	N	O	S	0	0
			1936	1224	360	349	3		

- Molecule 7 is a protein called 40S ribosomal protein rpS7 (S7e).

Mol	Chain	Residues	Atoms				AltConf	Trace
7	AG	143	Total	C	N	O	0	0
			716	429	143	144		

- Molecule 8 is a protein called 40S ribosomal protein rpS5 (S7p).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AF	199	Total	C	N	O	S	0	0
			1543	958	293	289	3		

- Molecule 9 is a protein called 40S ribosomal protein rpS22 (S8p).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AH	130	Total	C	N	O	S	0	0
			1030	655	189	182	4		

- Molecule 10 is a protein called 40S ribosomal protein rpS16 (S9p).

Mol	Chain	Residues	Atoms				AltConf	Trace
10	AI	126	Total	C	N	O	0	0
			998	639	184	175		

- Molecule 11 is a protein called 40S ribosomal protein rpS20 (S10p).

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AJ	113	Total	C	N	O	S	0	0
			849	528	158	162	1		

- Molecule 12 is a protein called 40S ribosomal protein rpS14 (S11p).

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AK	119	Total	C	N	O	S	0	0
			833	508	157	165	3		

- Molecule 13 is a protein called 40S ribosomal protein rpS23 (S12p).

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AL	145	Total	C	N	O	S	0	0
			978	588	203	184	3		

- Molecule 14 is a protein called 40S ribosomal protein rpS18 (S13p).

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AM	140	Total	C	N	O	S	0	0
			1156	719	231	204	2		

- Molecule 15 is a protein called 40S ribosomal protein rpS29 (S14p).

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AN	48	Total	C	N	O	S	0	0
			353	209	79	61	4		

- Molecule 16 is a protein called 40S ribosomal protein rpS13 (S15p).

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AO	121	Total	C	N	O	S	0	0
			978	624	183	170	1		

- Molecule 17 is a protein called 40S ribosomal protein rpS17 (S17e).

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	136	Total	C	N	O	S	0	0
			1098	682	213	201	2		

- Molecule 18 is a protein called 40S ribosomal protein rpS11 (S17p).

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AP	85	Total	C	N	O	S	0	0
			631	402	124	104	1		

- Molecule 19 is a protein called 40S ribosomal protein rpS15 (S19p).

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AR	88	Total	C	N	O	S	0	0
			676	429	123	118	6		

- Molecule 20 is a protein called 40S ribosomal protein rpS19 (S19e).

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AS	144	Total	C	N	O	S	0	0
			1120	699	209	209	3		

- Molecule 21 is a protein called 40S ribosomal protein rpS21 (S21e).

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AT	87	Total	C	N	O	S	0	0
			685	420	125	138	2		

- Molecule 22 is a protein called 40S ribosomal protein rpS25 (S25e).

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	85	Total	C	N	O	S	0	0
			688	437	128	122	1		

- Molecule 23 is a protein called 40S ribosomal protein rpS26 (S26e).

Mol	Chain	Residues	Atoms				AltConf	Trace
23	AW	92	Total	C	N	O	0	0
			461	276	92	93		

- Molecule 24 is a protein called 40S ribosomal protein rpS27 (S27e).

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	50	Total	C	N	O	S	0	0
			366	229	60	72	5		

- Molecule 25 is a protein called 40S ribosomal protein rpS28 (S28e).

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	60	Total	C	N	O	S	0	0
			445	276	80	87	2		

- Molecule 26 is a protein called 40S ribosomal protein rpS30 (S30e).

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AZ	63	Total	C	N	O	S	0	0
			492	307	102	81	2		

- Molecule 27 is a protein called Unknown 40S ribosomal protein XS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Ab	36	Total	C	N	O	0	0
			181	108	36	37		

- Molecule 28 is a protein called Unknown 40S ribosomal protein XS2.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	Ac	25	Total	C	N	O	0	0
			126	75	25	26		

- Molecule 29 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AU	96	Total	C	N	O	S	0	0
			714	450	134	129	1		

- Molecule 30 is a protein called 60S ribosomal protein rpL1 (L1p).

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BA	217	Total	C	N	O	S	0	0
			1718	1097	299	312	10		

- Molecule 31 is a protein called 60S ribosomal protein rpL2 (L2p).

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BB	254	Total	C	N	O	S	0	0
			1904	1183	385	334	2		

- Molecule 32 is a protein called 60S ribosomal protein rpL3 (L3p).

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BC	388	Total	C	N	O	S	0	0
			3055	1933	579	534	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BC	388	GLY	-	expression tag	UNP P14126

- Molecule 33 is a protein called 60S ribosomal protein rpL4 (L4p).

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BD	329	Total	C	N	O	S	0	0
			2486	1564	480	438	4		

- Molecule 34 is a protein called 60S ribosomal protein rpL11 (L5p).

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BE	168	Total	C	N	O	S	0	0
			1341	839	252	245	5		

- Molecule 35 is a protein called 60S ribosomal protein rpL6 (L6e).

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BG	176	Total	C	N	O	S	0	0
			1409	907	252	248	2		

- Molecule 36 is a protein called 60S ribosomal protein rpL9 (L6p).

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BF	191	Total	C	N	O	S	0	0
			1516	961	274	277	4		

- Molecule 37 is a protein called 60S ribosomal protein rpL8 (L7ae).

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BH	197	Total	C	N	O	S	0	0
			1505	959	269	274	3		

- Molecule 38 is a protein called 60S acidic ribosomal protein rpP0 (L10P).

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Bs	257	Total	C	N	O	S	0	0
			1976	1269	334	368	5		

- Molecule 39 is a protein called 60S ribosomal protein rpL12 (L11p).

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BJ	127	Total	C	N	O	S	0	0
			954	601	174	178	1		

- Molecule 40 is a protein called 60S ribosomal protein rpL16 (L13p).

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BK	199	Total	C	N	O	S	0	0
			1570	1011	291	266	2		

- Molecule 41 is a protein called 60S ribosomal protein rpL14 (L14e).

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BN	138	Total	C	N	O	S	0	0
			1068	683	201	181	3		

- Molecule 42 is a protein called 60S ribosomal protein rpL23 (L14p).

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BM	131	Total	C	N	O	S	0	0
			972	611	182	172	7		

- Molecule 43 is a protein called 60S ribosomal protein rpL15 (L15e).

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BP	193	Total	C	N	O	S	0	0
			1625	1016	341	266	2		

- Molecule 44 is a protein called 60S ribosomal protein rpL28 (L15p).

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BO	149	Total	C	N	O	S	0	0
			1182	754	232	192	4		

- Molecule 45 is a protein called 60S ribosomal protein rpL18 (L18e).

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BR	161	Total	C	N	O	S	0	0
			1243	786	242	212	3		

- Molecule 46 is a protein called 60S ribosomal protein rpL19 (L19e).

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BT	189	Total	C	N	O	S	0	0
			1530	940	327	262	1		

- Molecule 47 is a protein called 60S ribosomal protein rpL21 (L21e).

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BU	160	Total	C	N	O	S	0	0
			1261	793	242	222	4		

- Molecule 48 is a protein called 60S ribosomal protein rpL22 (L22e).

Mol	Chain	Residues	Atoms				AltConf	Trace
48	BW	105	Total	C	N	O	0	0
			830	535	140	155		

- Molecule 49 is a protein called 60S ribosomal protein rpL17 (L22p).

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BV	170	Total	C	N	O	S	0	0
			1312	814	254	243	1		

- Molecule 50 is a protein called 60S ribosomal protein rpL25 (L23p).

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BX	122	Total	C	N	O	S	0	0
			978	629	172	175	2		

- Molecule 51 is a protein called 60S ribosomal protein rpL24 (L24e).

Mol	Chain	Residues	Atoms				AltConf	Trace
51	BZ	73	Total	C	N	O	0	0
			579	366	115	98		

- Molecule 52 is a protein called 60S ribosomal protein rpL26 (L24p).

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BY	123	Total	C	N	O	S	0	0
			972	611	188	172	1		

- Molecule 53 is a protein called 60S ribosomal protein rpL27 (L27e).

Mol	Chain	Residues	Atoms				AltConf	Trace
53	Ba	95	Total	C	N	O	0	0
			708	455	134	119		

- Molecule 54 is a protein called 60S ribosomal protein rpL29 (L29e).

Mol	Chain	Residues	Atoms				AltConf	Trace
54	Bd	22	Total	C	N	O	0	0
			174	109	40	25		

- Molecule 55 is a protein called 60S ribosomal protein rpL35 (L29p).

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Bc	118	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 56 is a protein called 60S ribosomal protein rpL30 (L30e).

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Bf	105	Total	C	N	O	S	0	0
			785	501	133	150	1		

- Molecule 57 is a protein called 60S ribosomal protein rpL7 (L30p).

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Be	239	Total	C	N	O	S	0	0
			1919	1235	348	335	1		

- Molecule 58 is a protein called 60S ribosomal protein rpL31 (L31e).

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Bg	110	Total	C	N	O	S	0	0
			873	552	169	150	2		

- Molecule 59 is a protein called 60S ribosomal protein pL32 (L32e).

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Bh	130	Total	C	N	O	S	0	0
			1043	660	208	173	2		

- Molecule 60 is a protein called 60S ribosomal protein rpL34 (L34e).

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Bi	118	Total	C	N	O	S	0	0
			926	572	188	161	5		

- Molecule 61 is a protein called 60S ribosomal protein rpL33 (L35ae).

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Bj	100	Total	C	N	O	S	0	0
			738	461	147	128	2		

- Molecule 62 is a protein called 60S ribosomal protein rpL36 (L36e).

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Bk	77	Total	C	N	O	S	0	0
			619	384	129	105	1		

- Molecule 63 is a protein called 60S ribosomal protein rpL43 (L37ae).

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Bm	92	Total	C	N	O	S	0	0
			703	434	139	123	7		

- Molecule 64 is a protein called 60S ribosomal protein rpL37 (L37e).

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Bl	88	Total	C	N	O	S	0	0
			678	410	148	114	6		

- Molecule 65 is a protein called 60S ribosomal protein rpL38 (L38e).

Mol	Chain	Residues	Atoms				AltConf	Trace
65	Bn	78	Total	C	N	O	0	0
			604	385	113	106		

- Molecule 66 is a protein called 60S ribosomal protein rpL39 (L39e).

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bo	51	Total	C	N	O	S	0	0
			445	277	98	67	3		

- Molecule 67 is a protein called 60S ribosomal protein rpL40 (L40e).

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Bp	40	Total	C	N	O	S	0	0
			330	201	72	52	5		

- Molecule 68 is a protein called 60S ribosomal protein rpL41 (L41e).

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Bq	25	Total	C	N	O	S	0	0
			234	142	63	28	1		

- Molecule 69 is a protein called 60S ribosomal protein rpL42 (L44e).

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Br	106	Total	C	N	O	S	0	0
			834	521	169	138	6		

- Molecule 70 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bx	20	Total	C	N	O		0	0
			100	60	20	20			
70	By	20	Total	C	N	O		0	0
			100	60	20	20			

- Molecule 71 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Bz	14	Total	C	N	O		0	0
			70	42	14	14			

- Molecule 72 is a protein called 60S acidic ribosomal protein rpP11 (P1).

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bt	58	Total	C	N	O		0	0
			440	281	68	91			
72	Bu	58	Total	C	N	O		0	0
			440	281	68	91			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bt	37	ASP	VAL	conflict	UNP P05318
Bu	37	ASP	VAL	conflict	UNP P05318

- Molecule 73 is a protein called 60S acidic ribosomal protein (P2).

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bv	58	Total	C	N	O	S	0	0
			429	271	66	91	1		
73	Bw	58	Total	C	N	O	S	0	0
			429	271	66	91	1		

- Molecule 74 is a protein called 60S ribosomal protein rpL5 (L18p).

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BQ	297	Total	C	N	O	S	0	0
			2356	1485	414	454	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BQ	112	ARG	LYS	conflict	UNP P26321

- Molecule 75 is a protein called 60S ribosomal protein rpL13 (L13e).

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BL	169	Total	C	N	O		0	0
			845	507	169	169			

- Molecule 76 is a protein called 60S ribosomal protein rpL20 (L18ae).

Mol	Chain	Residues	Atoms					AltConf	Trace
76	BS	167	Total	C	N	O	S	0	0
			1420	916	263	234	7		

- Molecule 77 is a protein called 60S ribosomal protein rpL10 (L10e).

Mol	Chain	Residues	Atoms					AltConf	Trace
77	BI	181	Total	C	N	O	S	0	0
			1444	907	281	248	8		

- Molecule 78 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	CA	1721	Total	C	N	O	P	0	10
			33643	14904	5670	11348	1721		

- Molecule 79 is a RNA chain called P-SITE TRNA ASP.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	CB	75	Total	C	N	O	P	0	0
			1599	712	280	532	75		

- Molecule 80 is a RNA chain called MRNA, RNA (5'-R(P*AP*AP*AP*AP*GP*AP*CP*U P*UP*CP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CC	11	Total	C	N	O	P	0	0
			236	106	45	74	11		

- Molecule 81 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	DA	3354	Total	C	N	O	P	0	75
			68830	30640	12220	22616	3354		

- Molecule 82 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	DB	157	Total	C	N	O	P	0	0
			3129	1391	523	1058	157		

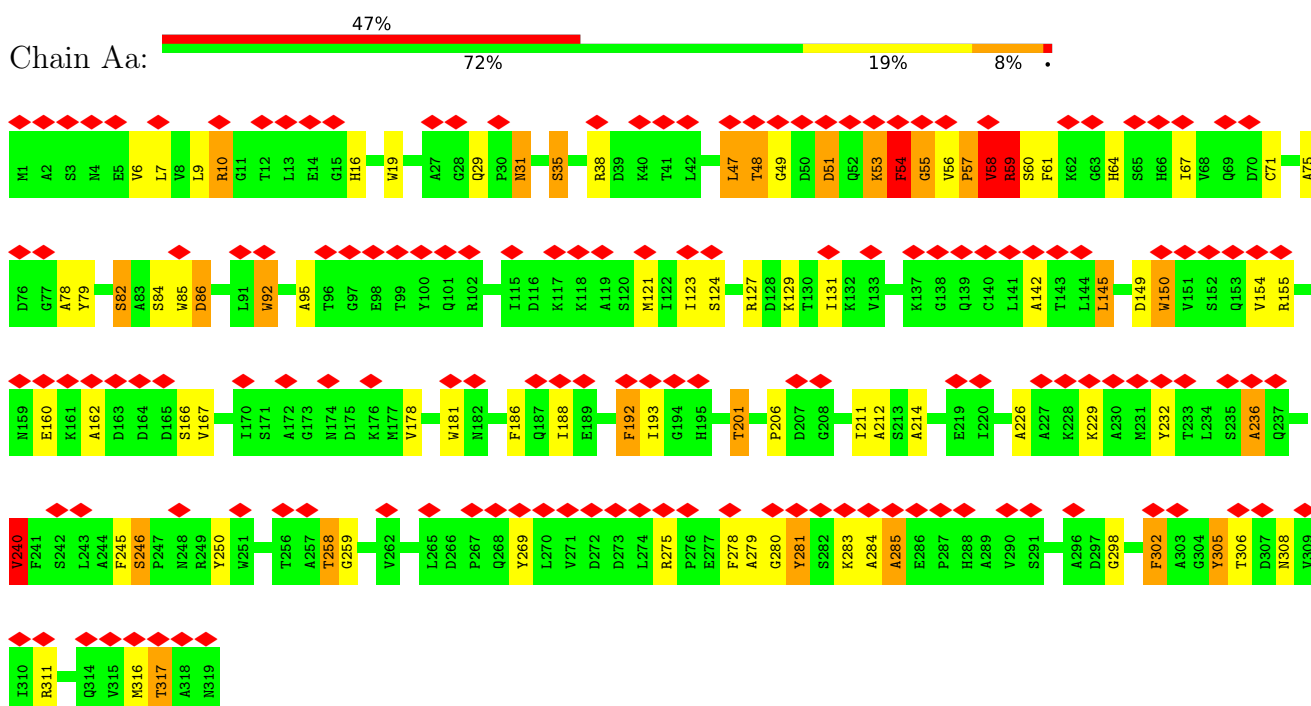
- Molecule 83 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	DC	118	Total	C	N	O	P	0	0
			2513	1122	446	827	118		

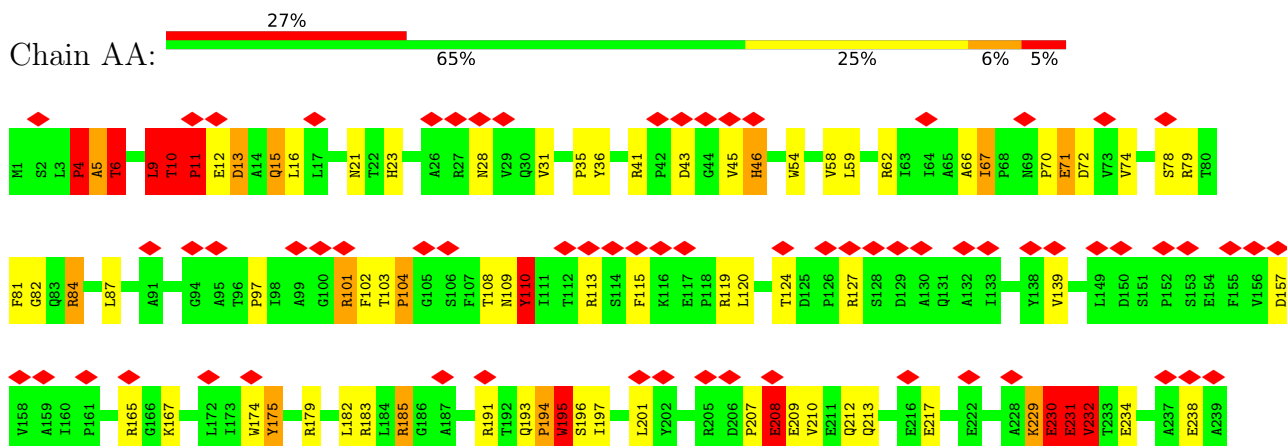
3 Residue-property plots

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: 40S ribosomal protein RACK1 (RACK1)

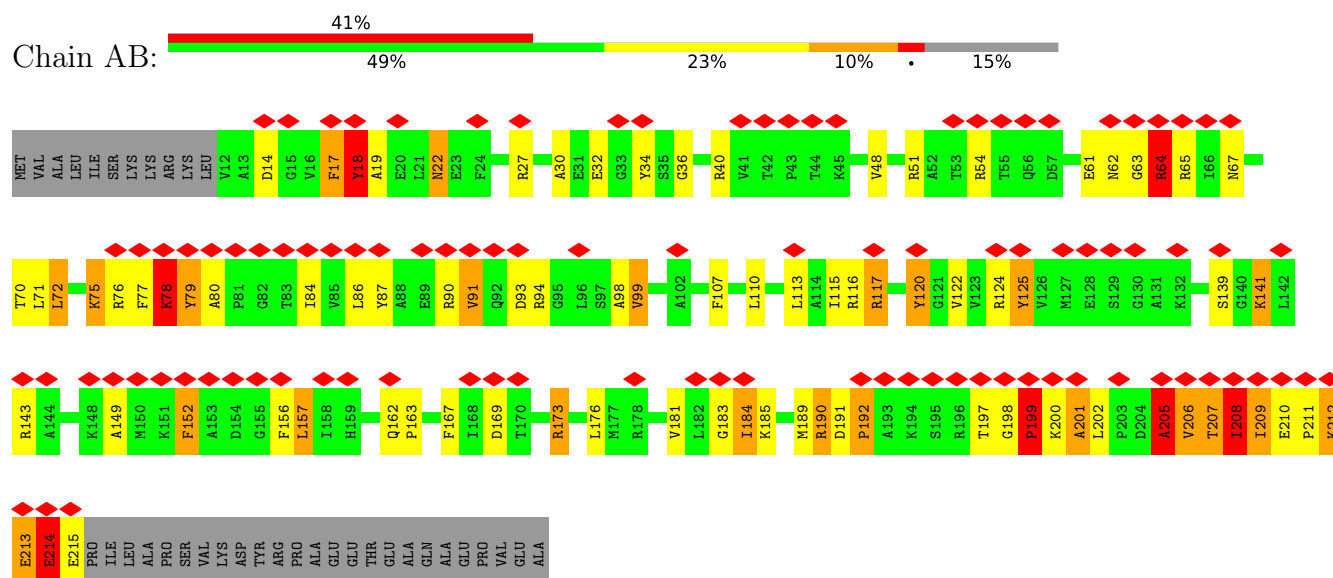


• Molecule 2: 40S ribosomal protein rpS0 (S2p)

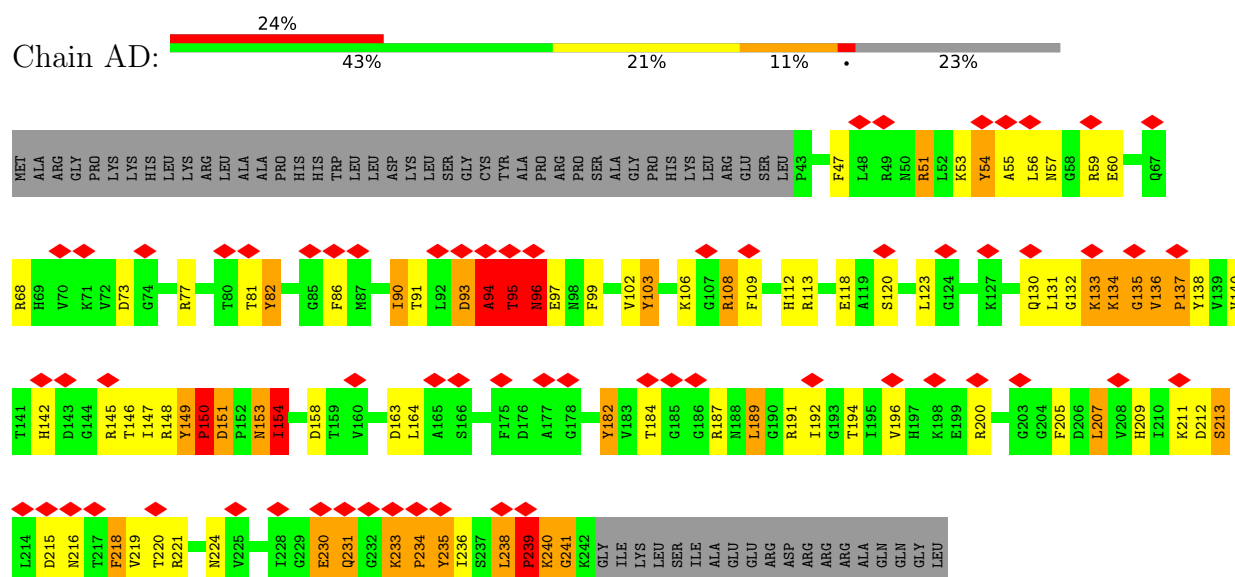




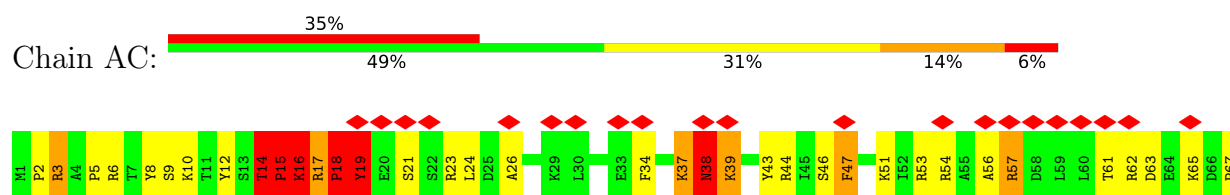
• Molecule 3: 40S ribosomal protein rpS3 (S3p)

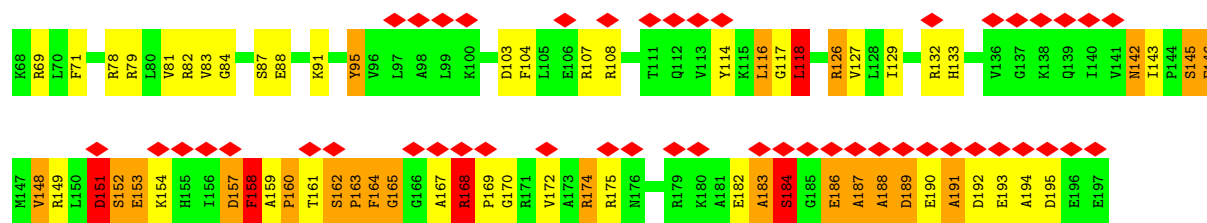


• Molecule 4: 40S ribosomal protein rpS4 (S4e)

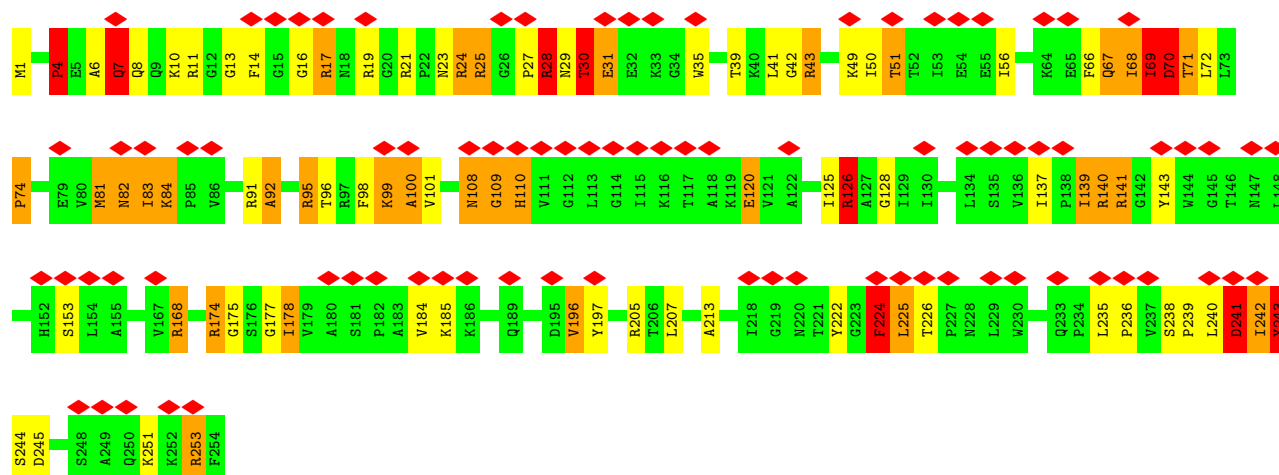


• Molecule 5: 40S ribosomal protein rpS9 (S4p)

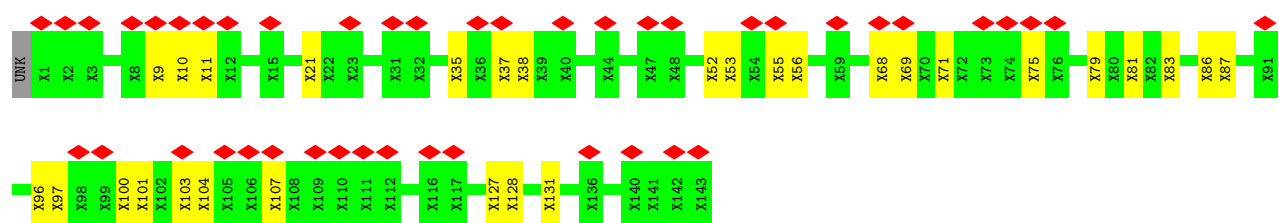
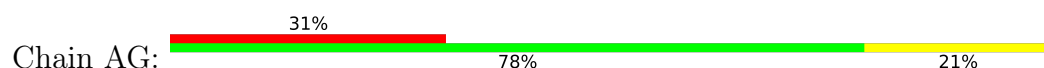




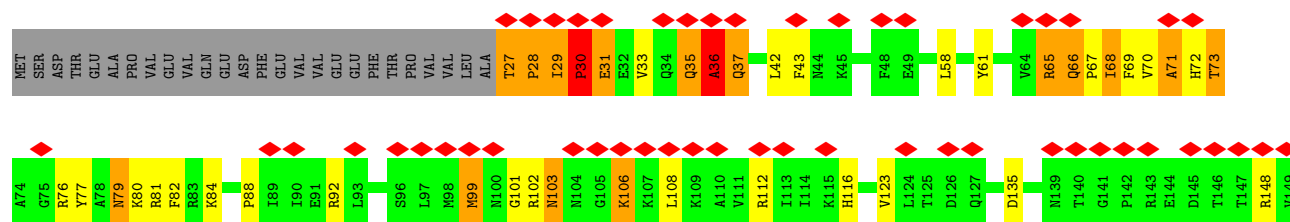
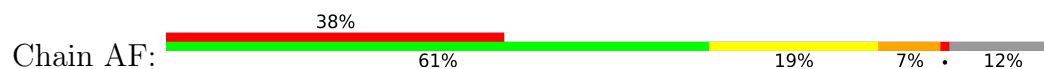
• Molecule 6: 40S ribosomal protein rpS2 (S5p)



• Molecule 7: 40S ribosomal protein rpS7 (S7e)

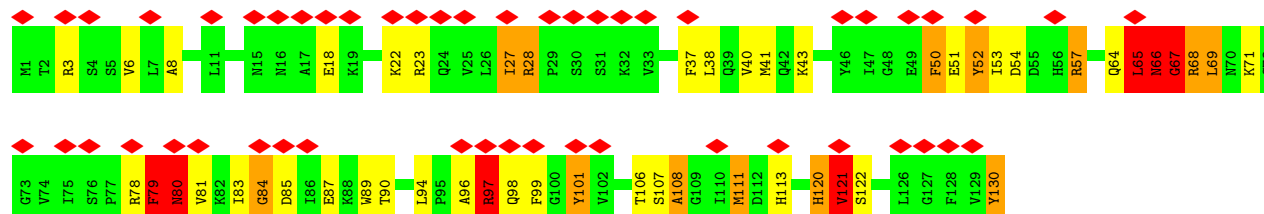
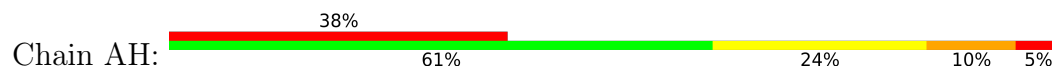


• Molecule 8: 40S ribosomal protein rpS5 (S7p)

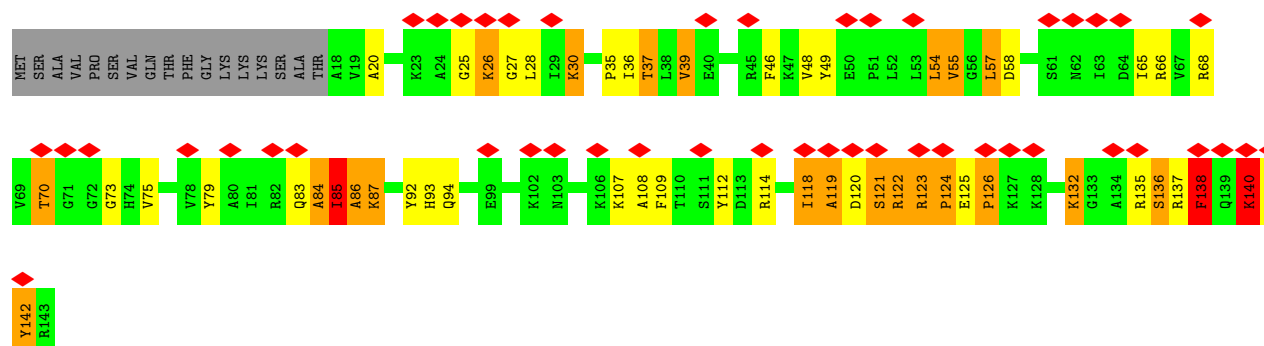




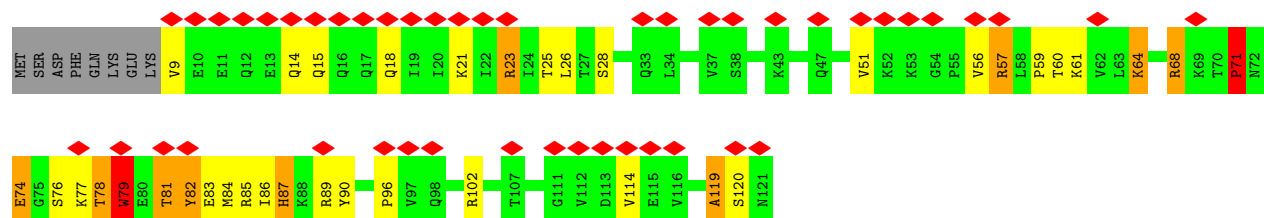
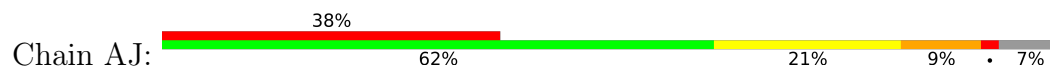
• Molecule 9: 40S ribosomal protein rpS22 (S8p)



• Molecule 10: 40S ribosomal protein rpS16 (S9p)



• Molecule 11: 40S ribosomal protein rpS20 (S10p)

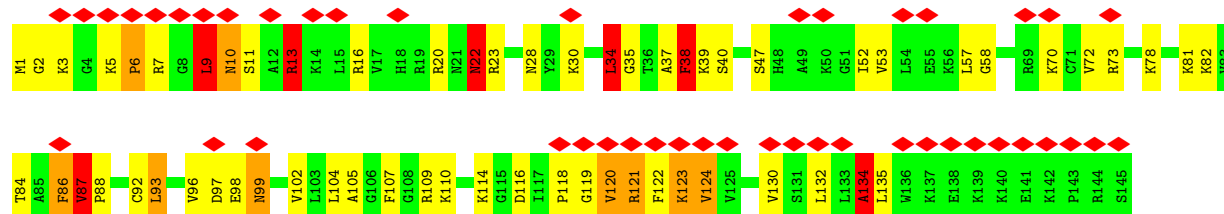


• Molecule 12: 40S ribosomal protein rpS14 (S11p)

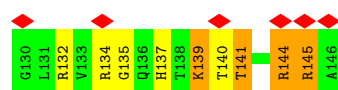
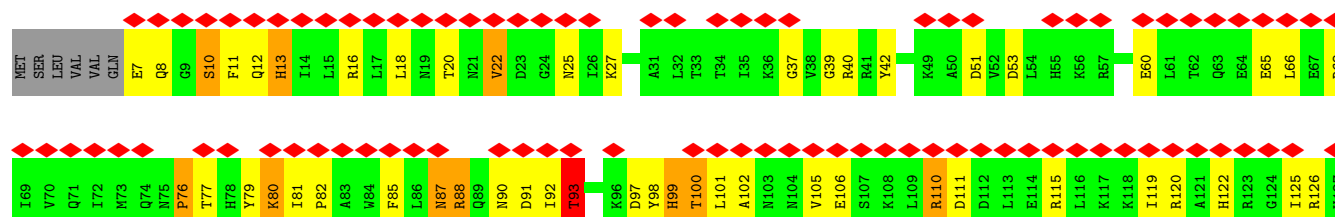




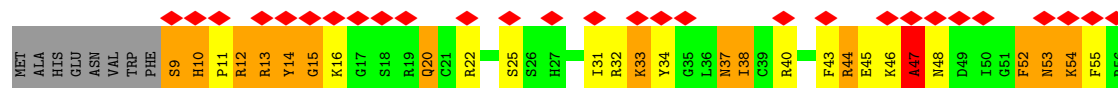
- Molecule 13: 40S ribosomal protein rpS23 (S12p)



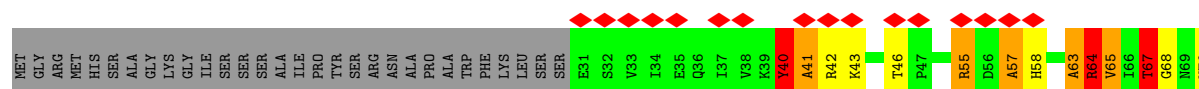
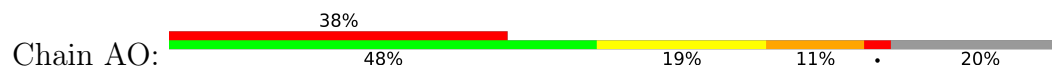
- Molecule 14: 40S ribosomal protein rpS18 (S13p)

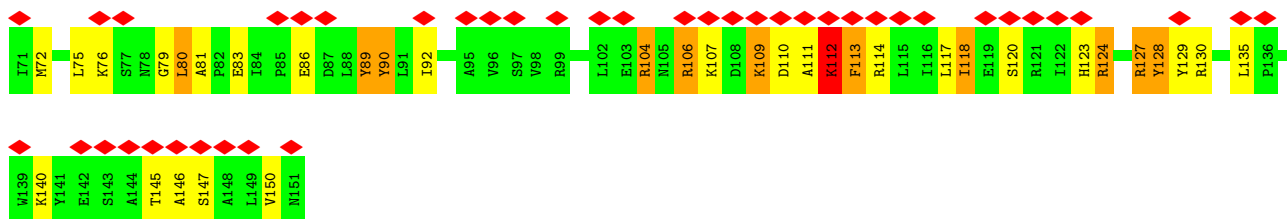


- Molecule 15: 40S ribosomal protein rpS29 (S14p)

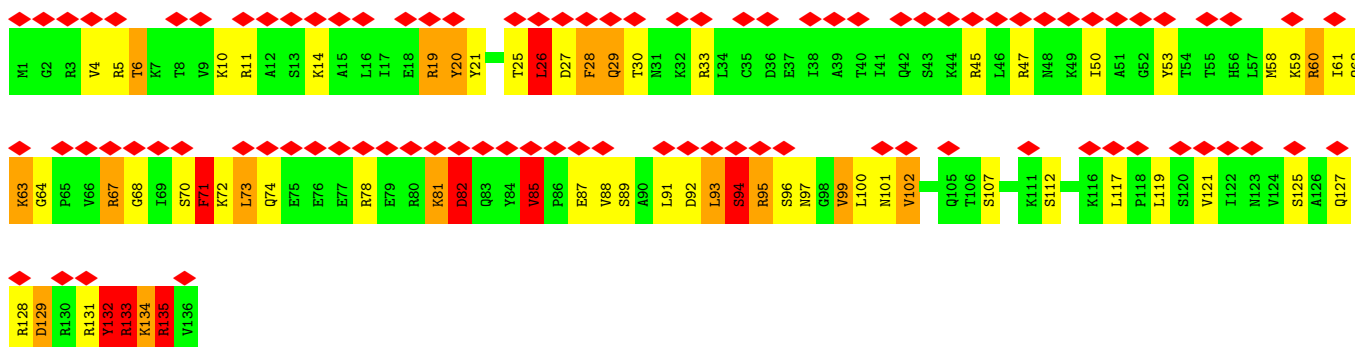


- Molecule 16: 40S ribosomal protein rpS13 (S15p)

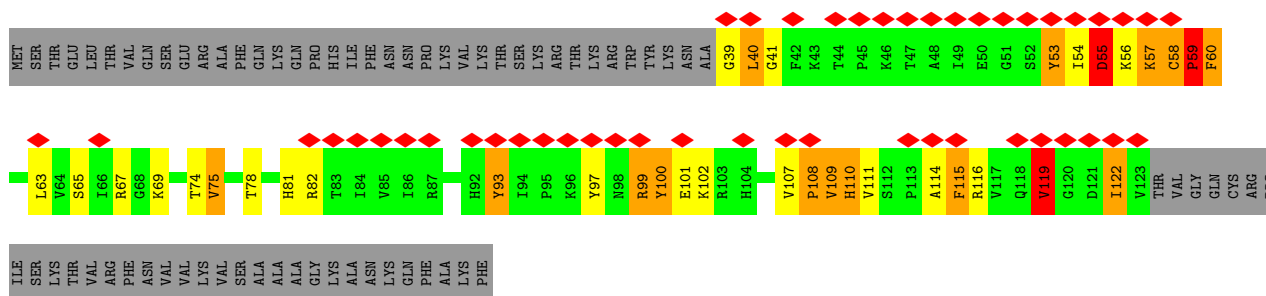
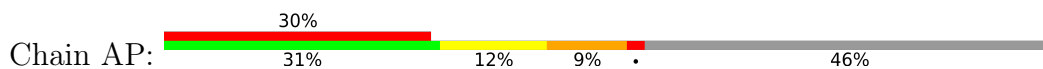




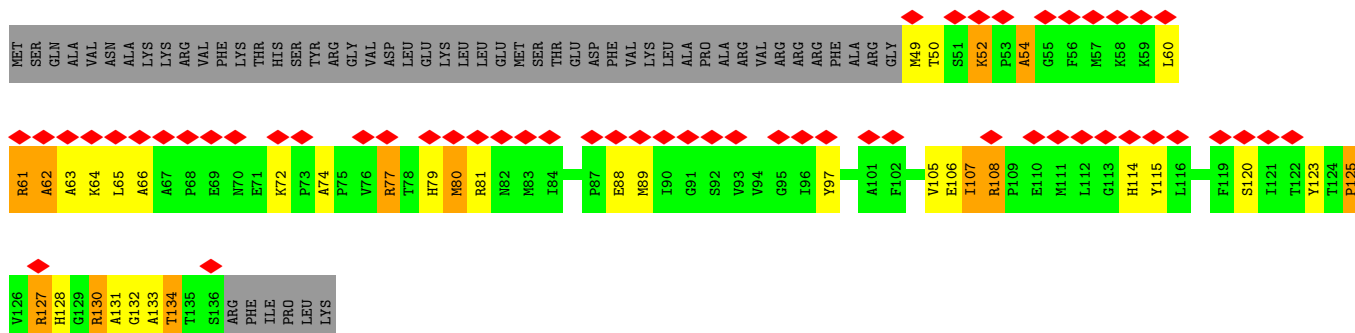
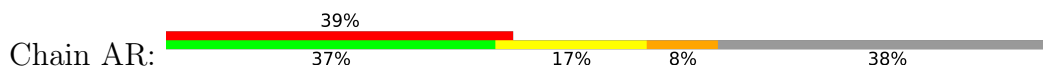
• Molecule 17: 40S ribosomal protein rpS17 (S17e)



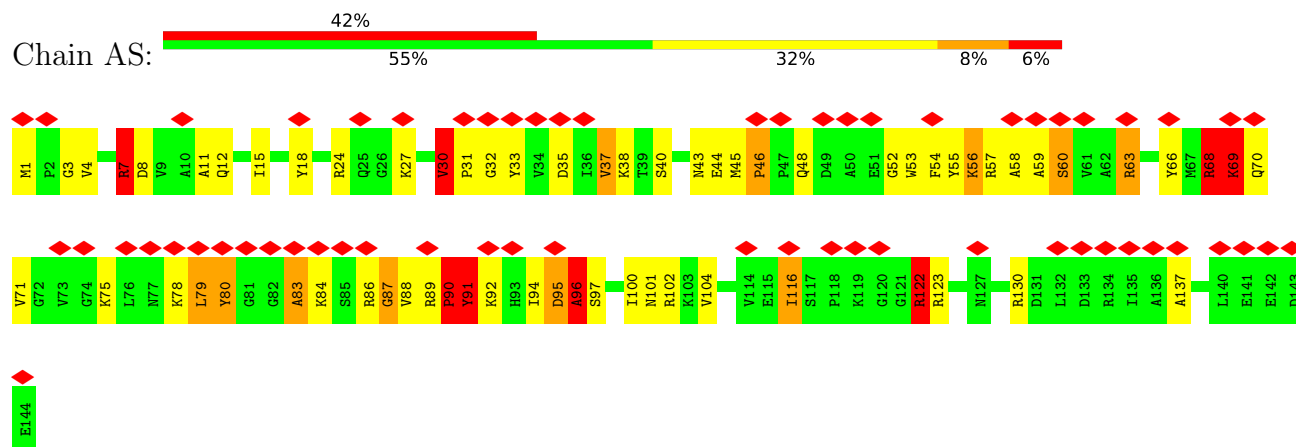
• Molecule 18: 40S ribosomal protein rpS11 (S17p)



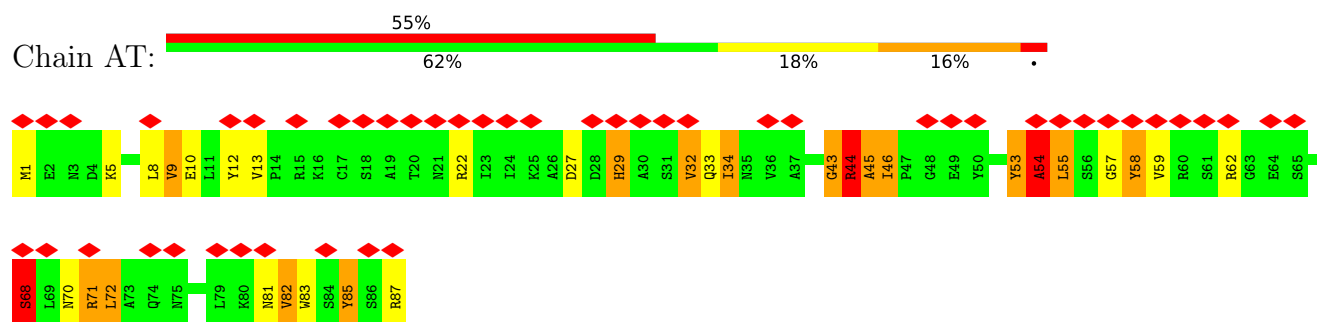
• Molecule 19: 40S ribosomal protein rpS15 (S19p)



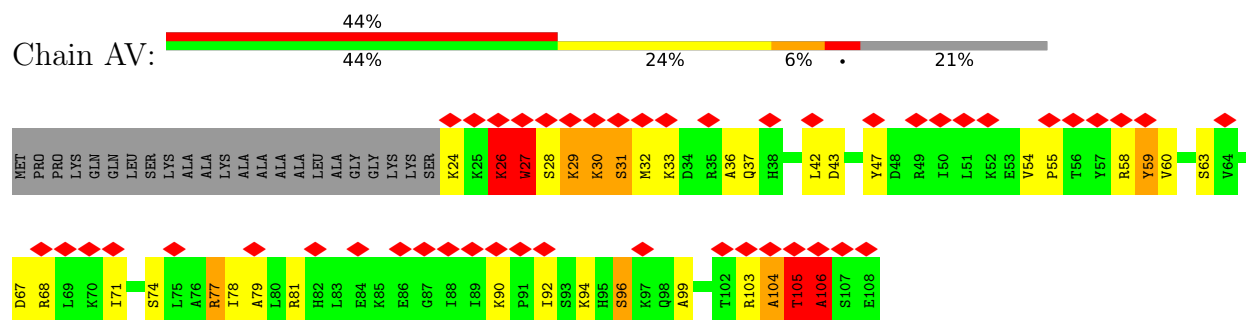
- Molecule 20: 40S ribosomal protein rpS19 (S19e)



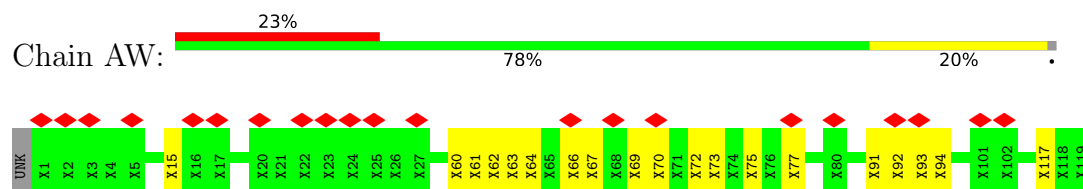
- Molecule 21: 40S ribosomal protein rpS21 (S21e)



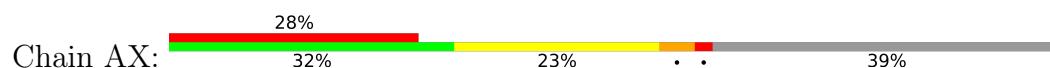
- Molecule 22: 40S ribosomal protein rpS25 (S25e)

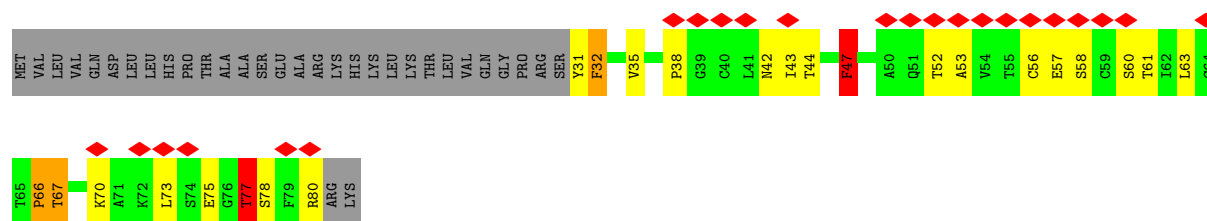


- Molecule 23: 40S ribosomal protein rpS26 (S26e)

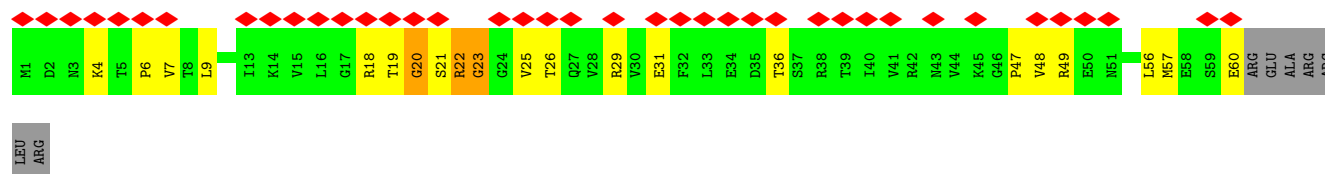


- Molecule 24: 40S ribosomal protein rpS27 (S27e)

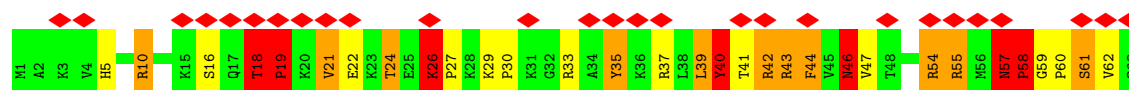
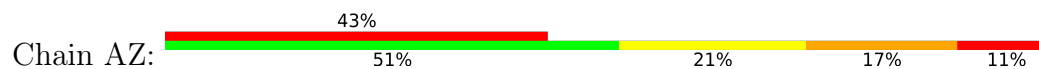




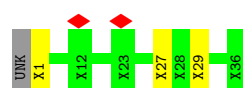
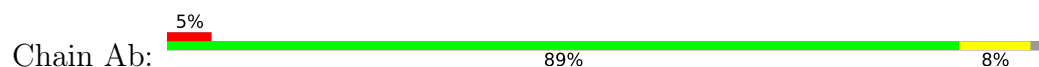
- Molecule 25: 40S ribosomal protein rpS28 (S28e)



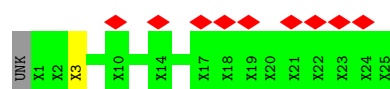
- Molecule 26: 40S ribosomal protein rpS30 (S30e)



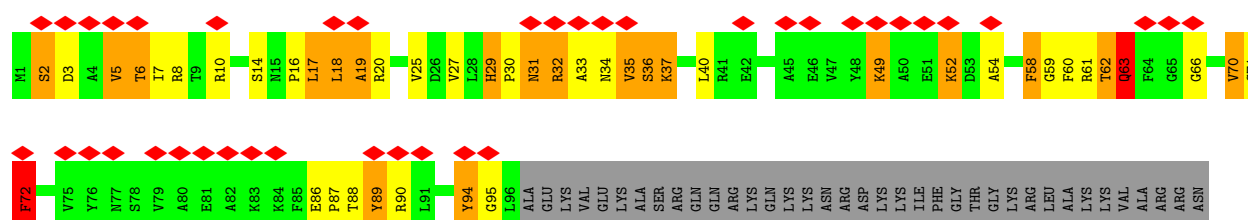
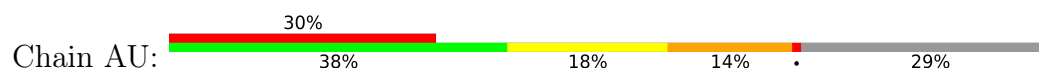
- Molecule 27: Unknown 40S ribosomal protein XS1



- Molecule 28: Unknown 40S ribosomal protein XS2

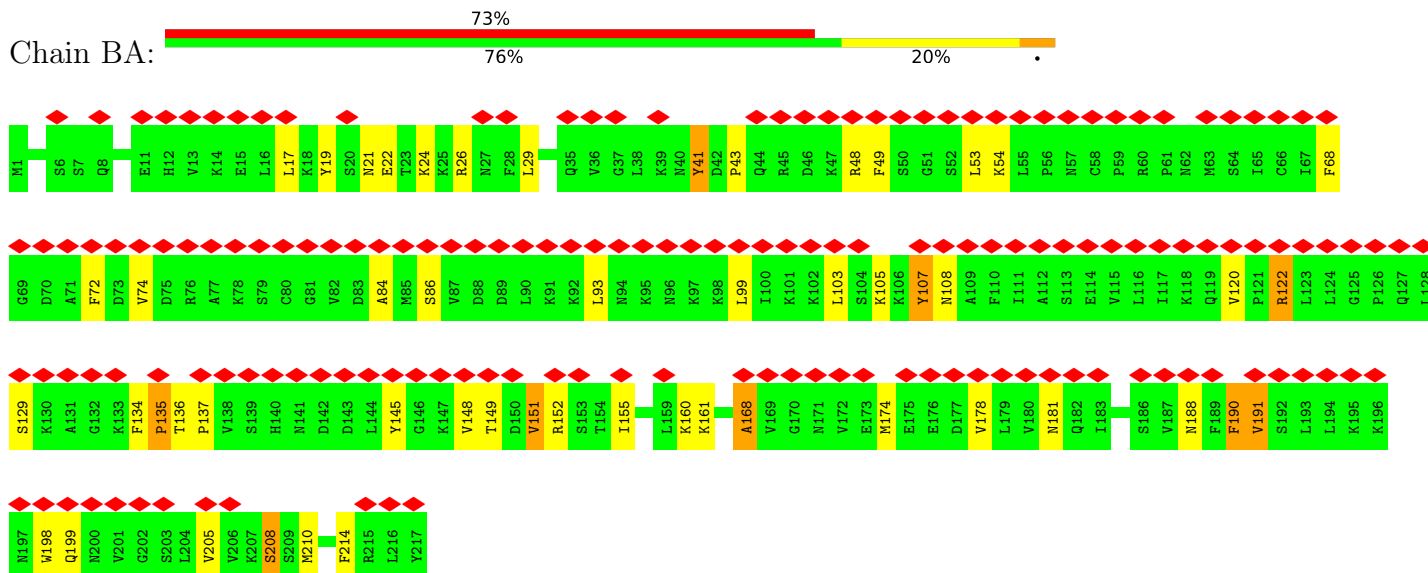


- Molecule 29: 40S ribosomal protein S24

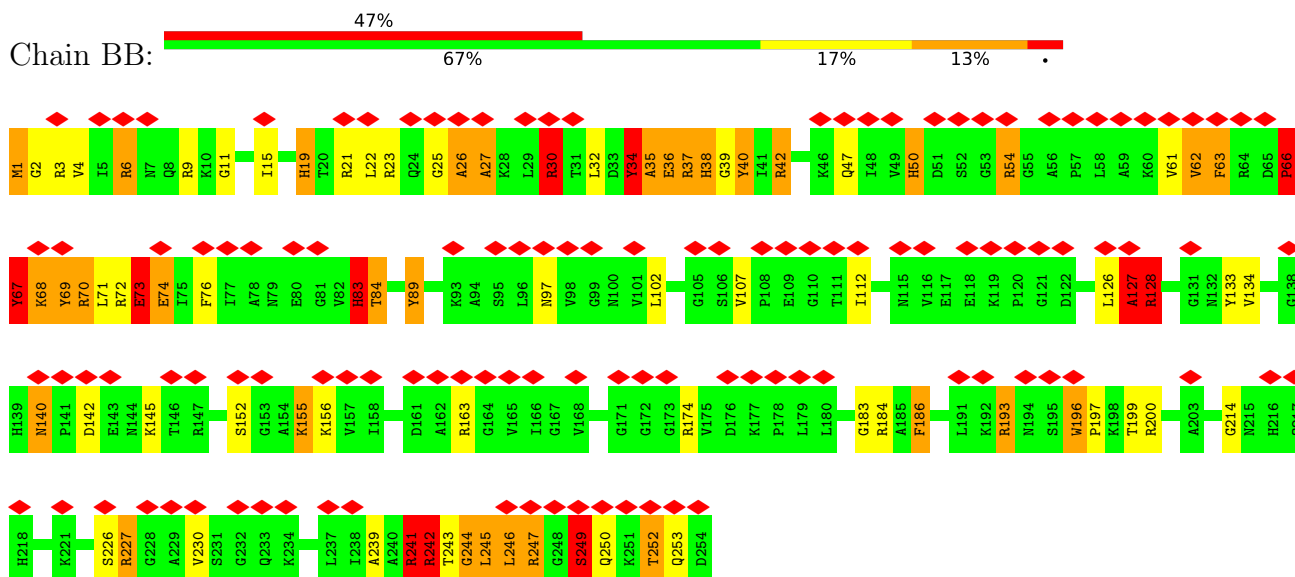


ALA
ASP

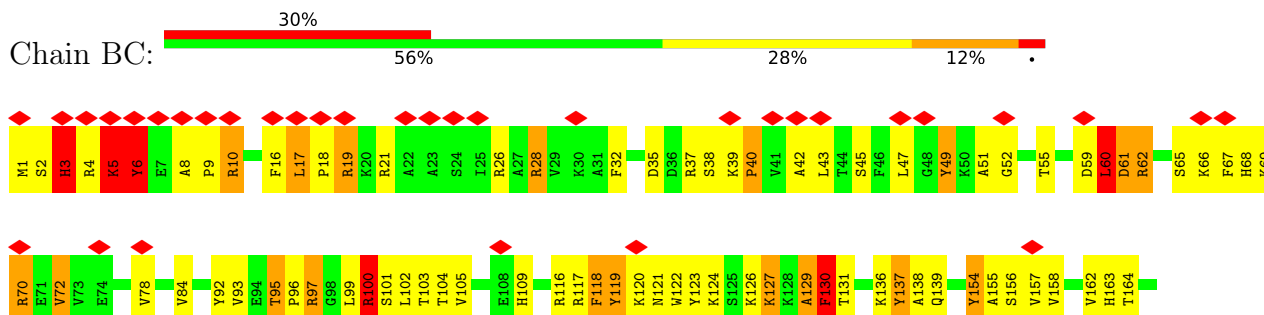
- Molecule 30: 60S ribosomal protein rpL1 (L1p)

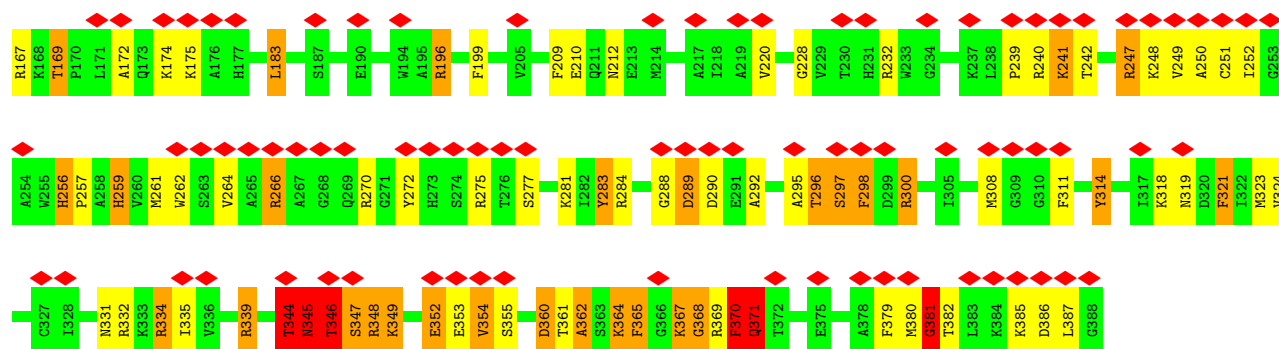


- Molecule 31: 60S ribosomal protein rpL2 (L2p)

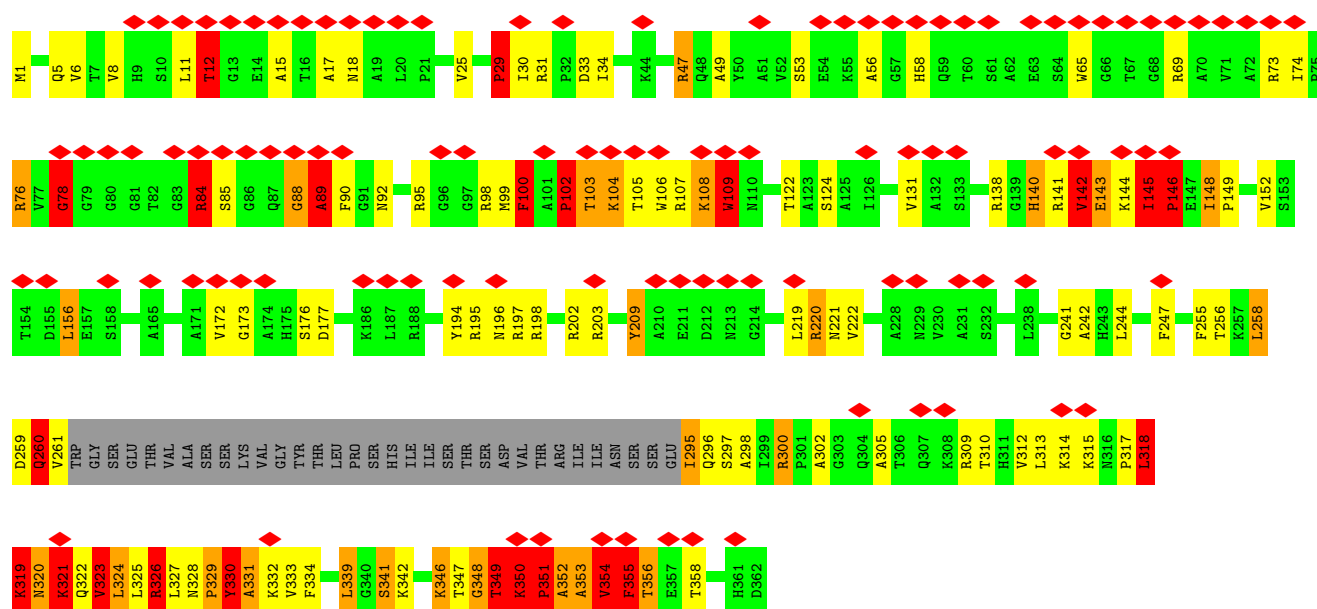


- Molecule 32: 60S ribosomal protein rpL3 (L3p)

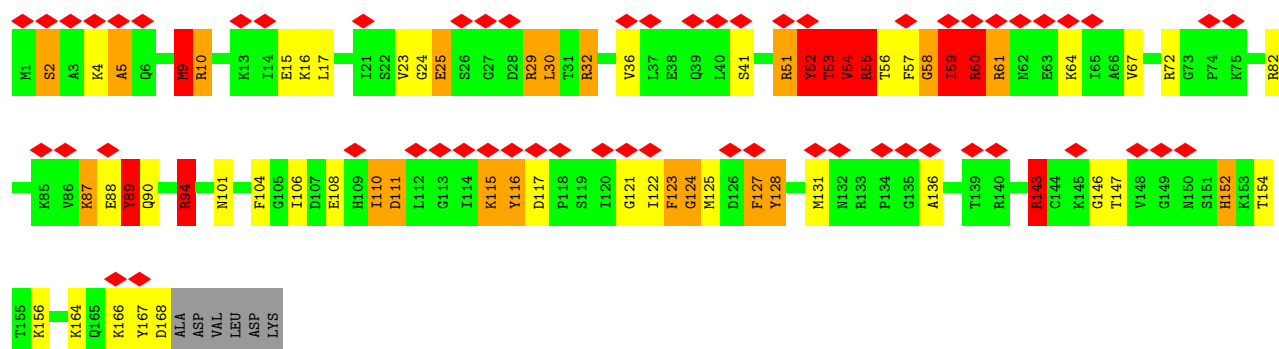




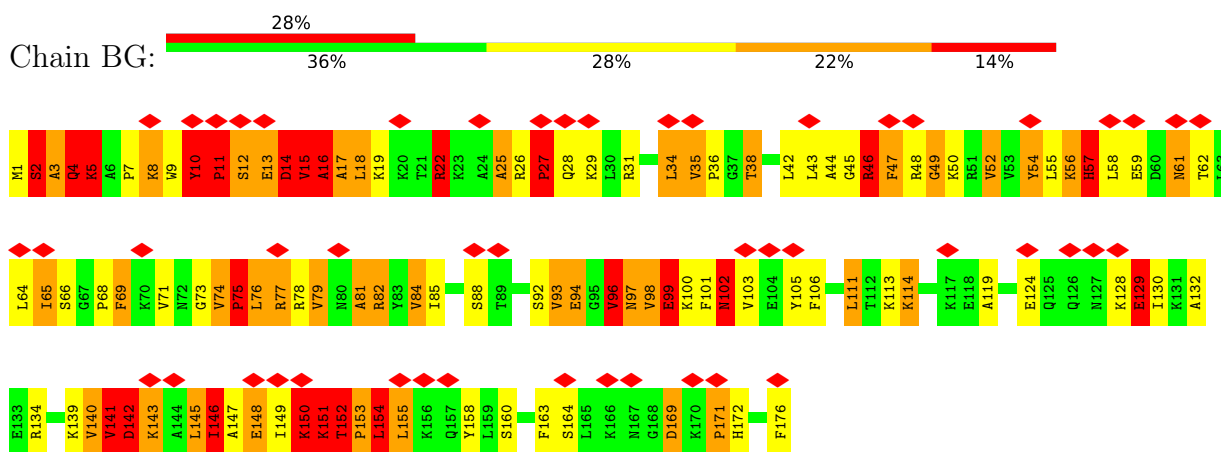
• Molecule 33: 60S ribosomal protein rpL4 (L4p)



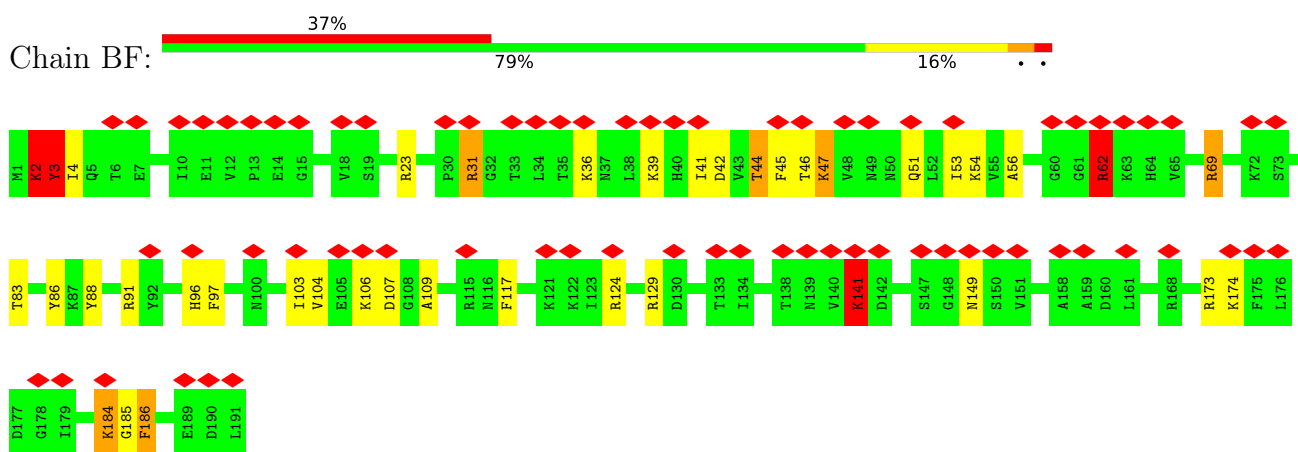
• Molecule 34: 60S ribosomal protein rpL11 (L5p)



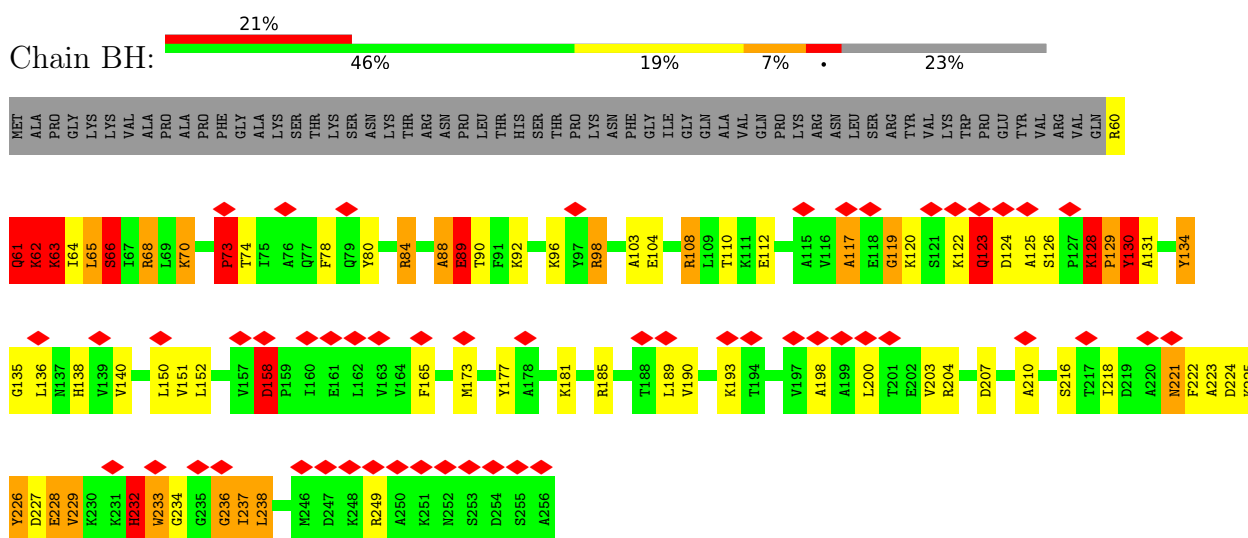
• Molecule 35: 60S ribosomal protein rpL6 (L6e)



• Molecule 36: 60S ribosomal protein rpL9 (L6p)

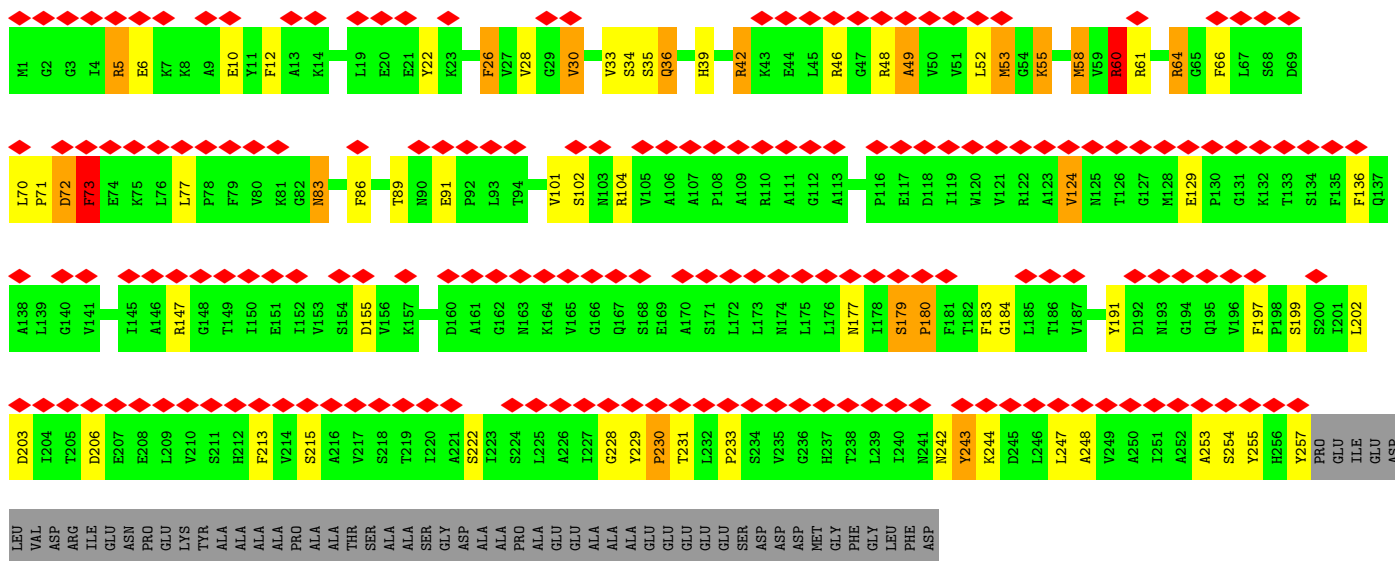


• Molecule 37: 60S ribosomal protein rpL8 (L7ae)

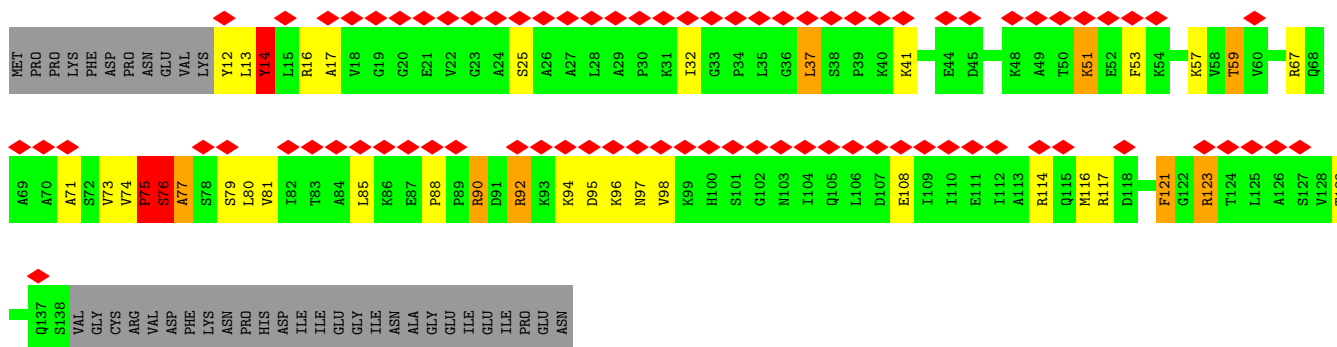


• Molecule 38: 60S acidic ribosomal protein rpP0 (L10P)

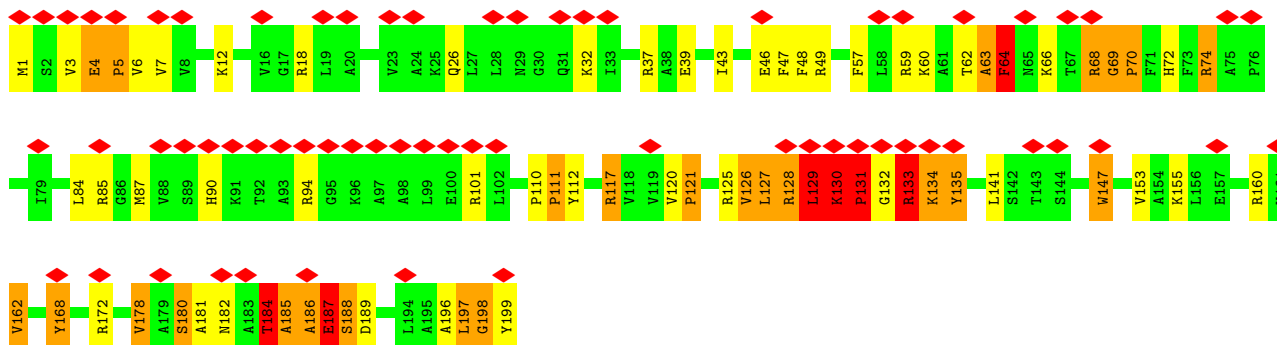




• Molecule 39: 60S ribosomal protein rpL12 (L11p)

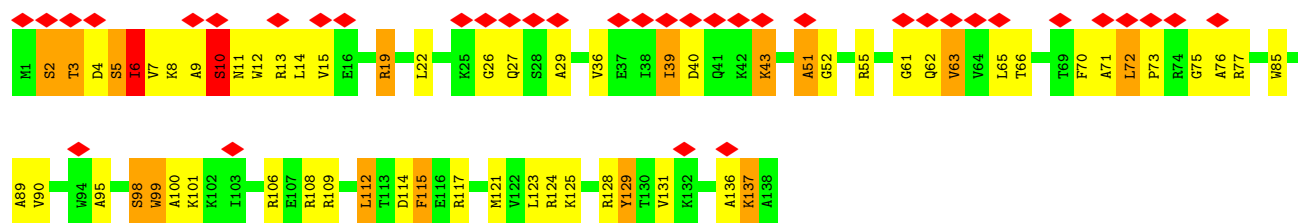


• Molecule 40: 60S ribosomal protein rpL16 (L13p)

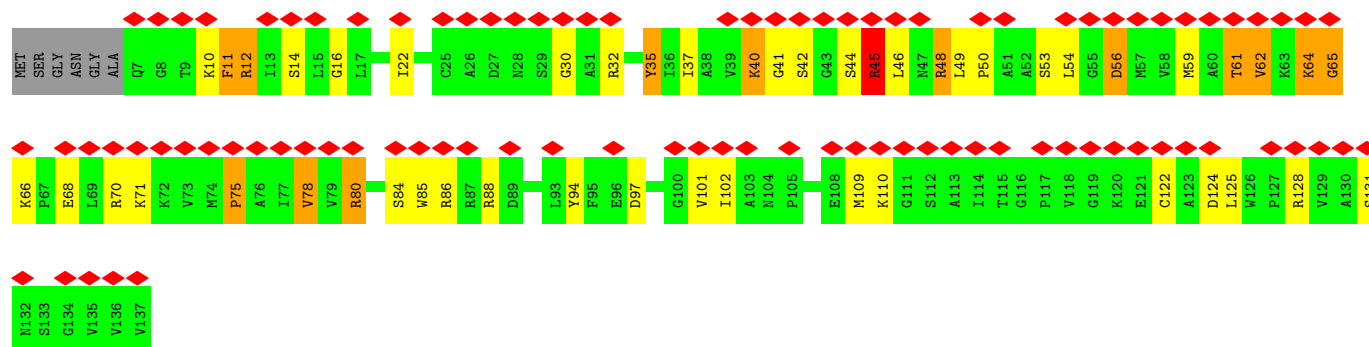


• Molecule 41: 60S ribosomal protein rpL14 (L14e)

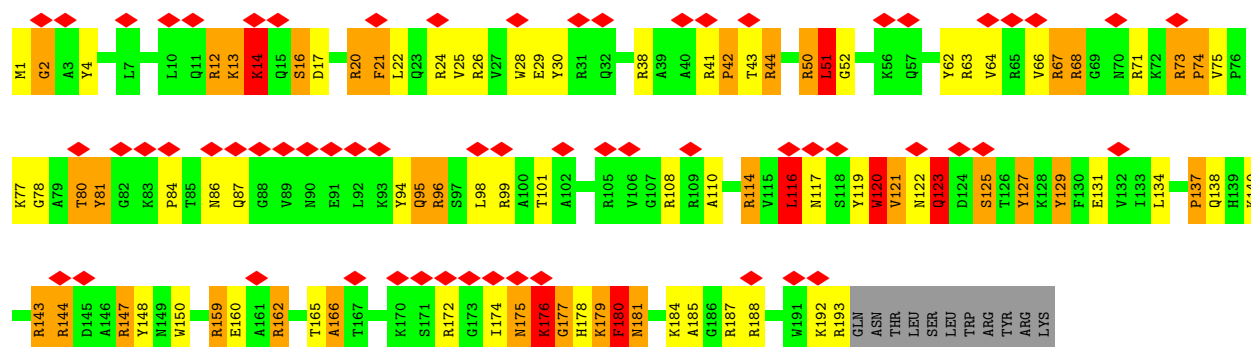




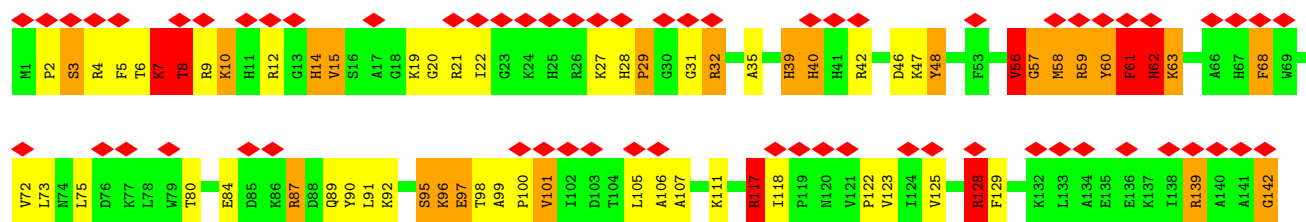
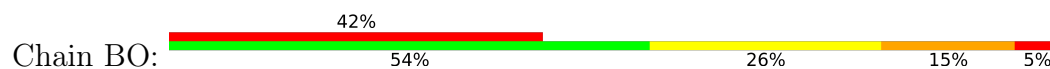
- Molecule 42: 60S ribosomal protein rpL23 (L14p)



- Molecule 43: 60S ribosomal protein rpL15 (L15e)

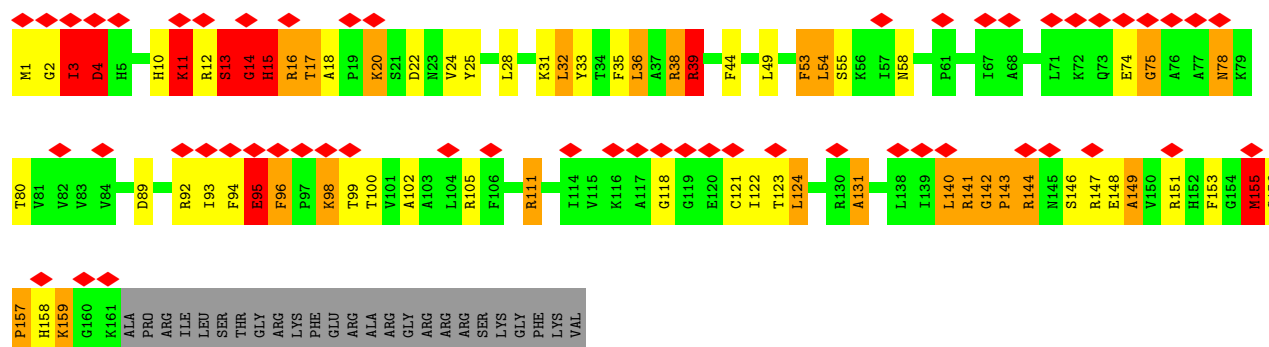


- Molecule 44: 60S ribosomal protein rpL28 (L15p)

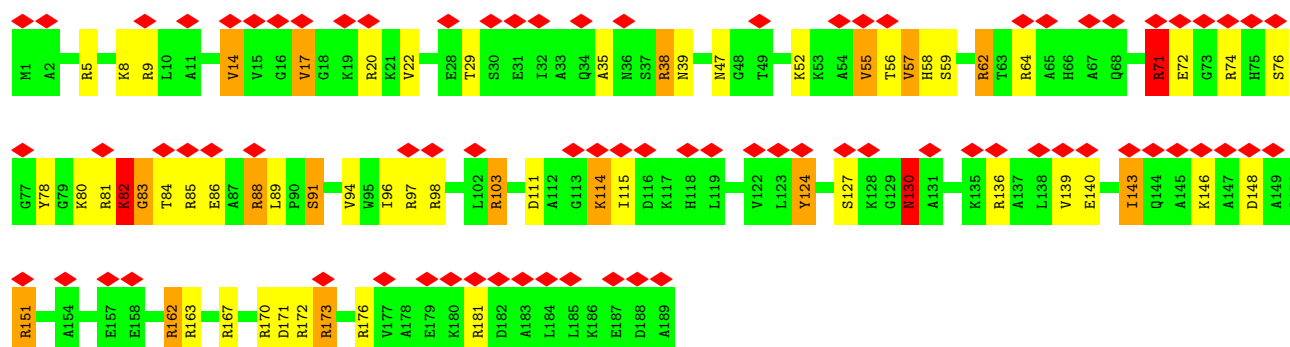




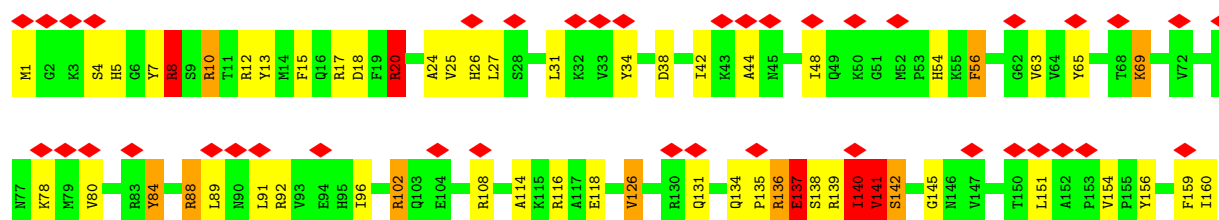
- Molecule 45: 60S ribosomal protein rpL18 (L18e)



- Molecule 46: 60S ribosomal protein rpL19 (L19e)

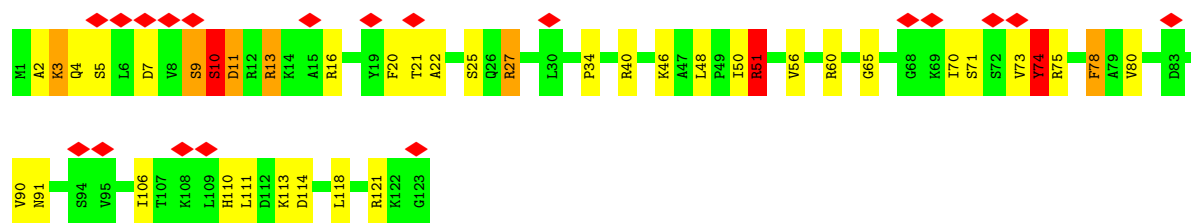


- Molecule 47: 60S ribosomal protein rpL21 (L21e)

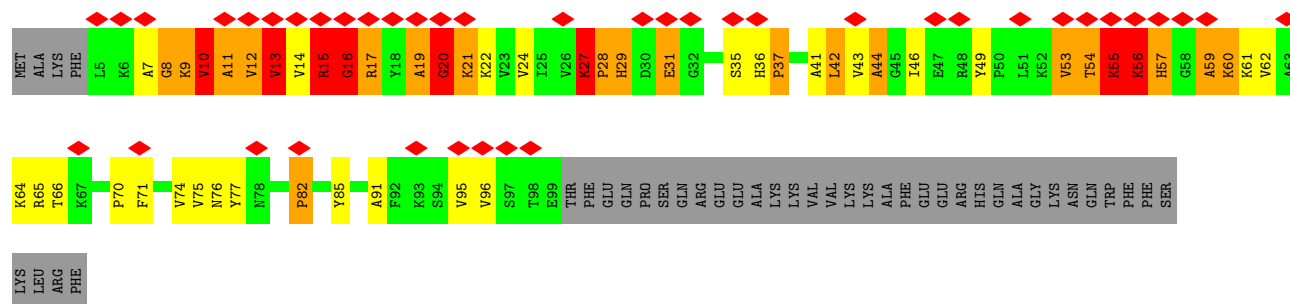
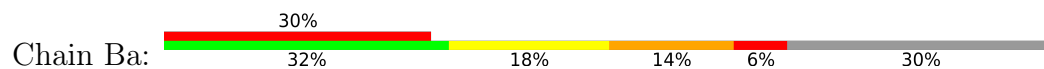


- Molecule 48: 60S ribosomal protein rpL22 (L22e)

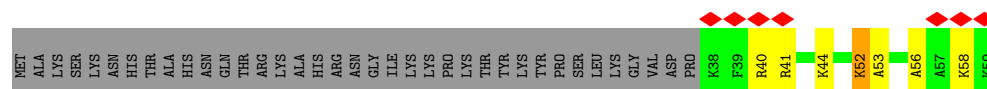




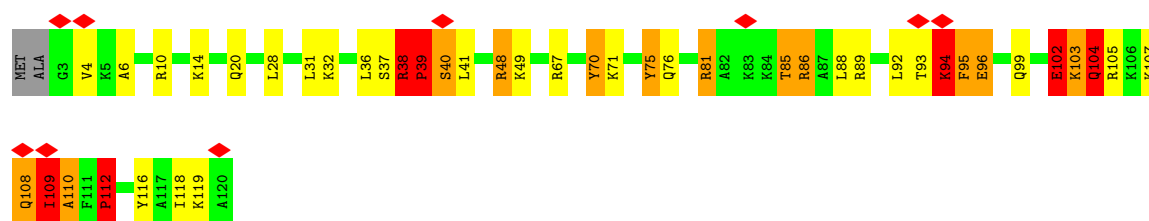
- Molecule 53: 60S ribosomal protein rpL27 (L27e)



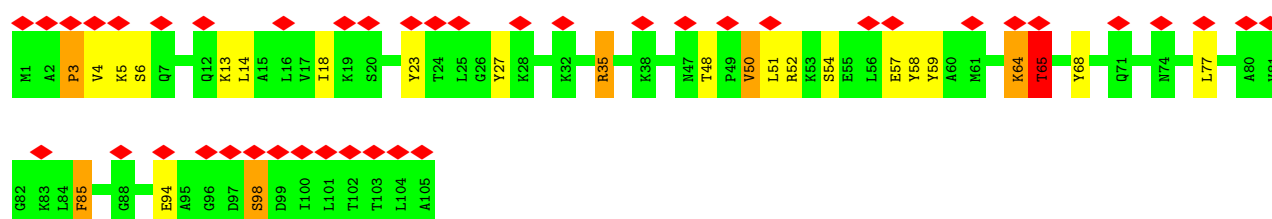
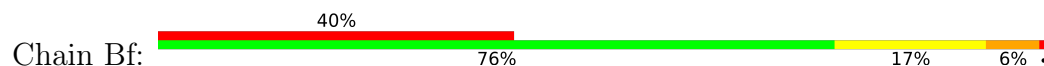
- Molecule 54: 60S ribosomal protein rpL29 (L29e)



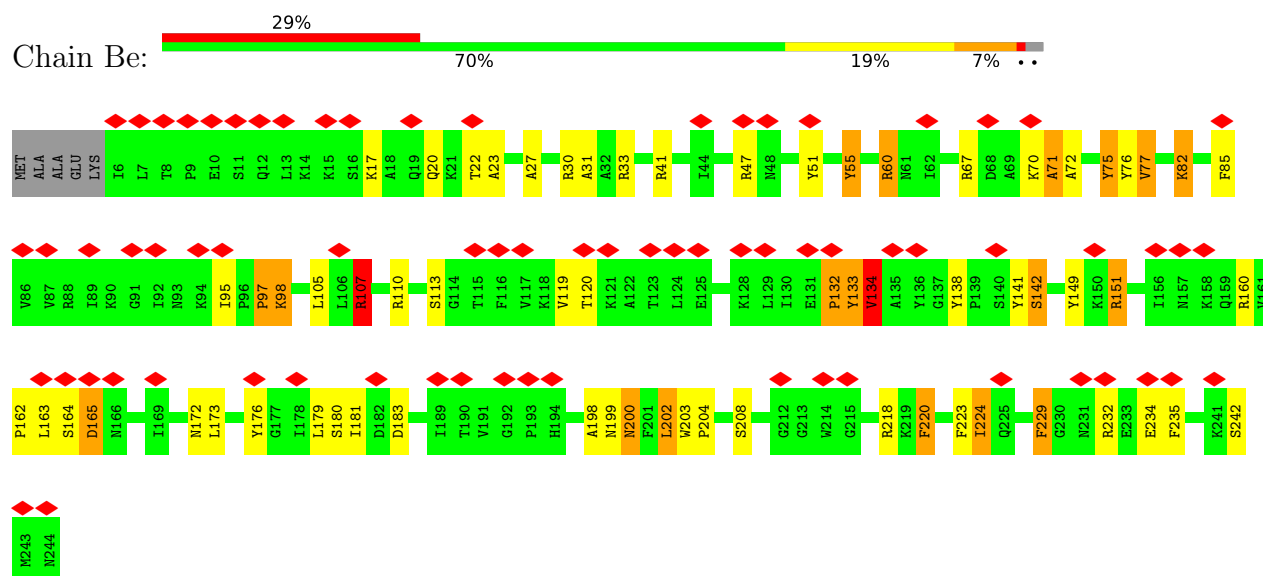
- Molecule 55: 60S ribosomal protein rpL35 (L29p)



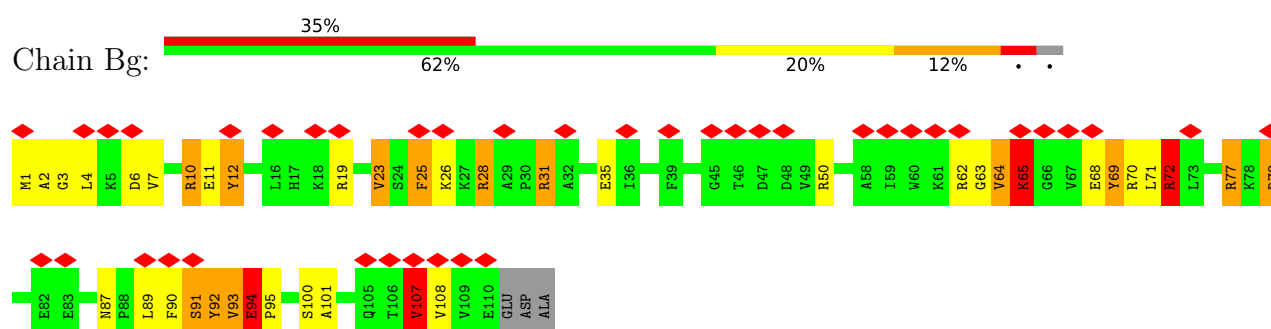
- Molecule 56: 60S ribosomal protein rpL30 (L30e)



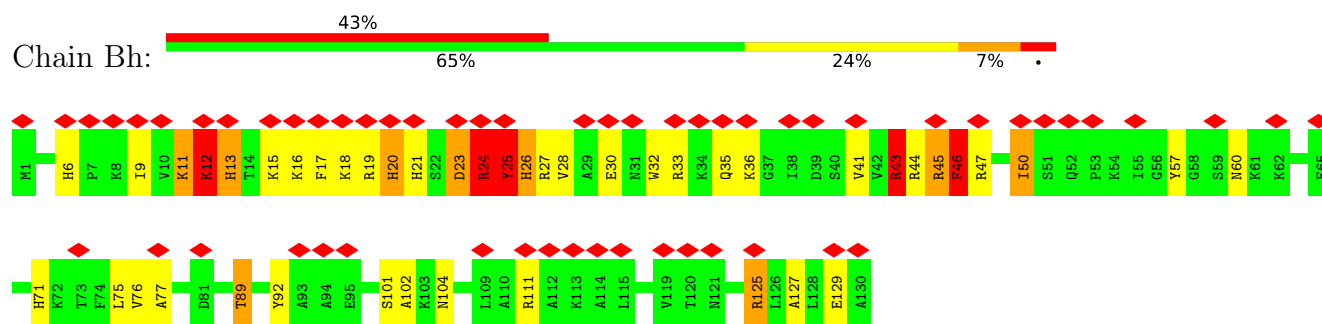
- Molecule 57: 60S ribosomal protein rpL7 (L30p)



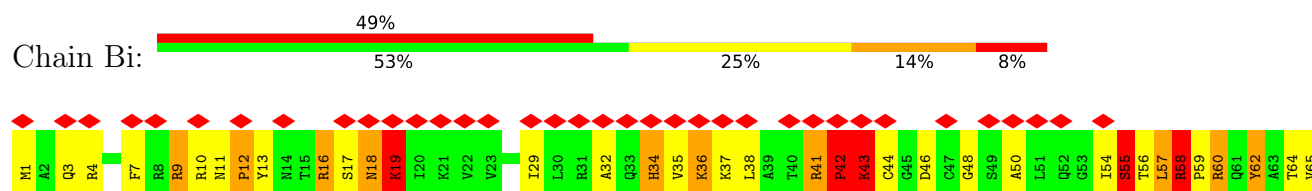
- Molecule 58: 60S ribosomal protein rpL31 (L31e)

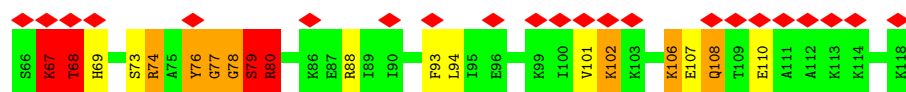


- Molecule 59: 60S ribosomal protein pL32 (L32e)

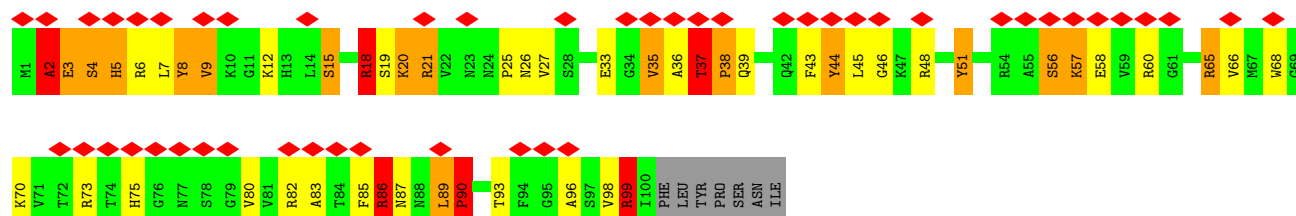


- Molecule 60: 60S ribosomal protein rpL34 (L34e)

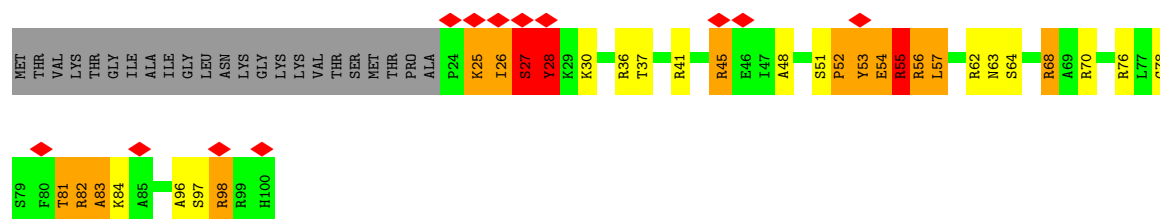




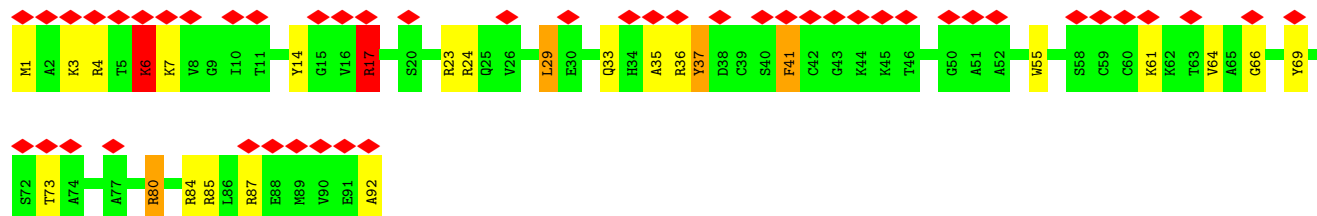
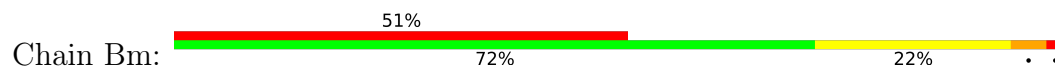
- Molecule 61: 60S ribosomal protein rpL33 (L35ae)



- Molecule 62: 60S ribosomal protein rpL36 (L36e)



- Molecule 63: 60S ribosomal protein rpL43 (L37ae)



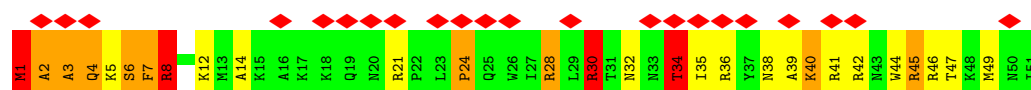
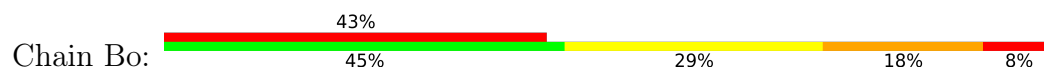
- Molecule 64: 60S ribosomal protein rpL37 (L37e)



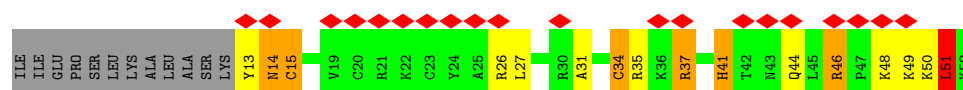
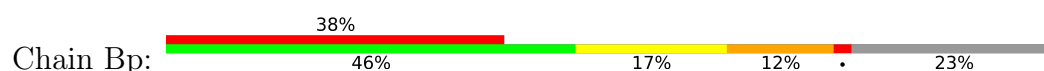
- Molecule 65: 60S ribosomal protein rpL38 (L38e)



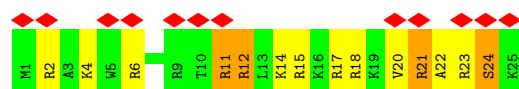
- Molecule 66: 60S ribosomal protein rpL39 (L39e)



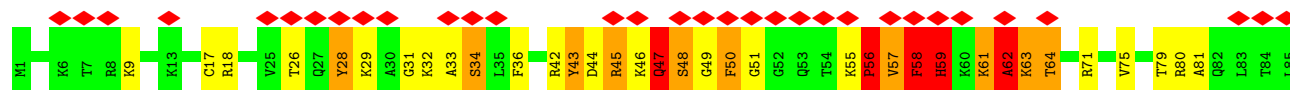
- Molecule 67: 60S ribosomal protein rpL40 (L40e)



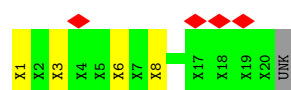
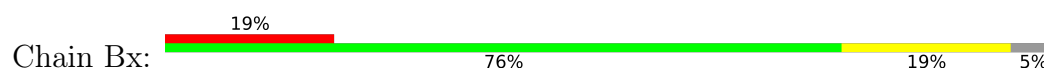
- Molecule 68: 60S ribosomal protein rpL41 (L41e)



- Molecule 69: 60S ribosomal protein rpL42 (L44e)



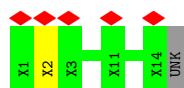
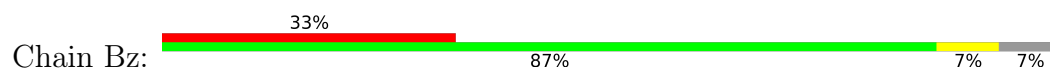
- Molecule 70: Unknown protein



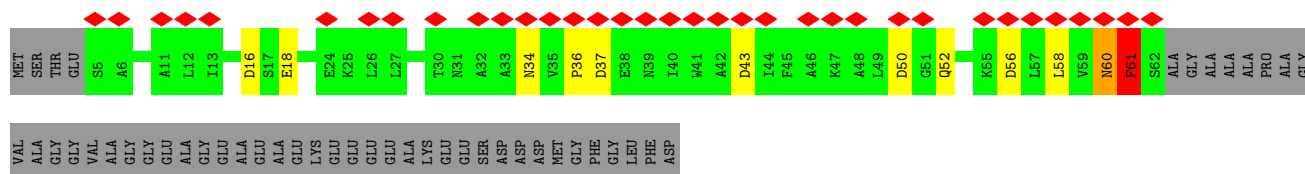
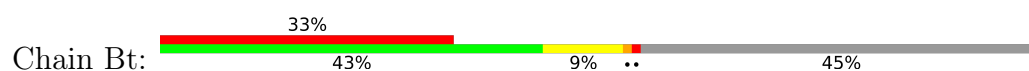
- Molecule 70: Unknown protein



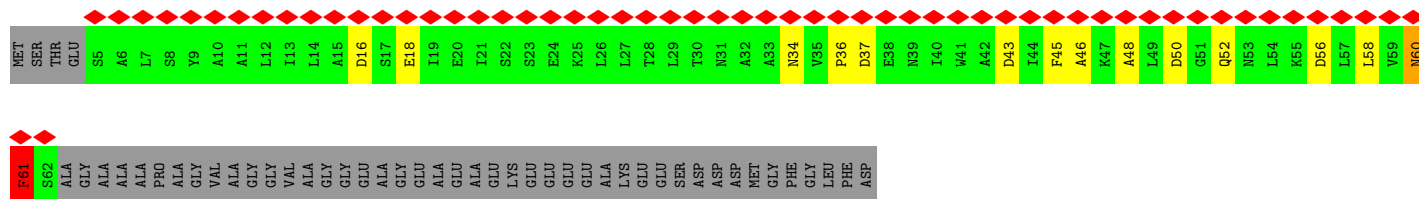
- Molecule 71: Unknown protein



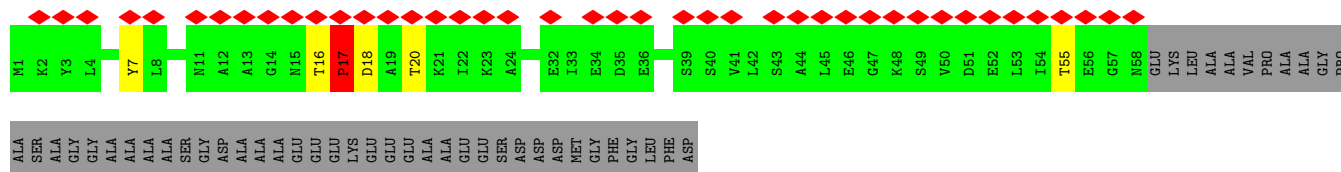
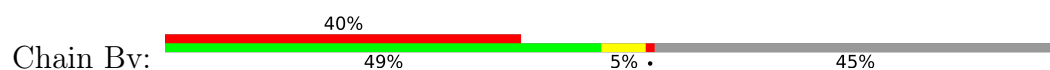
- Molecule 72: 60S acidic ribosomal protein rpP11 (P1)



- Molecule 72: 60S acidic ribosomal protein rpP11 (P1)

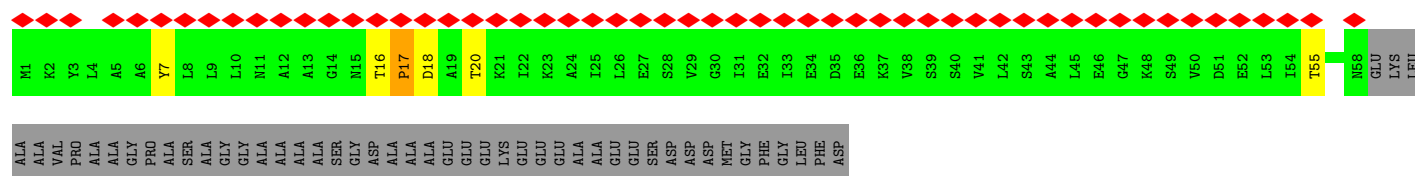


- Molecule 73: 60S acidic ribosomal protein (P2)

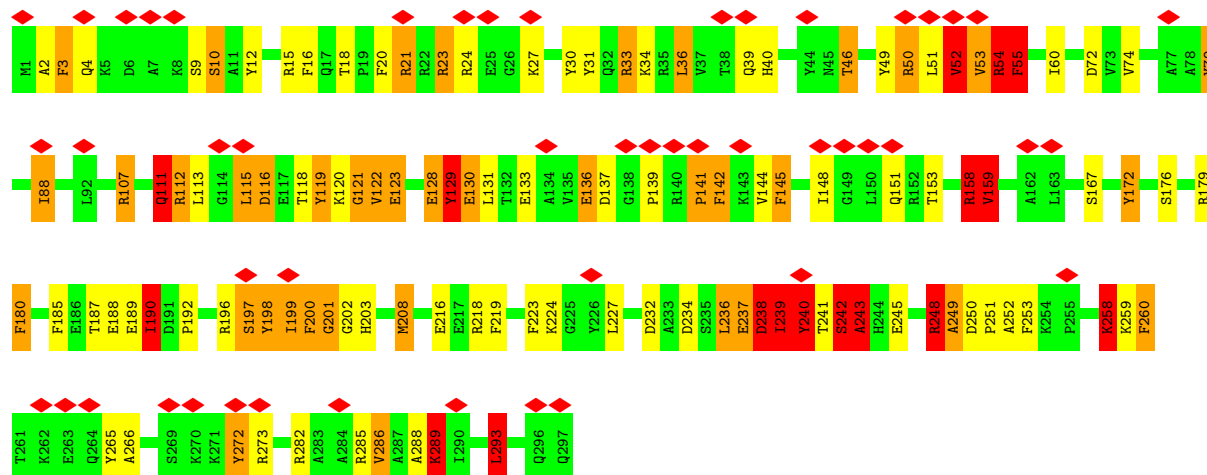


- Molecule 73: 60S acidic ribosomal protein (P2)

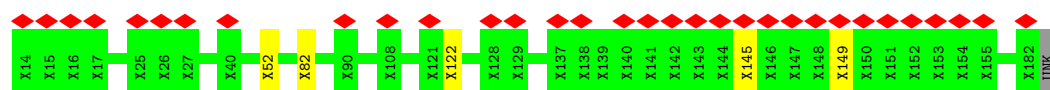




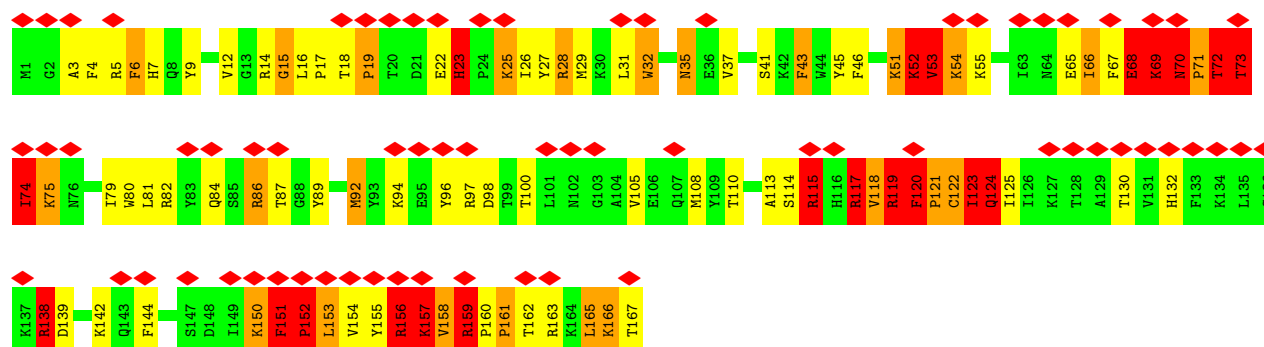
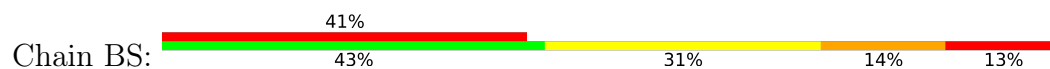
• Molecule 74: 60S ribosomal protein rpL5 (L18p)



• Molecule 75: 60S ribosomal protein rpL13 (L13e)

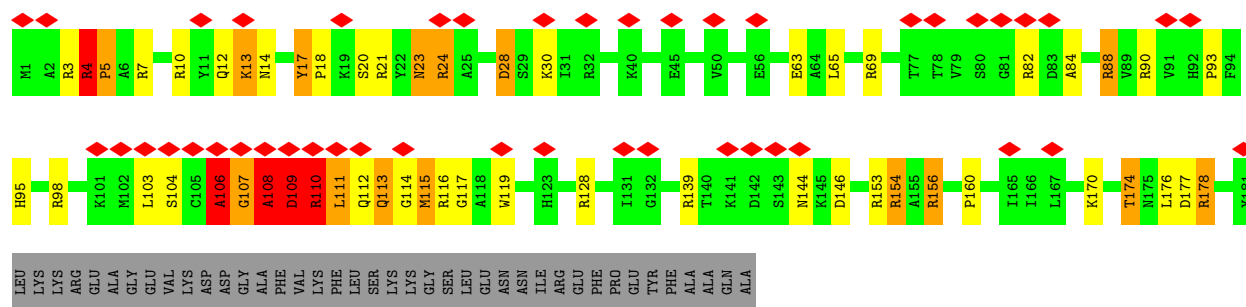


• Molecule 76: 60S ribosomal protein rpL20 (L18ae)

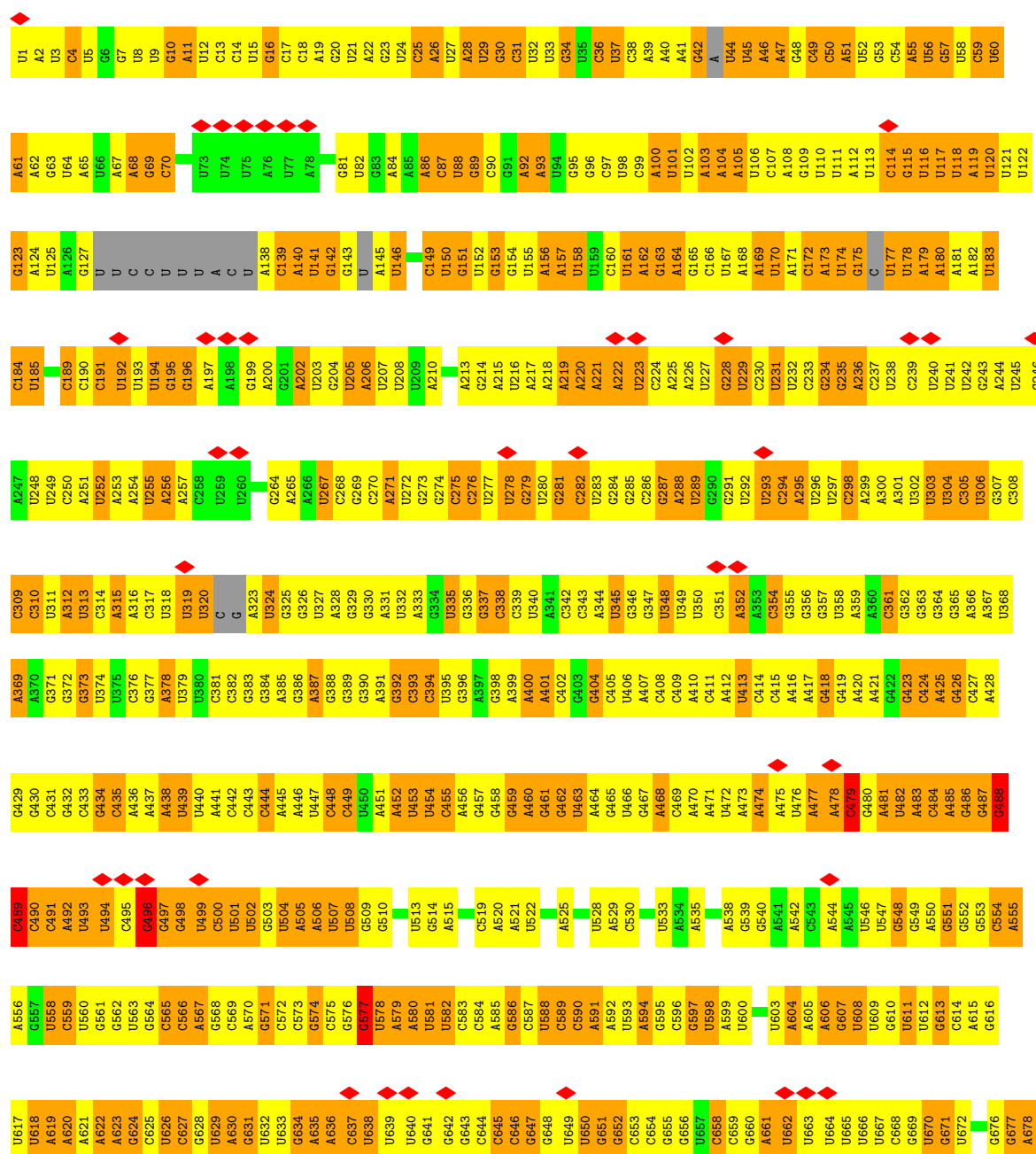
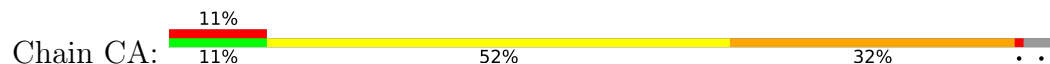


• Molecule 77: 60S ribosomal protein rpL10 (L10e)

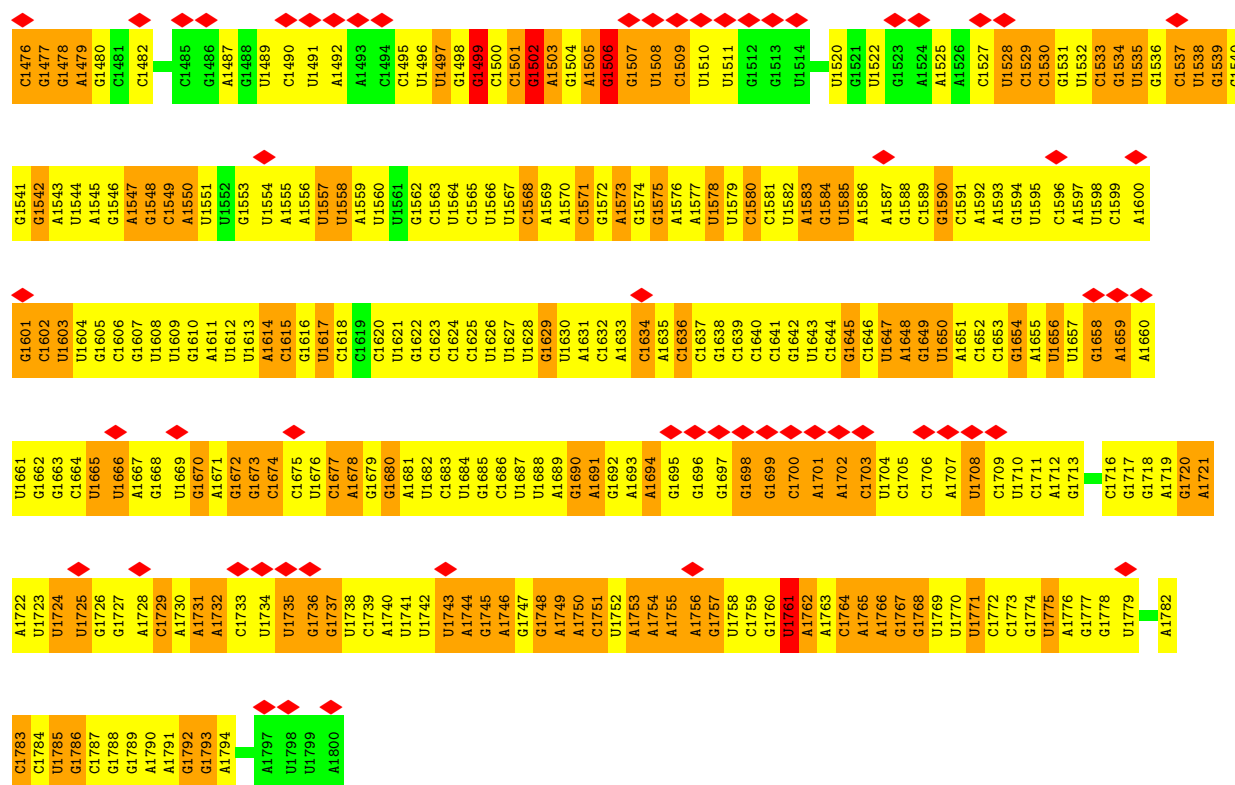




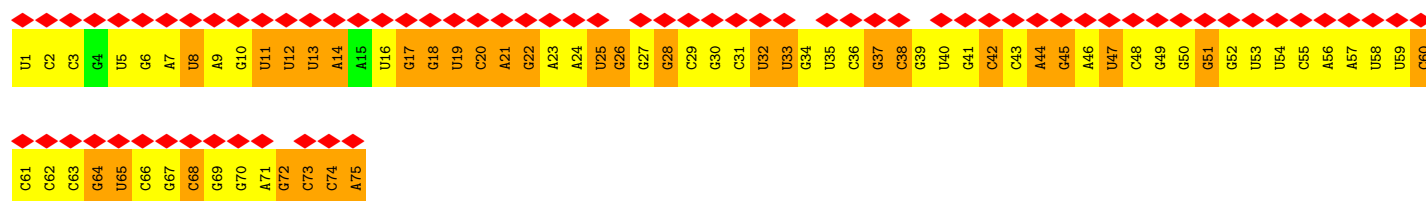
Molecule 78: 18S rRNA



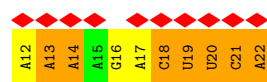




• Molecule 79: P-SITE TRNA ASP



• Molecule 80: MRNA, RNA (5'-R(P*AP*AP*AP*AP*GP*AP*CP*UP*UP*CP*A)-3')



• Molecule 81: 25S rRNA

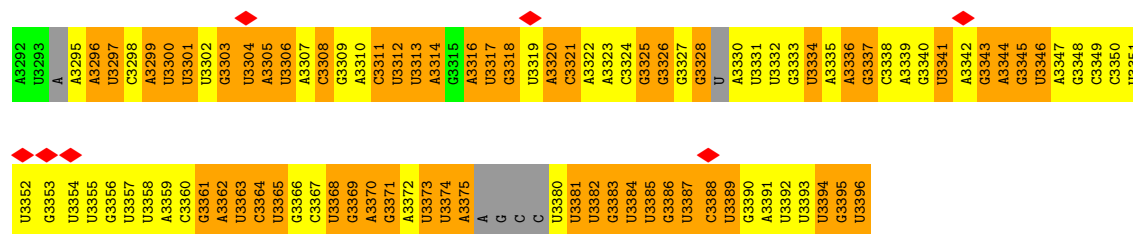


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U855	G795	A735	U615	G552	U492	U431	A369	U305	U245	C185	C125	A63
G856	U796	G676	U616	U553	G493	G432	U370	A306	U246	U186	U126	G64
G857	U797	A677	G617	U554	G494	U433	G371	A307	C247	A187	G127	A65
A858	G678	G738	U618	U555	G495	U434	A372	A308	U248	U188	G128	A66
G859	U679	A738	A619	U556	G496	U435	A373	U309	U249	G189	U129	A67
G860	G680	G739	U620	U557	C497	A436	A374	U310	U250	U190	C68	C68
A861	U681	U740	U621	U558	A498	G437	A375	U311	C130	A130	C130	C69
U862	U682	G742	U622	A559	G499		G376	C312	C132	C192	C132	A70
C863	U683	C743	A623	G560	C500	A440	A377	C313	U133	C193	U133	A71
G864	G684	A744	G624	C561	C501	U441	A378	U314	A253	C194	U134	C72
G865	G685	C745	G625	C562	U502	G442	C379	U314	A254	C195	U134	C73
A866	G686	G746	U626	U563	C503	G443	U380	C315	A255	U195	C135	C74
G867	U687	U747	U627	U564	C504	U444	U381	U316	G256	G136	G136	G75
G868	G688	A748	U628	U565	A504	G445	U382	A317	U257	G137	G137	G76
A869	U689	C749	U629	G566	G505		G383	A318	A198	U138	U138	A77
G870	A690	G750	A630	G567	U506	U446	A384	A319	G258	C139	U139	U78
U871	A691	A751	U631	G567	U507	U447	A385	G320	C200	C140	C140	U79
U872	G692	C752	U632	G568	U508	U448	A386	G321	C201	C141	C141	G80
C873	A693	G753	C633	A569	U509	U449	A387	U322	C202	G142	G142	C81
U874	G694	A754	C634	A670	G510	G450	G388	A323	C203	G143	G143	C82
G875	C695	U755	U635	A571	G511	U451	A389	U326	C205	A144	A144	C83
A876	C696	U756	U636	A572	U512	G452	G390	U327	G206	G145	G145	U84
A877	C697	C757	U637	C573	U513	C453	A391	U328	U207	U146	U146	U87
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U879	U698	G759	U639	C576	C515	C455	U393	U330	C208	U148	U148	C90
U880	A699	U760	U640	C577	A516	U456	A396	U331	A209	U149	U149	A90
C881	C700	A761	U641	A578	G517	G457	A397	G332	U210	A150	A150	U87
A882	G702	U762	U642	C580	A519	U458	A398	G333	A211	U151	U151	A89
C883	G703	U763	U643	U581	U520	U459	A399	G334	G212	U152	U152	G91
A884	U704	C764	U644	U582	A521	G460	G400	A334	A213	U153	U153	G92
U885	A705	U765	G645	G583	A522	G461	U401	A335	A214	U154	U154	G93
C886	U706	G766	A646	U584	A523	C462	A402	A336	G215	G155	G155	A95
A887	U707	U767	A647	C585	U524	U461	C403	G337	G216	G156	G156	G96
U888	G708	C768	C648	U586	C525	C462	G404	A338	G217	A157	A157	U97
U889	A709	G769	A649	U587	C526	C463	U405	C339	A219	G158	G158	G98
C890	U710	U770	C650	U588	U527	U464	A406	C340	G220	A159	A159	A99
G891	G711	U771	U651	C593	U528	U465	G412	G341	G221	G160	G160	A100
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C893	U713	G773	A653	G595	C530	G466	U414	G282	A222	C162	C162	G102
A894	G714	A774	C654	C596	G531	U467	A407	U343	G223	C163	C163	G103
U895	A715	U775	C655	C597	G532	G467	A408	A344	C224	A164	A164	G104
A896	U716	U776	A656	A598	A533	U467	G412	G345	C225	A	A	C105
U897	C	U777	G657	U599	U534	U467	U413	U346	G227	C166	C166	A106
G898	G	U778	U658	C599	U535	G468	U414	A349	U228	U167	U167	A107
U899	U	G779	U659	G600	U536	G469	G415	G350	G229	U168	U168	A108
C900	A720	A780	A660	U601	U537	U471	A416	A351	U230	U169	U169	A109
A841	G721	G781	G661	U602	G538	A472	A417	G352	G291	G170	G170	G110
G842	U722	U782	U662	A603	C539	G473	A418	G353	G232	G171	G171	C111
A843	U723	A783	C663	G604	U540	G474	G419	C293	C233	G172	G172	U112
U904	U724	G784	U664	U605	U541	G475	G420	U294	C234	G173	G173	C113
U905	G725	A785	A665	C606	C542	G476	G421	A295	C235	C174	C174	A114
A906	U726	U786	A666	A607	C543	U477	A422	A296	G236	A	A	A
G907	G727	G787	C667	G608	C544	G478	A423	G237	G237	U176	U176	U
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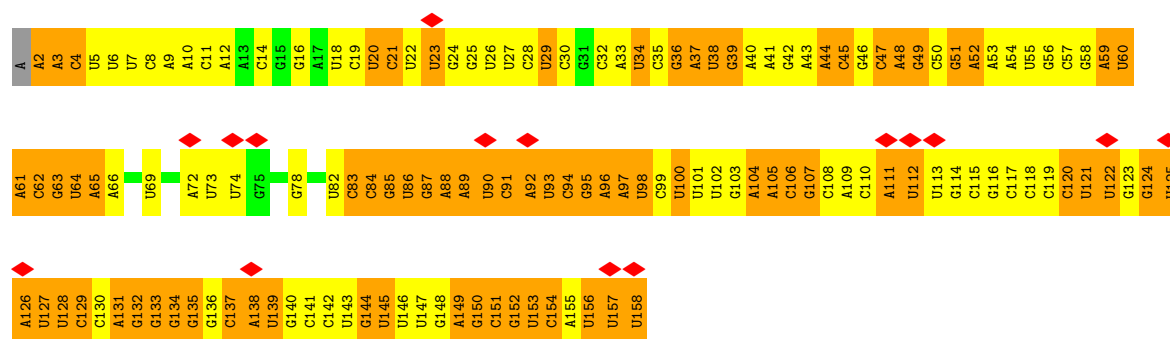


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G2478	G2418	U2358	A2295	G2235	U2173	G2110	C2049	G1993	U1936	G1810	G1751	G1751
A2479	A2419	C2359	U2296	G2236	G2174	U2112	G2050	G1994	U1937	A1812	A1752	A1752
G2480	C2420	U2360	U2297	C2237	U2175	G2113	G2051	A1995	G1938	A1813	G1753	G1753
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C2482	C2422	C2362	A2303	G2239	G2177	C2114	C2053	U1997	G1940	G1815	U1755	C1755
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G2484	A2424	C2364	G2305	U2241	C2179	G2116	G2056	U1999	U1942	U1817	G1758	G1758
U2485	G2425	G2365	C2306	A2243	G2180	A2117	G2057	C1999		A1881	U1818	U1818
A2486	U2426	C2366			C2181	C2118	U2059	U2001			G1759	G1759

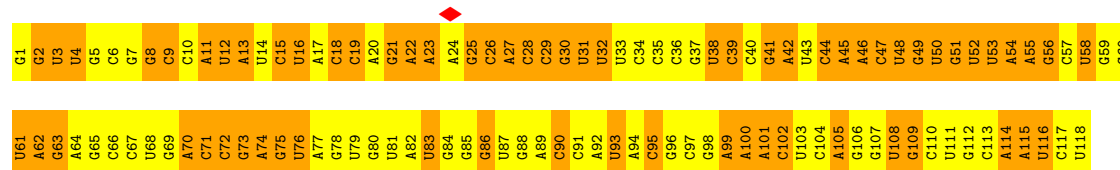
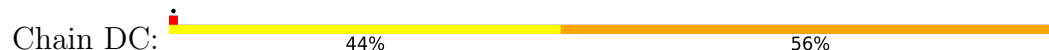




• Molecule 82: 5.8S rRNA



• Molecule 83: 5S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	20400	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	7.747	Depositor
Minimum map value	-3.672	Depositor
Average map value	0.049	Depositor
Map value standard deviation	0.609	Depositor
Recommended contour level	1.75	Depositor
Map size (\AA)	455.4, 455.4, 455.4	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.2375, 1.2375, 1.2375	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Aa	1.65	23/2495 (0.9%)	2.01	81/3391 (2.4%)
2	AA	1.99	33/1962 (1.7%)	2.62	83/2674 (3.1%)
3	AB	1.87	20/1530 (1.3%)	2.48	72/2049 (3.5%)
4	AD	1.95	29/1620 (1.8%)	2.88	94/2182 (4.3%)
5	AC	2.12	34/1544 (2.2%)	3.02	112/2059 (5.4%)
6	AE	1.82	21/1971 (1.1%)	2.46	79/2664 (3.0%)
8	AF	1.70	13/1561 (0.8%)	1.94	47/2103 (2.2%)
9	AH	1.85	10/1047 (1.0%)	2.39	47/1405 (3.3%)
10	AI	1.94	15/1016 (1.5%)	2.50	48/1362 (3.5%)
11	AJ	1.93	13/857 (1.5%)	2.90	38/1148 (3.3%)
12	AK	1.98	14/843 (1.7%)	2.28	38/1134 (3.4%)
13	AL	2.41	23/990 (2.3%)	3.21	80/1304 (6.1%)
14	AM	1.85	23/1175 (2.0%)	2.38	47/1577 (3.0%)
15	AN	1.78	5/358 (1.4%)	2.77	29/469 (6.2%)
16	AO	1.85	10/994 (1.0%)	2.70	58/1339 (4.3%)
17	AQ	2.16	24/1109 (2.2%)	3.08	59/1483 (4.0%)
18	AP	2.29	17/646 (2.6%)	3.39	49/867 (5.7%)
19	AR	1.65	5/691 (0.7%)	2.07	20/931 (2.1%)
20	AS	1.83	17/1138 (1.5%)	2.73	74/1527 (4.8%)
21	AT	2.06	13/694 (1.9%)	2.67	32/935 (3.4%)
22	AV	1.91	14/698 (2.0%)	2.68	44/932 (4.7%)
24	AX	1.77	5/372 (1.3%)	2.15	13/504 (2.6%)
25	AY	1.80	3/447 (0.7%)	2.08	19/601 (3.2%)
26	AZ	2.63	17/499 (3.4%)	3.77	31/660 (4.7%)
29	AU	1.93	8/725 (1.1%)	2.49	45/969 (4.6%)
30	BA	1.42	4/1745 (0.2%)	1.78	32/2342 (1.4%)
31	BB	2.07	31/1938 (1.6%)	2.90	100/2600 (3.8%)
32	BC	2.25	65/3124 (2.1%)	3.27	171/4196 (4.1%)
33	BD	2.15	53/2531 (2.1%)	2.93	146/3414 (4.3%)
34	BE	2.08	25/1362 (1.8%)	3.17	79/1824 (4.3%)
35	BG	2.50	42/1433 (2.9%)	3.60	142/1922 (7.4%)
36	BF	1.65	9/1537 (0.6%)	2.05	27/2068 (1.3%)
37	BH	2.09	26/1527 (1.7%)	2.60	82/2052 (4.0%)
38	Bs	1.71	18/2013 (0.9%)	2.32	75/2731 (2.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	BJ	1.89	16/964 (1.7%)	2.63	44/1295 (3.4%)
40	BK	1.93	21/1600 (1.3%)	2.78	76/2146 (3.5%)
41	BN	1.88	15/1083 (1.4%)	2.30	56/1456 (3.8%)
42	BM	1.73	12/987 (1.2%)	2.20	45/1326 (3.4%)
43	BP	2.03	23/1659 (1.4%)	2.68	113/2221 (5.1%)
44	BO	2.47	29/1213 (2.4%)	3.20	74/1623 (4.6%)
45	BR	2.41	29/1264 (2.3%)	3.18	68/1701 (4.0%)
46	BT	1.82	26/1547 (1.7%)	2.27	54/2060 (2.6%)
47	BU	1.78	21/1285 (1.6%)	2.44	54/1720 (3.1%)
48	BW	2.02	13/846 (1.5%)	2.75	47/1142 (4.1%)
49	BV	1.71	14/1335 (1.0%)	2.03	40/1794 (2.2%)
50	BX	1.58	5/993 (0.5%)	2.19	41/1336 (3.1%)
51	BZ	2.29	14/590 (2.4%)	2.74	40/783 (5.1%)
52	BY	1.61	10/983 (1.0%)	1.95	25/1312 (1.9%)
53	Ba	2.24	20/722 (2.8%)	3.30	75/967 (7.8%)
54	Bd	1.63	2/177 (1.1%)	1.91	5/231 (2.2%)
55	Bc	2.06	14/974 (1.4%)	2.76	53/1294 (4.1%)
56	Bf	1.59	7/793 (0.9%)	1.92	17/1062 (1.6%)
57	Be	1.85	25/1957 (1.3%)	2.29	69/2631 (2.6%)
58	Bg	1.83	16/887 (1.8%)	2.38	32/1185 (2.7%)
59	Bh	1.80	11/1064 (1.0%)	2.30	47/1423 (3.3%)
60	Bi	2.51	24/935 (2.6%)	3.64	59/1242 (4.8%)
61	Bj	2.79	19/751 (2.5%)	3.05	68/1004 (6.8%)
62	Bk	2.48	19/625 (3.0%)	3.48	45/826 (5.4%)
63	Bm	1.73	9/710 (1.3%)	2.09	24/944 (2.5%)
64	Bl	2.03	9/693 (1.3%)	2.42	34/915 (3.7%)
65	Bn	2.32	13/610 (2.1%)	3.37	37/813 (4.6%)
66	Bo	1.80	4/452 (0.9%)	2.23	17/598 (2.8%)
67	Bp	1.57	2/335 (0.6%)	2.25	18/442 (4.1%)
68	Bq	1.98	3/235 (1.3%)	2.32	14/300 (4.7%)
69	Br	2.01	14/846 (1.7%)	2.74	44/1113 (4.0%)
72	Bt	0.69	1/445 (0.2%)	1.49	16/606 (2.6%)
72	Bu	0.92	1/445 (0.2%)	1.63	18/606 (3.0%)
73	Bv	0.97	0/431	1.29	4/582 (0.7%)
73	Bw	0.96	0/431	1.28	4/582 (0.7%)
74	BQ	2.23	50/2404 (2.1%)	3.27	146/3236 (4.5%)
76	BS	1.92	23/1458 (1.6%)	2.70	109/1957 (5.6%)
77	BI	0.95	1/1473 (0.1%)	1.60	29/1976 (1.5%)
78	CA	2.64	1783/37406 (4.8%)	2.65	3176/57948 (5.5%)
79	CB	2.75	77/1785 (4.3%)	2.58	142/2779 (5.1%)
80	CC	3.40	11/264 (4.2%)	3.22	29/407 (7.1%)
81	DA	2.74	3996/76832 (5.2%)	2.77	7042/119578 (5.9%)
82	DB	2.68	166/3480 (4.8%)	2.64	305/5395 (5.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
83	DC	2.90	156/2808 (5.6%)	3.09	331/4372 (7.6%)
All	All	2.44	7406/202969 (3.6%)	2.70	14979/298347 (5.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	Aa	0	18
2	AA	1	30
3	AB	0	29
4	AD	0	36
5	AC	2	40
6	AE	3	29
7	AG	0	52
8	AF	0	14
9	AH	0	15
10	AI	0	14
11	AJ	0	17
12	AK	1	15
13	AL	0	14
14	AM	0	12
15	AN	0	12
16	AO	2	15
17	AQ	0	29
18	AP	0	15
19	AR	0	8
20	AS	0	19
21	AT	0	15
22	AV	0	12
23	AW	0	20
24	AX	0	2
25	AY	0	4
26	AZ	0	25
27	Ab	0	3
28	Ac	0	1
29	AU	2	12
30	BA	0	8
31	BB	2	45
32	BC	2	56
33	BD	2	53

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	BE	2	25
35	BG	2	57
36	BF	0	10
37	BH	0	36
38	Bs	0	18
39	BJ	1	10
40	BK	0	29
41	BN	1	13
42	BM	0	11
43	BP	4	44
44	BO	1	28
45	BR	0	31
46	BT	0	17
47	BU	1	16
48	BW	0	12
49	BV	0	20
50	BX	0	13
51	BZ	0	18
52	BY	0	8
53	Ba	0	25
54	Bd	0	1
55	Bc	0	16
56	Bf	0	6
57	Be	1	14
58	Bg	0	13
59	Bh	0	14
60	Bi	0	25
61	Bj	1	26
62	Bk	1	15
63	Bm	1	5
64	Bl	0	13
65	Bn	0	15
66	Bo	0	15
67	Bp	0	8
68	Bq	0	4
69	Br	0	23
70	Bx	0	7
71	Bz	0	1
72	Bt	0	3
72	Bu	0	3
73	Bv	0	1
73	Bw	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
74	BQ	0	48
75	BL	0	5
76	BS	1	41
77	BI	2	24
78	CA	10	22
79	CB	1	0
80	CC	1	0
81	DA	32	15
82	DB	5	0
All	All	85	1514

The worst 5 of 7406 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	DA	1261	G	C2'-C1'	59.16	2.18	1.53
79	CB	55	C	C2'-C1'	-55.11	0.92	1.53
78	CA	636	A	C2'-C1'	54.35	2.13	1.53
81	DA	3215	A	C2'-C1'	-49.15	0.99	1.53
78	CA	1190	C	O5'-C5'	-48.72	0.65	1.42

The worst 5 of 14979 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	BC	266	ARG	NE-CZ-NH1	-73.84	83.38	120.30
81	DA	3305	A	P-O3'-C3'	50.10	179.82	119.70
81	DA	3047	U	P-O3'-C3'	47.61	176.83	119.70
81	DA	2046	U	P-O3'-C3'	47.25	176.40	119.70
81	DA	2071	A	P-O3'-C3'	46.20	175.13	119.70

5 of 85 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	AA	241	GLU	CA
5	AC	129	ILE	CA
5	AC	162	SER	CA
6	AE	28	ARG	CA
6	AE	30	THR	CA

5 of 1514 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Aa	10	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	Aa	48	THR	Peptide
1	Aa	49	GLY	Peptide
1	Aa	53	LYS	Mainchain,Peptide
1	Aa	54	PHE	Mainchain

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	Aa	317/319 (99%)	274 (86%)	23 (7%)	20 (6%)	1	17
2	AA	250/252 (99%)	199 (80%)	21 (8%)	30 (12%)	0	6
3	AB	202/240 (84%)	137 (68%)	30 (15%)	35 (17%)	0	3
4	AD	198/261 (76%)	160 (81%)	17 (9%)	21 (11%)	0	8
5	AC	192/197 (98%)	136 (71%)	28 (15%)	28 (15%)	0	4
6	AE	252/254 (99%)	176 (70%)	36 (14%)	40 (16%)	0	3
8	AF	197/225 (88%)	170 (86%)	9 (5%)	18 (9%)	1	11
9	AH	128/130 (98%)	95 (74%)	17 (13%)	16 (12%)	0	5
10	AI	124/143 (87%)	84 (68%)	16 (13%)	24 (19%)	0	2
11	AJ	108/121 (89%)	92 (85%)	8 (7%)	8 (7%)	1	14
12	AK	117/137 (85%)	81 (69%)	9 (8%)	27 (23%)	0	1
13	AL	143/145 (99%)	100 (70%)	22 (15%)	21 (15%)	0	4
14	AM	138/146 (94%)	107 (78%)	21 (15%)	10 (7%)	1	14
15	AN	46/56 (82%)	31 (67%)	2 (4%)	13 (28%)	0	0
16	AO	119/151 (79%)	95 (80%)	12 (10%)	12 (10%)	0	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	AQ	134/136 (98%)	90 (67%)	22 (16%)	22 (16%)	0	3
18	AP	83/156 (53%)	65 (78%)	12 (14%)	6 (7%)	1	14
19	AR	86/142 (61%)	64 (74%)	10 (12%)	12 (14%)	0	4
20	AS	142/144 (99%)	118 (83%)	8 (6%)	16 (11%)	0	7
21	AT	85/87 (98%)	66 (78%)	10 (12%)	9 (11%)	0	8
22	AV	83/108 (77%)	66 (80%)	7 (8%)	10 (12%)	0	6
24	AX	48/82 (58%)	37 (77%)	7 (15%)	4 (8%)	1	12
25	AY	58/67 (87%)	46 (79%)	7 (12%)	5 (9%)	1	12
26	AZ	61/63 (97%)	41 (67%)	6 (10%)	14 (23%)	0	1
29	AU	94/135 (70%)	62 (66%)	14 (15%)	18 (19%)	0	2
30	BA	215/217 (99%)	194 (90%)	11 (5%)	10 (5%)	2	21
31	BB	252/254 (99%)	208 (82%)	18 (7%)	26 (10%)	0	8
32	BC	386/388 (100%)	316 (82%)	33 (8%)	37 (10%)	0	10
33	BD	325/362 (90%)	250 (77%)	34 (10%)	41 (13%)	0	5
34	BE	166/174 (95%)	136 (82%)	11 (7%)	19 (11%)	0	7
35	BG	174/176 (99%)	108 (62%)	15 (9%)	51 (29%)	0	0
36	BF	189/191 (99%)	173 (92%)	13 (7%)	3 (2%)	9	44
37	BH	195/256 (76%)	156 (80%)	18 (9%)	21 (11%)	0	8
38	Bs	255/312 (82%)	224 (88%)	16 (6%)	15 (6%)	1	17
39	BJ	125/165 (76%)	107 (86%)	11 (9%)	7 (6%)	2	19
40	BK	197/199 (99%)	161 (82%)	15 (8%)	21 (11%)	0	8
41	BN	136/138 (99%)	104 (76%)	14 (10%)	18 (13%)	0	5
42	BM	129/137 (94%)	124 (96%)	5 (4%)	0	100	100
43	BP	191/204 (94%)	168 (88%)	14 (7%)	9 (5%)	2	21
44	BO	147/149 (99%)	100 (68%)	24 (16%)	23 (16%)	0	3
45	BR	159/186 (86%)	116 (73%)	22 (14%)	21 (13%)	0	5
46	BT	187/189 (99%)	163 (87%)	14 (8%)	10 (5%)	2	19
47	BU	158/160 (99%)	144 (91%)	7 (4%)	7 (4%)	2	22
48	BW	103/121 (85%)	79 (77%)	15 (15%)	9 (9%)	1	11
49	BV	168/170 (99%)	135 (80%)	20 (12%)	13 (8%)	1	13
50	BX	120/142 (84%)	95 (79%)	11 (9%)	14 (12%)	0	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	BZ	71/155 (46%)	48 (68%)	13 (18%)	10 (14%)	0	4
52	BY	121/123 (98%)	115 (95%)	2 (2%)	4 (3%)	4	26
53	Ba	93/136 (68%)	62 (67%)	15 (16%)	16 (17%)	0	3
54	Bd	20/59 (34%)	19 (95%)	1 (5%)	0	100	100
55	Bc	116/120 (97%)	92 (79%)	11 (10%)	13 (11%)	0	7
56	Bf	103/105 (98%)	91 (88%)	7 (7%)	5 (5%)	2	20
57	Be	237/244 (97%)	213 (90%)	14 (6%)	10 (4%)	3	22
58	Bg	108/113 (96%)	95 (88%)	4 (4%)	9 (8%)	1	12
59	Bh	128/130 (98%)	115 (90%)	7 (6%)	6 (5%)	2	21
60	Bi	116/118 (98%)	76 (66%)	13 (11%)	27 (23%)	0	1
61	Bj	98/107 (92%)	66 (67%)	15 (15%)	17 (17%)	0	3
62	Bk	75/100 (75%)	61 (81%)	6 (8%)	8 (11%)	0	8
63	Bm	90/92 (98%)	78 (87%)	10 (11%)	2 (2%)	6	35
64	Bl	86/88 (98%)	65 (76%)	14 (16%)	7 (8%)	1	12
65	Bn	76/78 (97%)	56 (74%)	10 (13%)	10 (13%)	0	5
66	Bo	49/51 (96%)	38 (78%)	3 (6%)	8 (16%)	0	3
67	Bp	38/52 (73%)	28 (74%)	7 (18%)	3 (8%)	1	13
68	Bq	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	2	22
69	Br	104/106 (98%)	71 (68%)	14 (14%)	19 (18%)	0	3
72	Bt	56/106 (53%)	53 (95%)	0	3 (5%)	2	19
72	Bu	56/106 (53%)	53 (95%)	0	3 (5%)	2	19
73	Bv	56/106 (53%)	53 (95%)	1 (2%)	2 (4%)	3	25
73	Bw	56/106 (53%)	53 (95%)	1 (2%)	2 (4%)	3	25
74	BQ	295/297 (99%)	232 (79%)	27 (9%)	36 (12%)	0	6
76	BS	165/167 (99%)	116 (70%)	15 (9%)	34 (21%)	0	2
77	BI	179/221 (81%)	135 (75%)	23 (13%)	21 (12%)	0	6
All	All	9997/11298 (88%)	7958 (80%)	949 (10%)	1090 (11%)	1	8

5 of 1090 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Aa	29	GLN
1	Aa	51	ASP

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Mol	Chain	Res	Type
1	Aa	55	GLY
1	Aa	57	PRO
1	Aa	84	SER

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	Aa	259/262 (99%)	238 (92%)	21 (8%)	11	35
2	AA	198/210 (94%)	180 (91%)	18 (9%)	9	29
3	AB	148/195 (76%)	136 (92%)	12 (8%)	11	35
4	AD	173/222 (78%)	158 (91%)	15 (9%)	10	31
5	AC	153/166 (92%)	132 (86%)	21 (14%)	3	17
6	AE	205/205 (100%)	188 (92%)	17 (8%)	11	34
8	AF	163/191 (85%)	144 (88%)	19 (12%)	5	21
9	AH	111/111 (100%)	98 (88%)	13 (12%)	5	21
10	AI	105/119 (88%)	93 (89%)	12 (11%)	5	21
11	AJ	93/114 (82%)	88 (95%)	5 (5%)	22	47
12	AK	82/105 (78%)	77 (94%)	5 (6%)	18	44
13	AL	87/120 (72%)	75 (86%)	12 (14%)	3	17
14	AM	123/129 (95%)	104 (85%)	19 (15%)	2	14
15	AN	34/49 (69%)	30 (88%)	4 (12%)	5	20
16	AO	105/128 (82%)	91 (87%)	14 (13%)	4	18
17	AQ	122/124 (98%)	109 (89%)	13 (11%)	6	23
18	AP	63/137 (46%)	56 (89%)	7 (11%)	6	22
19	AR	71/118 (60%)	62 (87%)	9 (13%)	4	18
20	AS	115/116 (99%)	100 (87%)	15 (13%)	4	18
21	AT	74/74 (100%)	67 (90%)	7 (10%)	8	27
22	AV	74/89 (83%)	67 (90%)	7 (10%)	8	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	AX	43/71 (61%)	33 (77%)	10 (23%)	1	4
25	AY	50/60 (83%)	47 (94%)	3 (6%)	19	44
26	AZ	51/54 (94%)	47 (92%)	4 (8%)	12	36
29	AU	72/113 (64%)	62 (86%)	10 (14%)	3	17
30	BA	198/198 (100%)	184 (93%)	14 (7%)	14	39
31	BB	189/196 (96%)	177 (94%)	12 (6%)	18	43
32	BC	315/323 (98%)	265 (84%)	50 (16%)	2	13
33	BD	253/289 (88%)	222 (88%)	31 (12%)	4	19
34	BE	145/150 (97%)	118 (81%)	27 (19%)	1	9
35	BG	153/153 (100%)	124 (81%)	29 (19%)	1	8
36	BF	170/171 (99%)	152 (89%)	18 (11%)	6	24
37	BH	154/208 (74%)	136 (88%)	18 (12%)	5	21
38	Bs	216/254 (85%)	209 (97%)	7 (3%)	39	61
39	BJ	102/136 (75%)	94 (92%)	8 (8%)	12	36
40	BK	162/162 (100%)	143 (88%)	19 (12%)	5	21
41	BN	109/109 (100%)	96 (88%)	13 (12%)	5	20
42	BM	101/105 (96%)	85 (84%)	16 (16%)	2	13
43	BP	165/176 (94%)	141 (86%)	24 (14%)	3	15
44	BO	119/119 (100%)	100 (84%)	19 (16%)	2	13
45	BR	131/151 (87%)	106 (81%)	25 (19%)	1	8
46	BT	154/154 (100%)	144 (94%)	10 (6%)	17	42
47	BU	132/137 (96%)	113 (86%)	19 (14%)	3	16
48	BW	90/107 (84%)	77 (86%)	13 (14%)	3	16
49	BV	131/137 (96%)	117 (89%)	14 (11%)	6	23
50	BX	106/118 (90%)	99 (93%)	7 (7%)	16	41
51	BZ	59/129 (46%)	51 (86%)	8 (14%)	3	17
52	BY	107/107 (100%)	93 (87%)	14 (13%)	4	18
53	Ba	73/116 (63%)	63 (86%)	10 (14%)	3	17
54	Bd	15/47 (32%)	13 (87%)	2 (13%)	4	18
55	Bc	104/105 (99%)	88 (85%)	16 (15%)	2	14
56	Bf	83/88 (94%)	75 (90%)	8 (10%)	8	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	Be	202/205 (98%)	182 (90%)	20 (10%)	8	26
58	Bg	90/97 (93%)	79 (88%)	11 (12%)	5	20
59	Bh	111/111 (100%)	95 (86%)	16 (14%)	3	16
60	Bi	99/101 (98%)	87 (88%)	12 (12%)	5	20
61	Bj	71/91 (78%)	63 (89%)	8 (11%)	6	21
62	Bk	64/82 (78%)	58 (91%)	6 (9%)	8	28
63	Bm	72/72 (100%)	67 (93%)	5 (7%)	15	40
64	Bl	68/71 (96%)	61 (90%)	7 (10%)	7	25
65	Bn	66/69 (96%)	53 (80%)	13 (20%)	1	8
66	Bo	46/46 (100%)	38 (83%)	8 (17%)	2	11
67	Bp	37/47 (79%)	35 (95%)	2 (5%)	22	47
68	Bq	23/23 (100%)	21 (91%)	2 (9%)	10	31
69	Br	87/91 (96%)	76 (87%)	11 (13%)	4	19
72	Bt	48/76 (63%)	48 (100%)	0	100	100
72	Bu	48/76 (63%)	48 (100%)	0	100	100
73	Bv	47/74 (64%)	45 (96%)	2 (4%)	29	53
73	Bw	47/74 (64%)	46 (98%)	1 (2%)	53	72
74	BQ	238/245 (97%)	196 (82%)	42 (18%)	2	11
76	BS	153/153 (100%)	116 (76%)	37 (24%)	0	4
77	BI	151/187 (81%)	133 (88%)	18 (12%)	5	20
All	All	8278/9418 (88%)	7314 (88%)	964 (12%)	9	21

5 of 964 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	BF	47	LYS
74	BQ	131	LEU
43	BP	174	ILE
74	BQ	53	VAL
77	BI	4	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 133 such sidechains are listed below:

Mol	Chain	Res	Type
60	Bi	52	GLN
61	Bj	13	HIS
76	BS	124	GLN
31	BB	216	HIS
31	BB	205	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
78	CA	1485/1800 (82%)	521 (35%)	209 (14%)
79	CB	74/75 (98%)	26 (35%)	10 (13%)
80	CC	10/11 (90%)	7 (70%)	1 (10%)
81	DA	3156/3396 (92%)	1246 (39%)	607 (19%)
82	DB	142/158 (89%)	65 (45%)	36 (25%)
83	DC	117/118 (99%)	60 (51%)	26 (22%)
All	All	4984/5558 (89%)	1925 (38%)	889 (17%)

5 of 1925 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
78	CA	3	U
78	CA	4	C
78	CA	5	U
78	CA	10	G
78	CA	11	A

5 of 889 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
81	DA	1526	U
83	DC	75	G
81	DA	2031	U
83	DC	32	U
81	DA	3258	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
78	CA	4
44	BO	3
23	AW	1
80	CC	1
74	BQ	1
76	BS	1
20	AS	1
7	AG	1
14	AM	1
34	BE	1
32	BC	1

The worst 5 of 16 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	31:UNK	C	59:UNK	N	10.96
1	CC	18:C	O3'	19:U	P	2.07
1	CA	1255:G	O3'	1256:A	P	1.94
1	BQ	39:GLN	C	40:HIS	N	1.90
1	CA	1254:U	O3'	1255:G	P	1.83

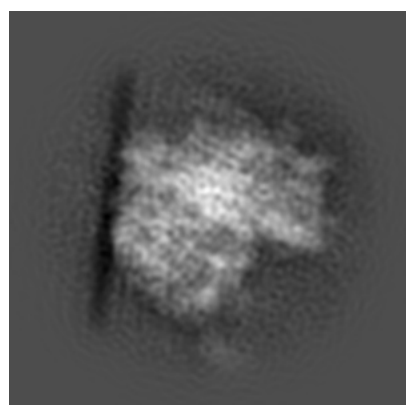
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1669. These allow visual inspection of the internal detail of the map and identification of artifacts.

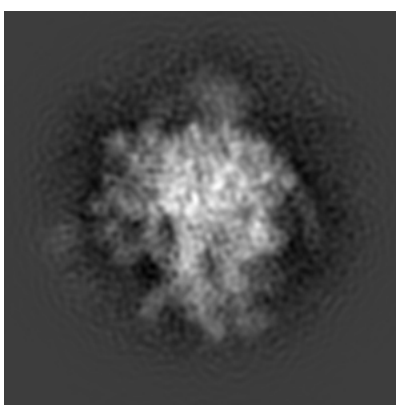
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

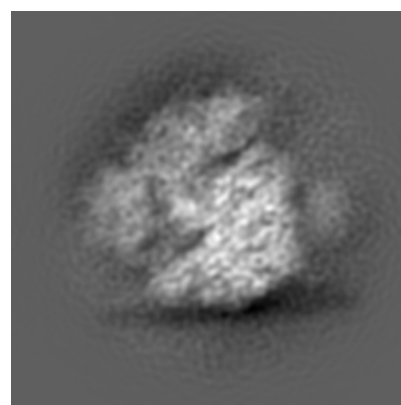
6.1.1 Primary map



X



Y

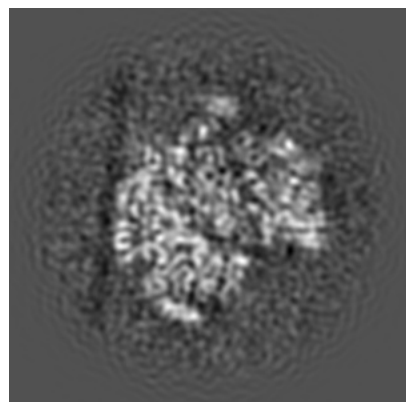


Z

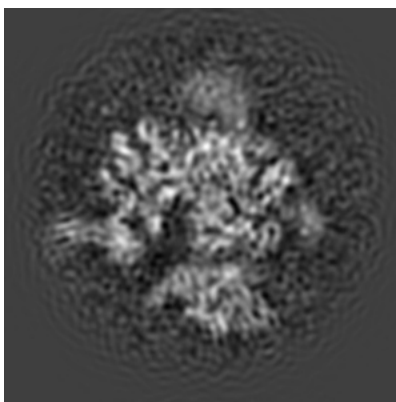
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

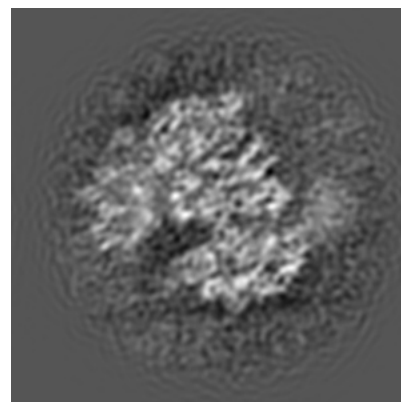
6.2.1 Primary map



X Index: 184



Y Index: 184

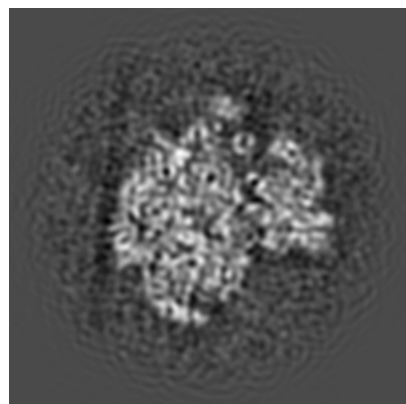


Z Index: 184

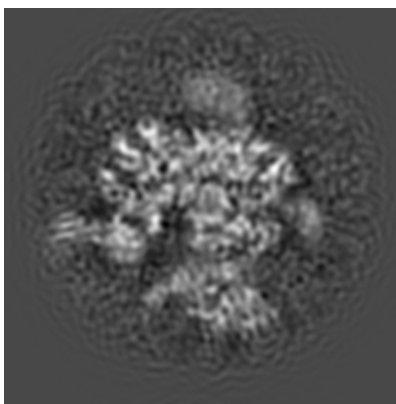
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

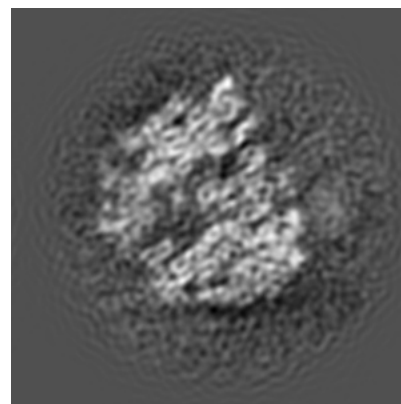
6.3.1 Primary map



X Index: 188



Y Index: 187

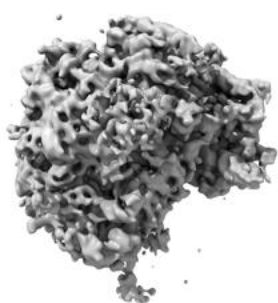


Z Index: 172

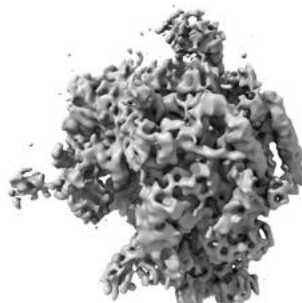
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

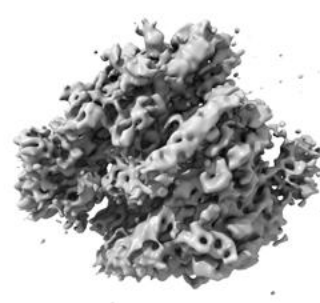
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.75. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

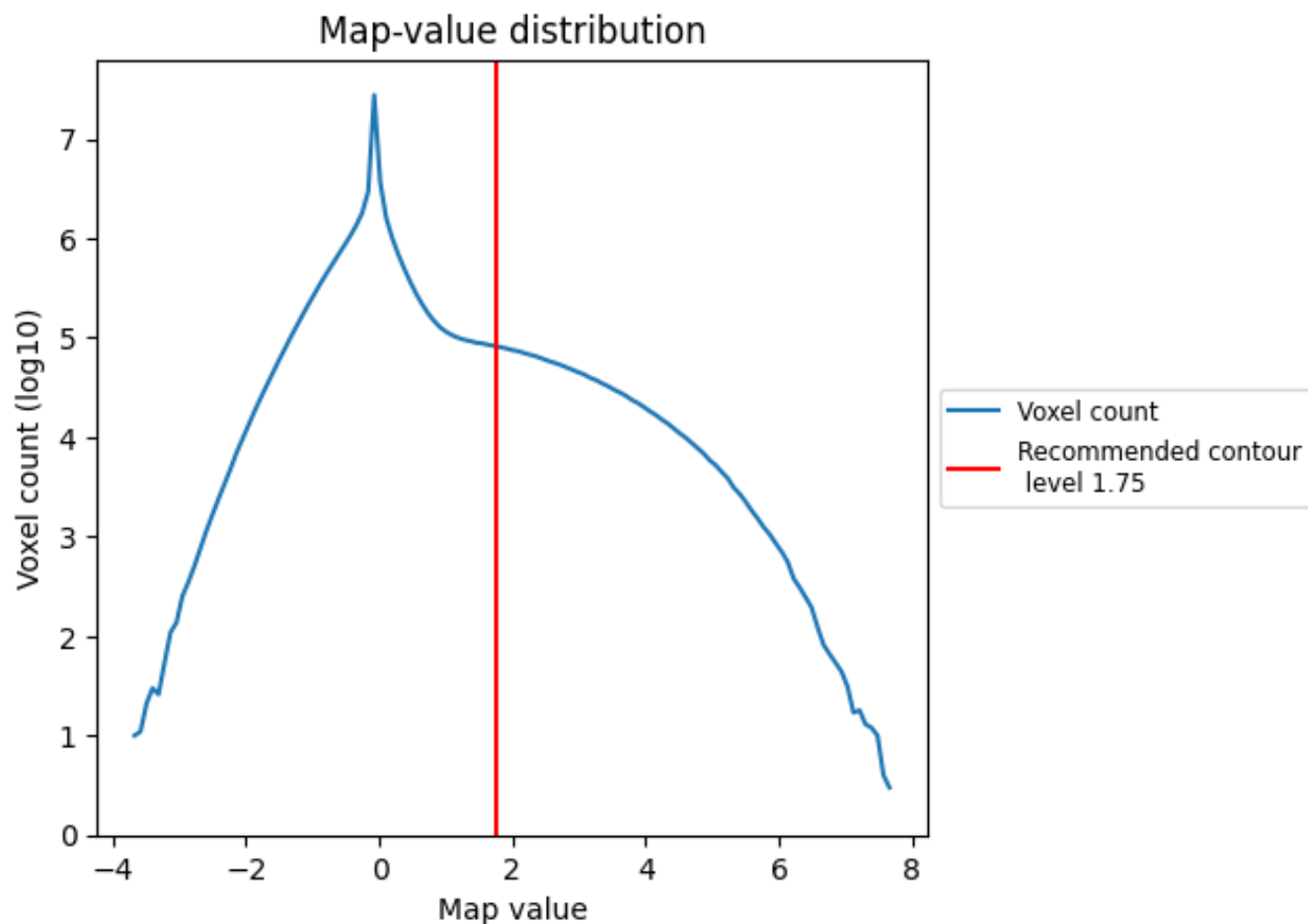
6.5 Mask visualisation

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

7 Map analysis [i](#)

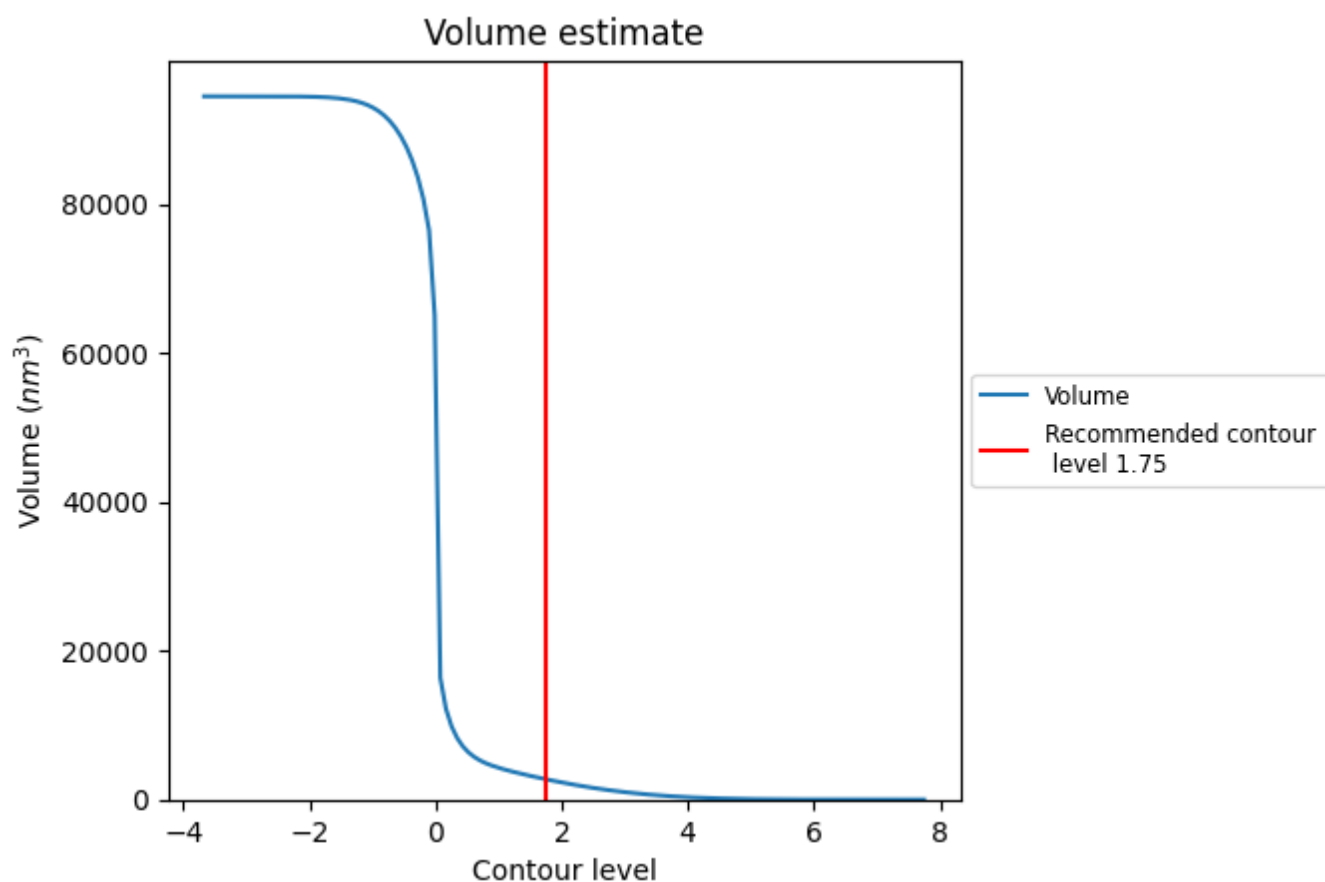
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

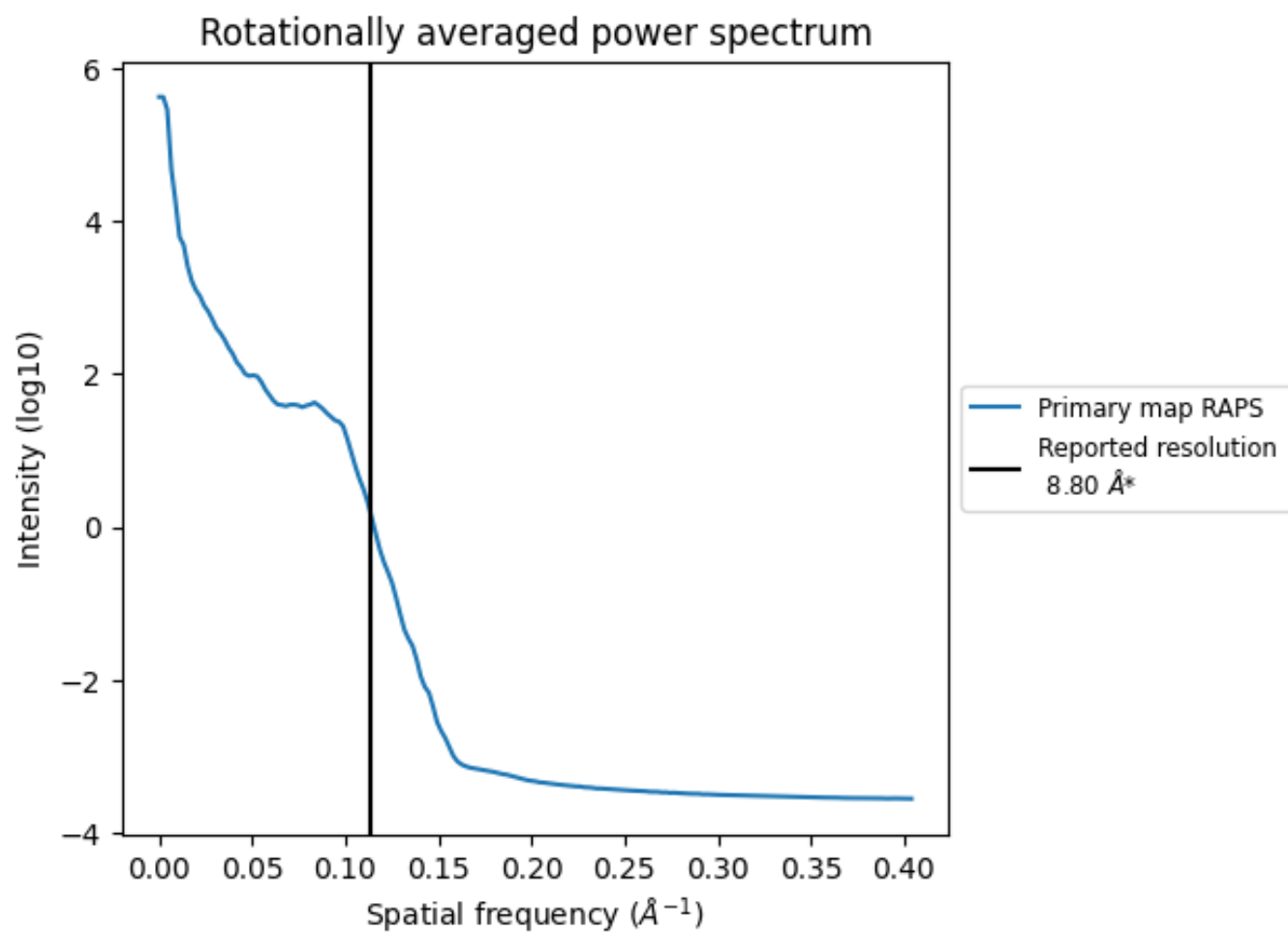
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2728 nm³; this corresponds to an approximate mass of 2464 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 0.114 Å⁻¹

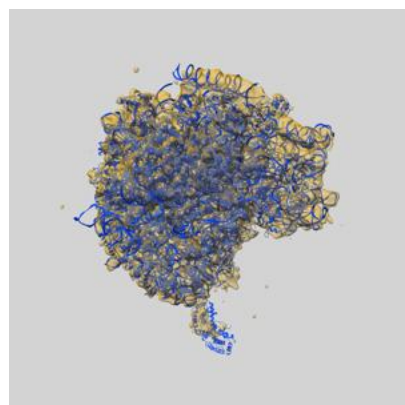
8 Fourier-Shell correlation

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

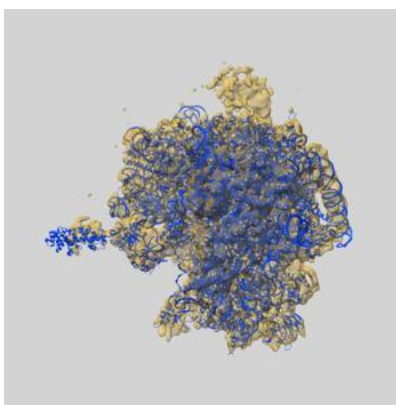
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1669 and PDB model 4V6I. Per-residue inclusion information can be found in section 3 on page 20.

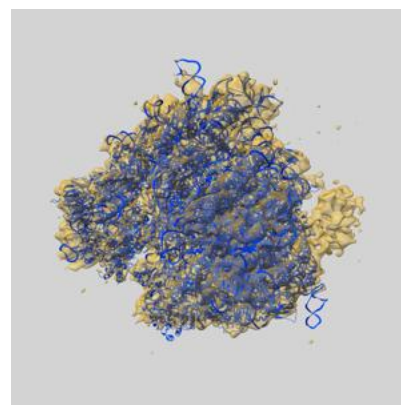
9.1 Map-model overlay [i](#)



X



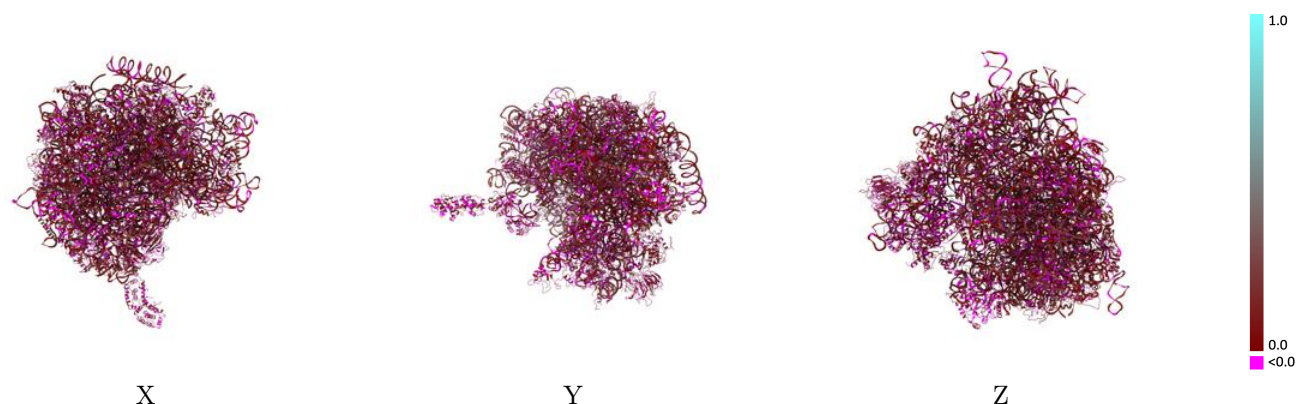
Y



Z

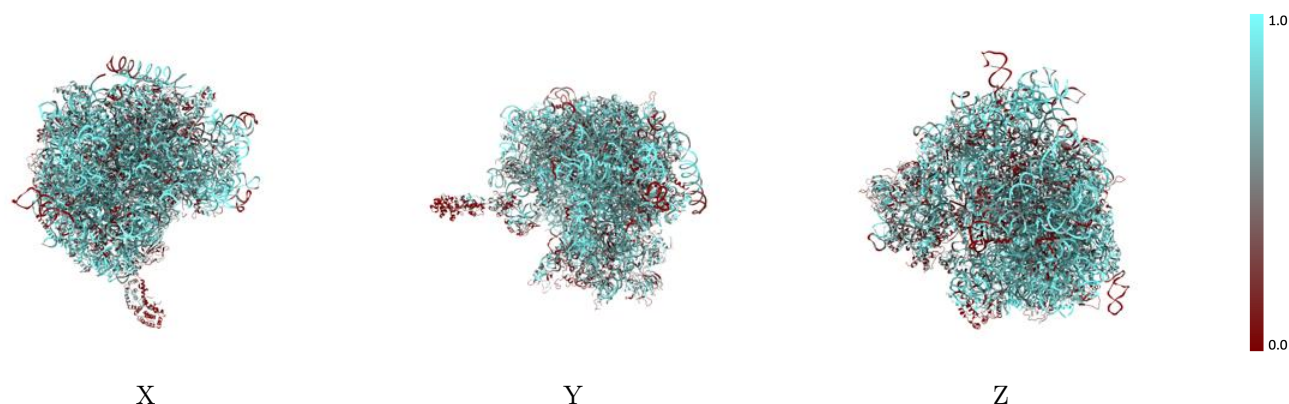
The images above show the 3D surface view of the map at the recommended contour level 1.75 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



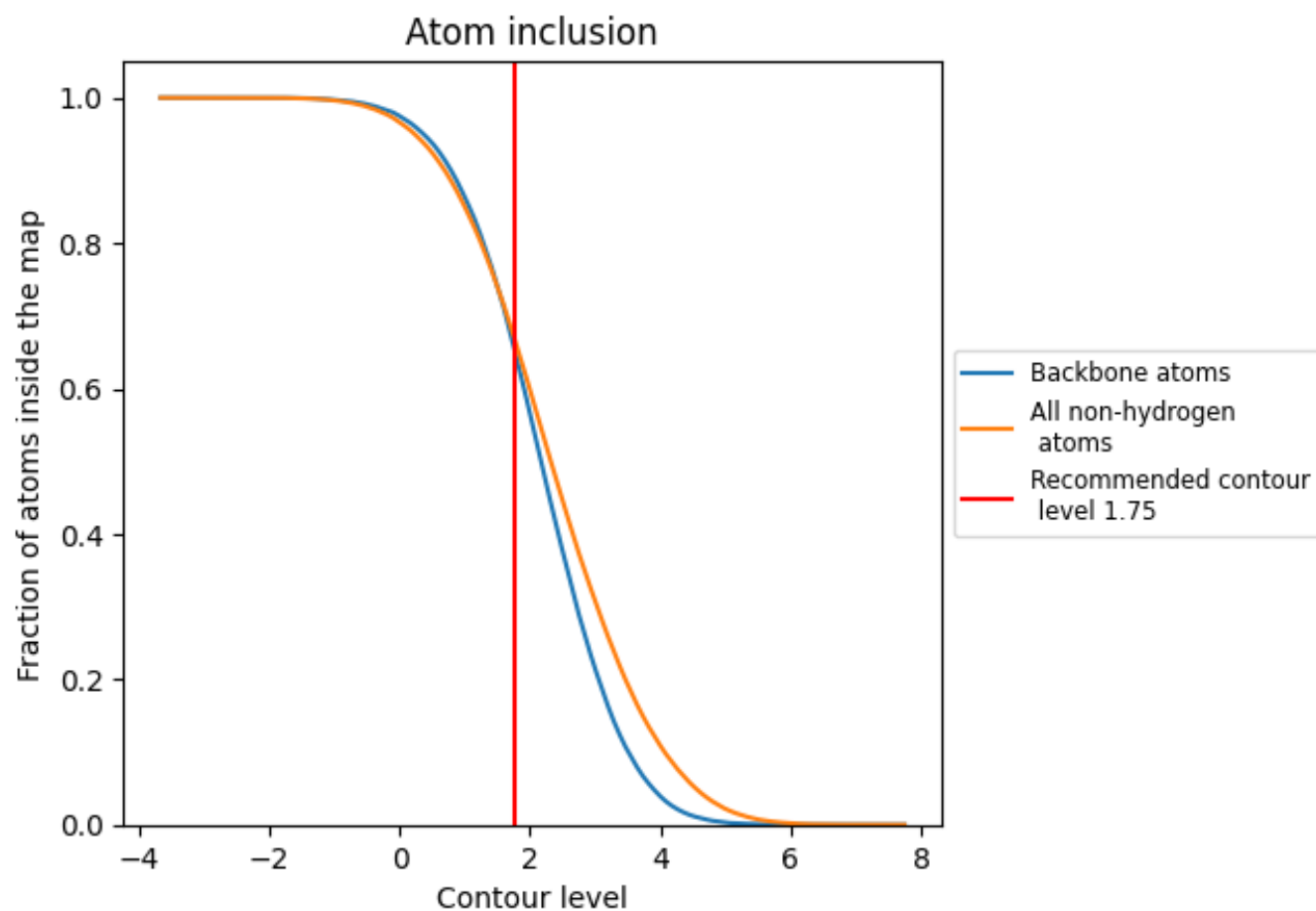
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.75).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 67% 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 (1.75) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6720	 0.0940
AA	 0.6074	 0.1010
AB	 0.4528	 0.0770
AC	 0.5848	 0.0770
AD	 0.5781	 0.0860
AE	 0.5526	 0.0920
AF	 0.5030	 0.0710
AG	 0.6844	 0.1610
AH	 0.5134	 0.0870
AI	 0.5432	 0.0530
AJ	 0.5000	 0.0680
AK	 0.5767	 0.0700
AL	 0.6538	 0.0570
AM	 0.2952	 0.0500
AN	 0.3769	 0.0420
AO	 0.4520	 0.0830
AP	 0.4144	 0.0750
AQ	 0.2997	 0.0670
AR	 0.3298	 0.0730
AS	 0.5262	 0.0540
AT	 0.4165	 0.1050
AU	 0.5374	 0.0730
AV	 0.3767	 0.0800
AW	 0.7202	 0.1670
AX	 0.4821	 0.0640
AY	 0.3318	 0.0120
AZ	 0.4958	 0.0540
Aa	 0.4646	 0.0690
Ab	 0.8674	 0.2310
Ac	 0.6349	 0.2370
BA	 0.2178	 0.0010
BB	 0.4621	 0.0460
BC	 0.5826	 0.0580
BD	 0.5836	 0.0660
BE	 0.5587	 0.0870























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Chain	Atom inclusion	Q-score
BF	 0.5296	 0.0860
BG	 0.5857	 0.0780
BH	 0.6208	 0.0830
BI	 0.6600	 0.0620
BJ	 0.3380	 0.0300
BK	 0.5742	 0.0870
BL	 0.7799	 0.1700
BM	 0.2616	 0.0860
BN	 0.6398	 0.0980
BO	 0.4909	 0.0400
BP	 0.5556	 0.0370
BQ	 0.7449	 0.0610
BR	 0.5524	 0.1000
BS	 0.5018	 0.0650
BT	 0.4789	 0.0960
BU	 0.6287	 0.0650
BV	 0.5071	 0.0570
BW	 0.6069	 0.0800
BX	 0.5126	 0.0770
BY	 0.6952	 0.0860
BZ	 0.3936	 0.0600
Ba	 0.4835	 0.0350
Bc	 0.7380	 0.1170
Bd	 0.6176	 0.0590
Be	 0.5653	 0.0900
Bf	 0.4787	 0.1190
Bg	 0.5584	 0.0760
Bh	 0.4621	 0.0730
Bi	 0.4370	 0.0580
Bj	 0.4448	 0.0490
Bk	 0.6897	 0.0950
Bl	 0.6733	 0.0500
Bm	 0.3923	 0.0810
Bn	 0.5632	 0.0860
Bo	 0.4717	 0.0500
Bp	 0.4367	 -0.0300
Bq	 0.4883	 0.1170
Br	 0.4650	 0.0650
Bs	 0.2769	 0.0350
Bt	 0.3562	 0.0260
Bu	 0.0000	 0.0530
Bv	 0.2740	 0.0480

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Chain	Atom inclusion	Q-score
Bw	 0.0375	 0.0100
Bx	 0.7900	 0.1580
By	 0.9100	 0.2380
Bz	 0.6143	 0.2150
CA	 0.7887	 0.1050
CB	 0.0688	 0.0440
CC	 0.1441	 -0.0370
DA	 0.7960	 0.1160
DB	 0.8124	 0.1140
DC	 0.9133	 0.1250