



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 10:04 PM UTC

PDB ID : 4V6I / pdb_00004v6i
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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

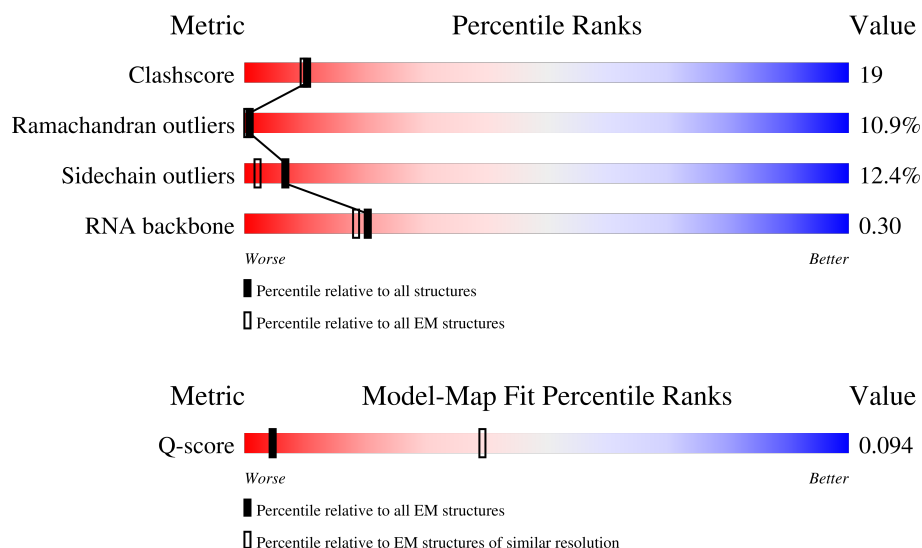
1 Overall quality at a glance

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	265 (8.30 - 9.30)

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	
2	AA	252	
3	AB	240	

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Mol	Chain	Length	Quality of chain
4	AD	261	
5	AC	197	
6	AE	254	
7	AG	144	
8	AF	225	
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	

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Mol	Chain	Length	Quality of chain
29	AU	135	
30	BA	217	
31	BB	254	
32	BC	388	
33	BD	362	
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	

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Mol	Chain	Length	Quality of chain
54	Bd	59	
55	Bc	120	
56	Bf	105	
57	Be	244	
58	Bg	113	
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	

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Mol	Chain	Length	Quality of chain
76	BS	167	
77	BI	221	
78	CA	1800	
79	CB	75	
80	CC	11	
81	DA	3396	
82	DB	158	
83	DC	118	

2 Entry composition [i](#)

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		

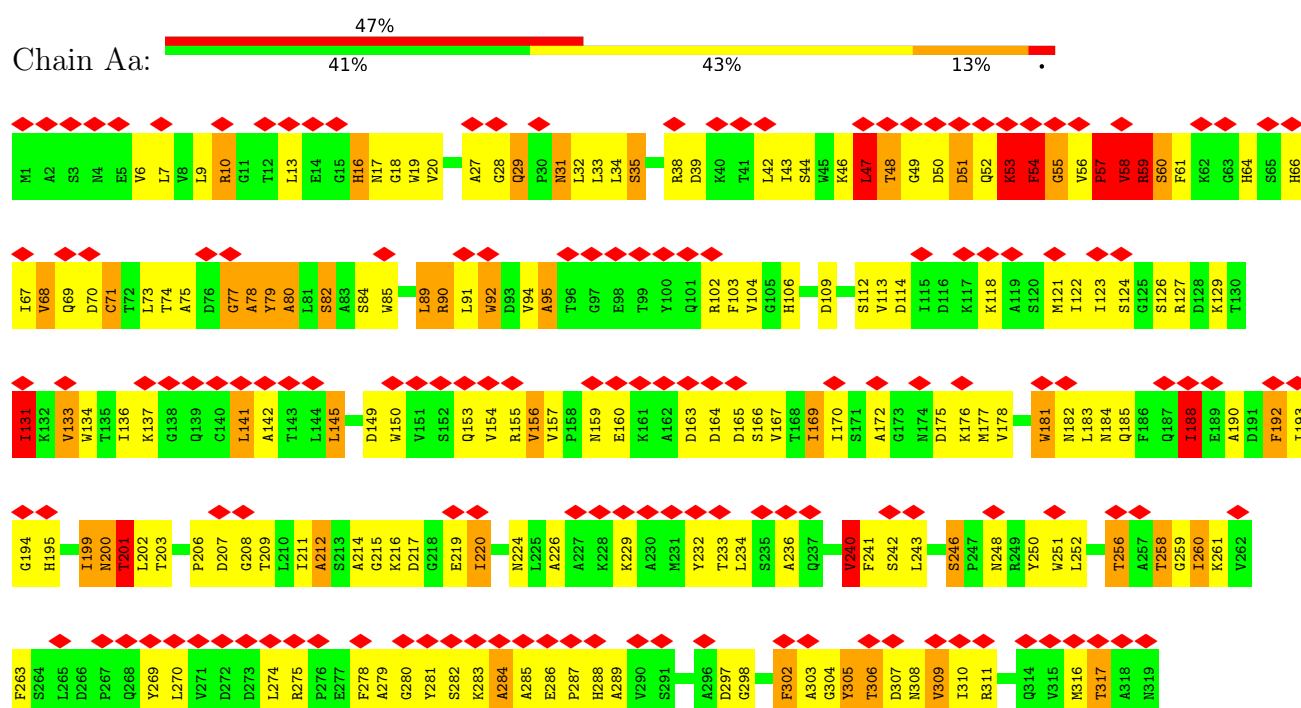
- Molecule 83 is a RNA chain called 5S rRNA.

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

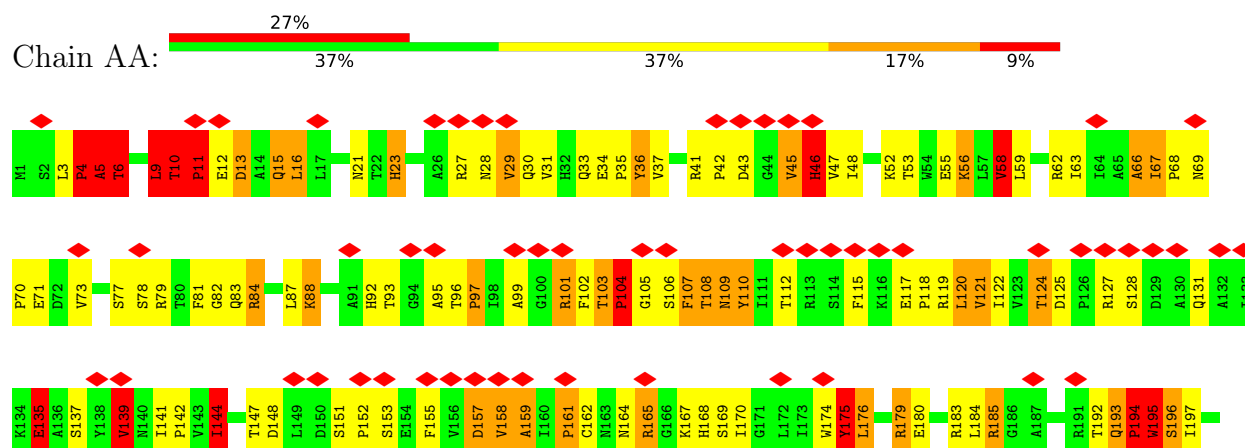
3 Residue-property plots [i](#)

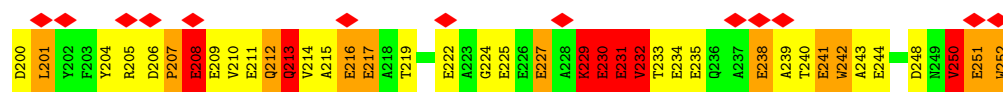
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 40S ribosomal protein RACK1 (RACK1)

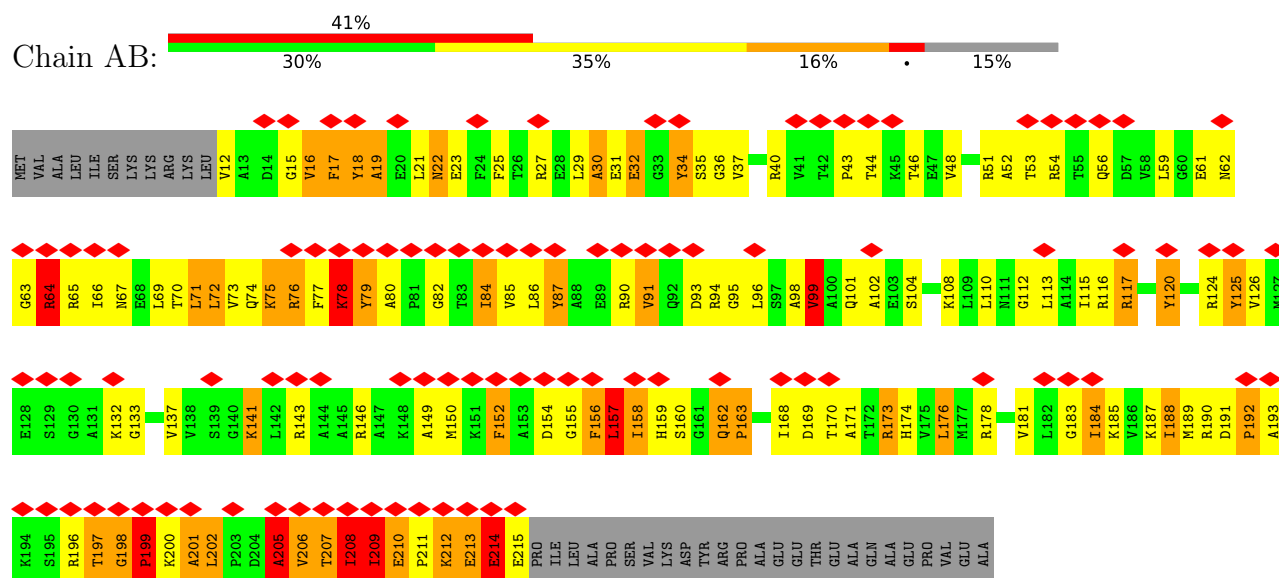


• Molecule 2: 40S ribosomal protein rpS0 (S2p)

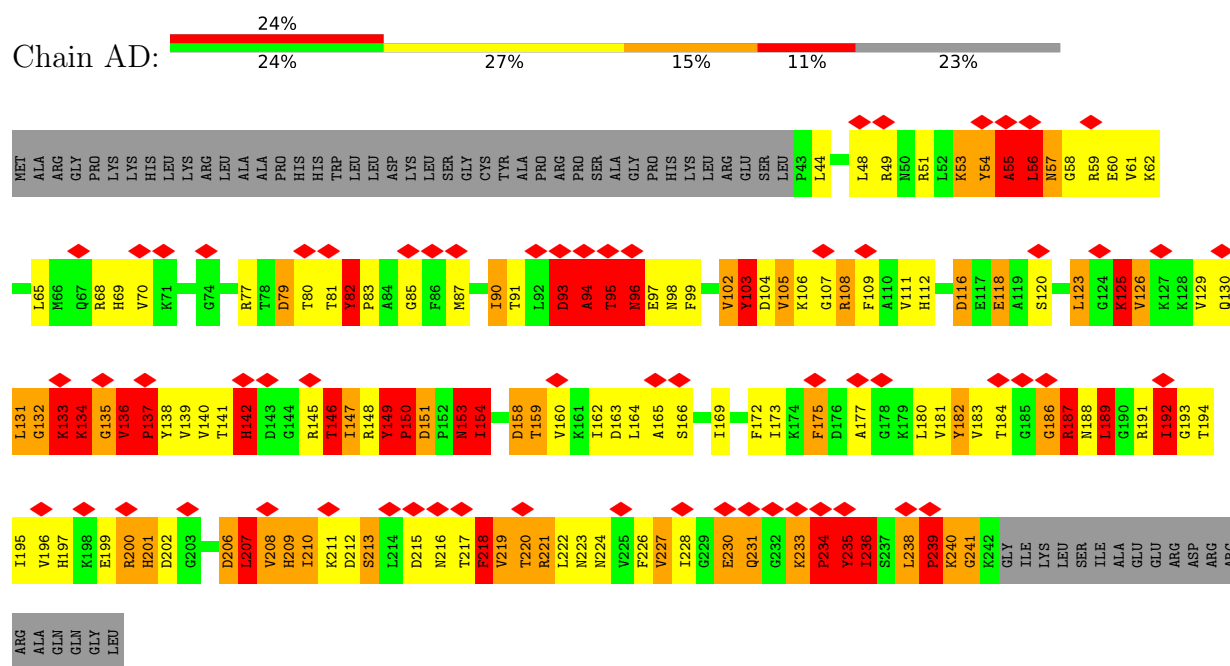




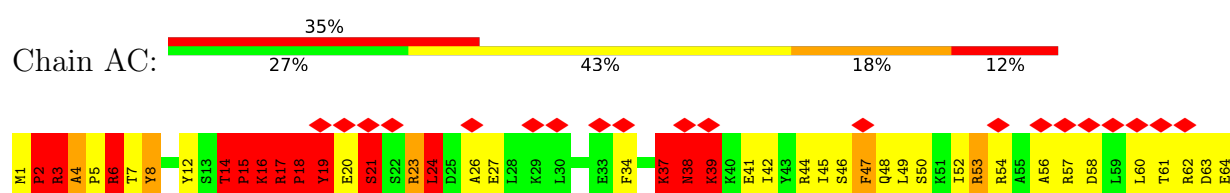
• Molecule 3: 40S ribosomal protein rpS3 (S3p)

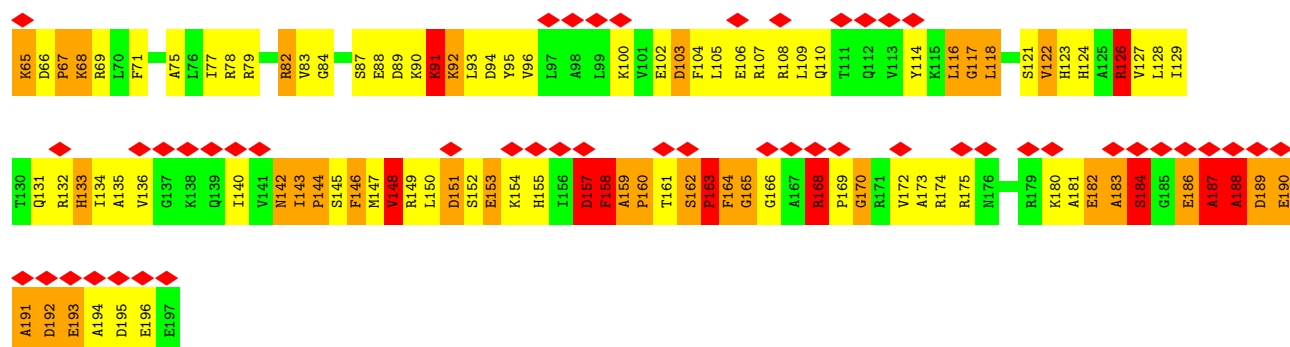


• Molecule 4: 40S ribosomal protein rpS4 (S4e)

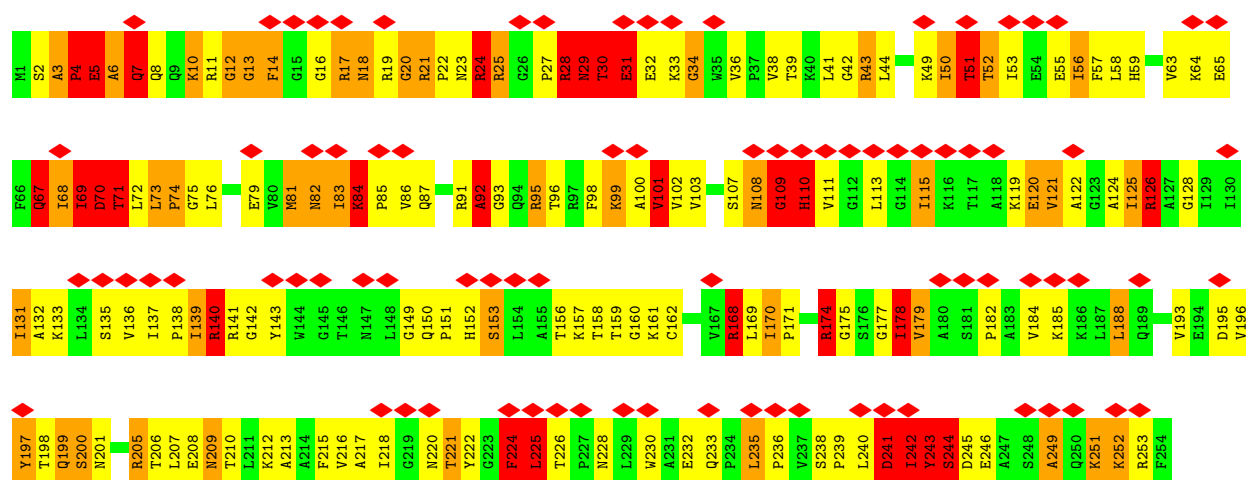


• Molecule 5: 40S ribosomal protein rpS9 (S4p)

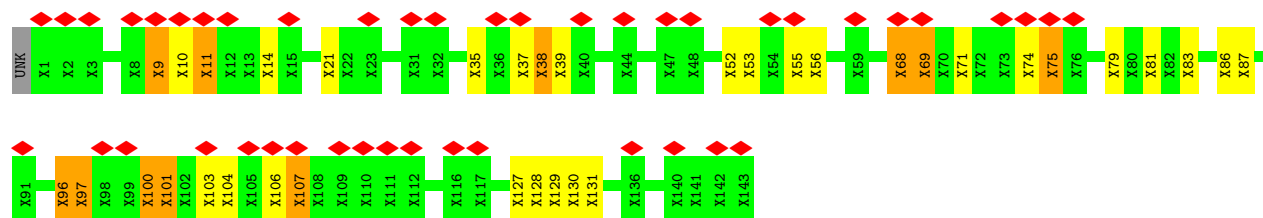
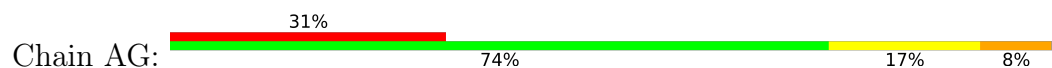




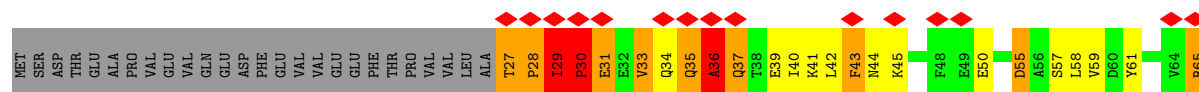
• Molecule 6: 40S ribosomal protein rpS2 (S5p)

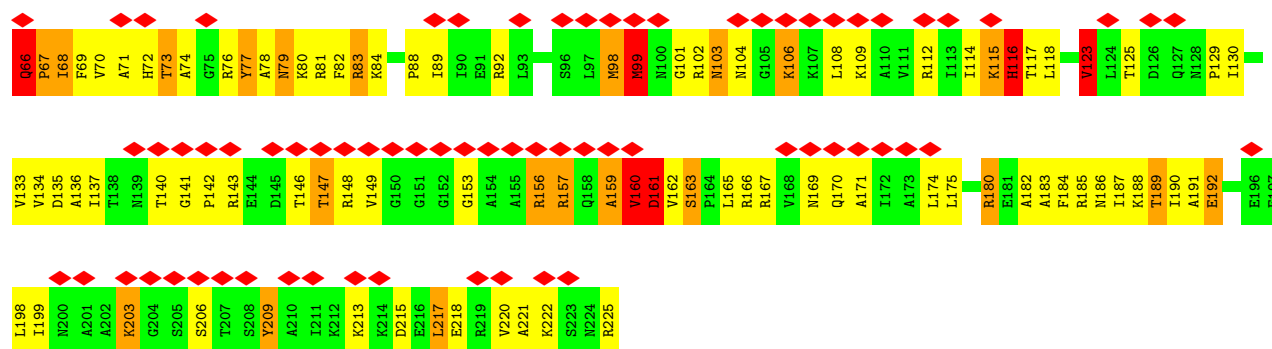


• Molecule 7: 40S ribosomal protein rpS7 (S7e)

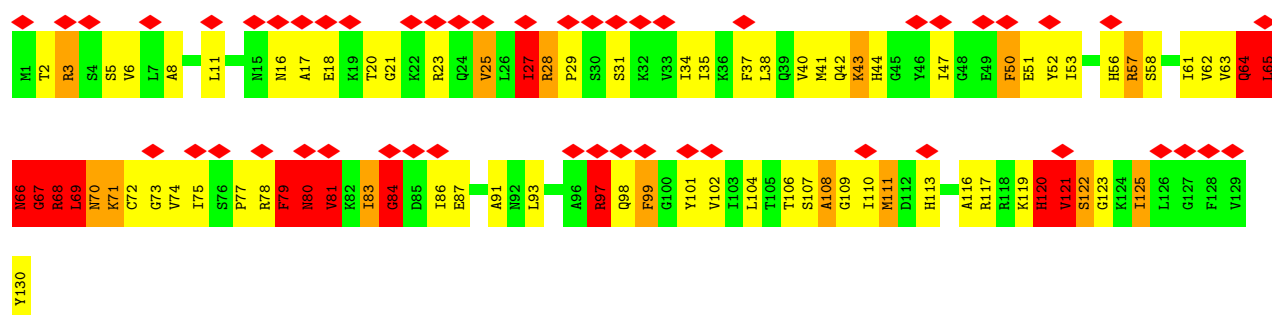
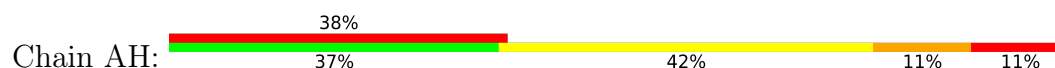


• Molecule 8: 40S ribosomal protein rpS5 (S7p)

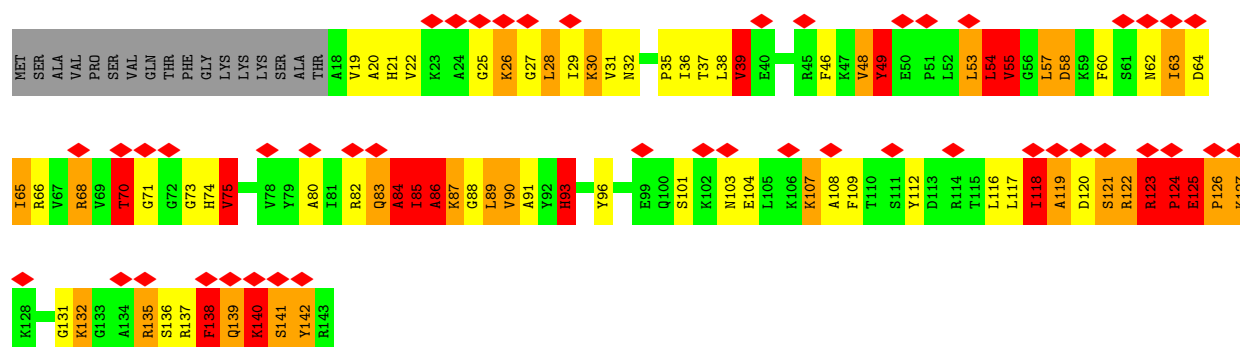




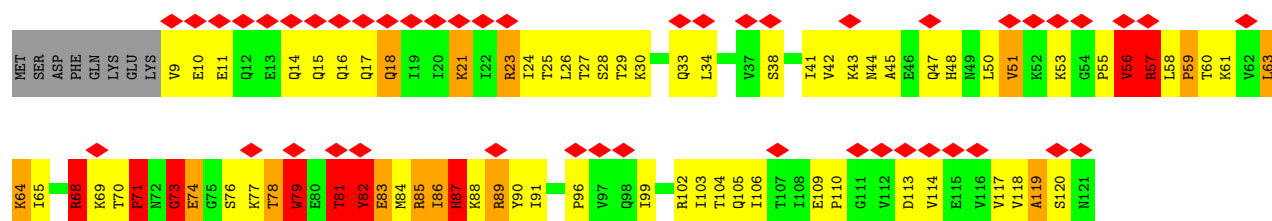
• Molecule 9: 40S ribosomal protein rpS22 (S8p)



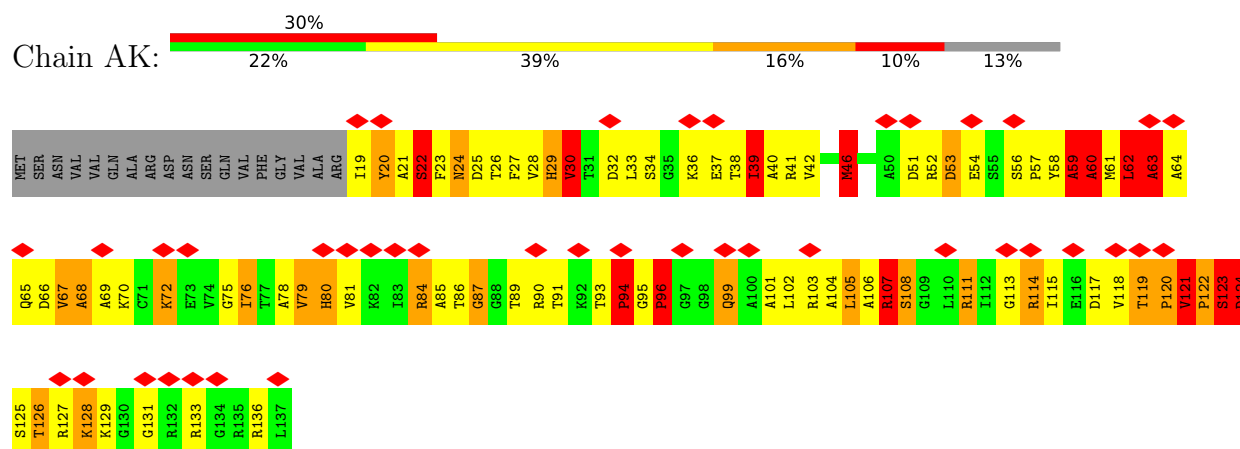
• Molecule 10: 40S ribosomal protein rpS16 (S9p)



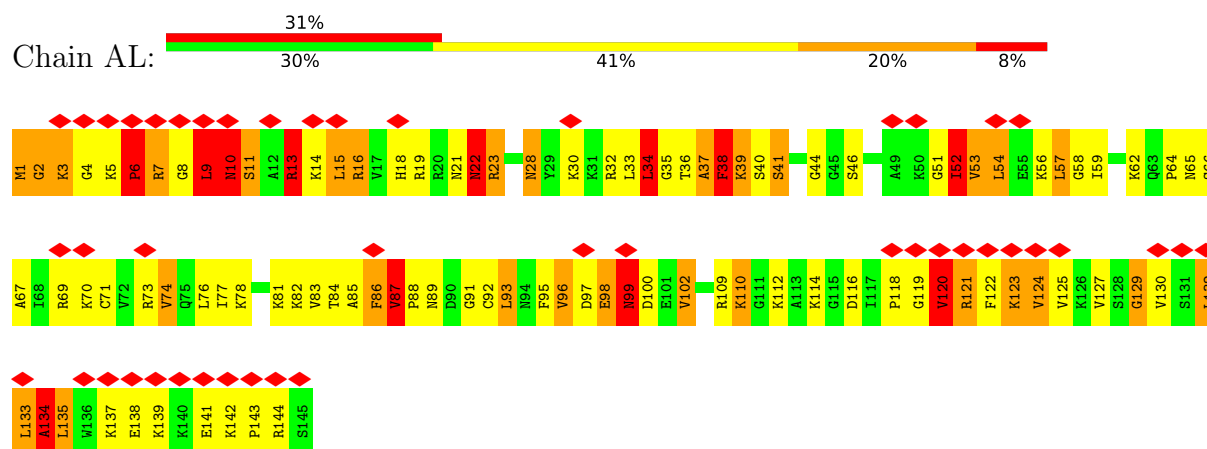
• Molecule 11: 40S ribosomal protein rpS20 (S10p)



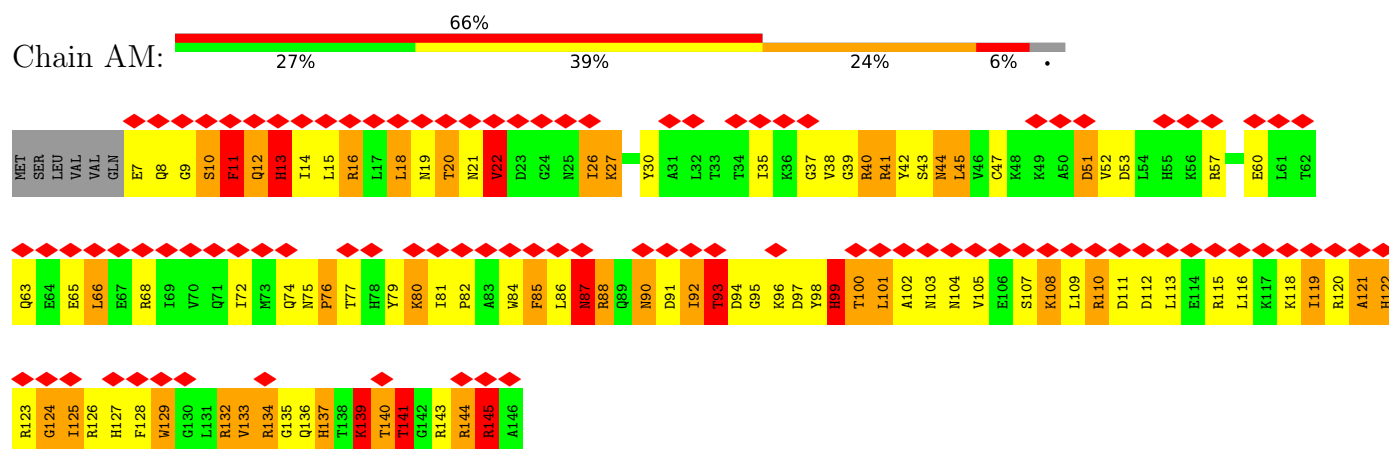
- Molecule 12: 40S ribosomal protein rpS14 (S11p)



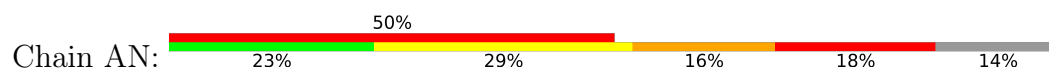
- Molecule 13: 40S ribosomal protein rpS23 (S12p)

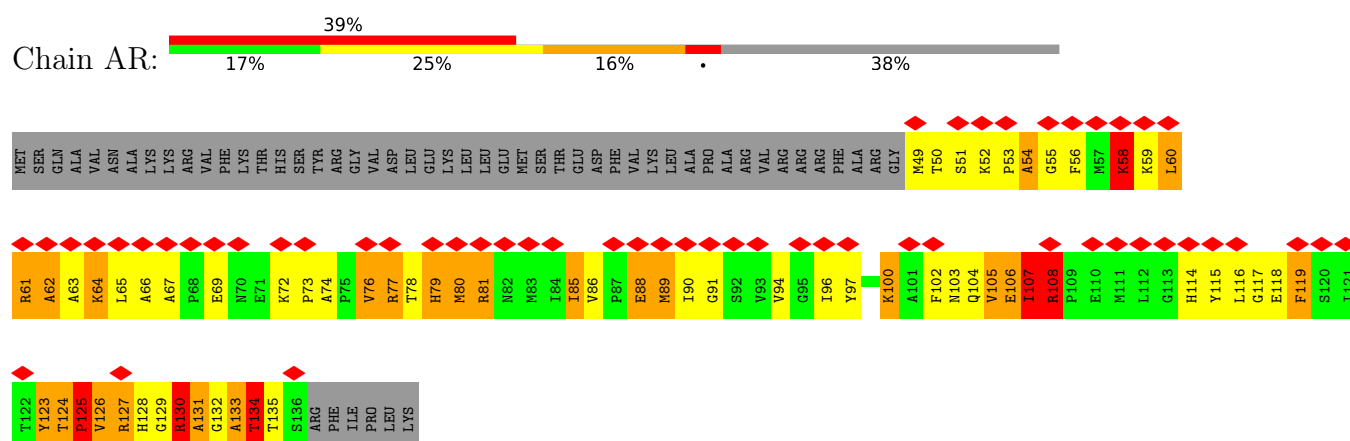


- Molecule 14: 40S ribosomal protein rpS18 (S13p)

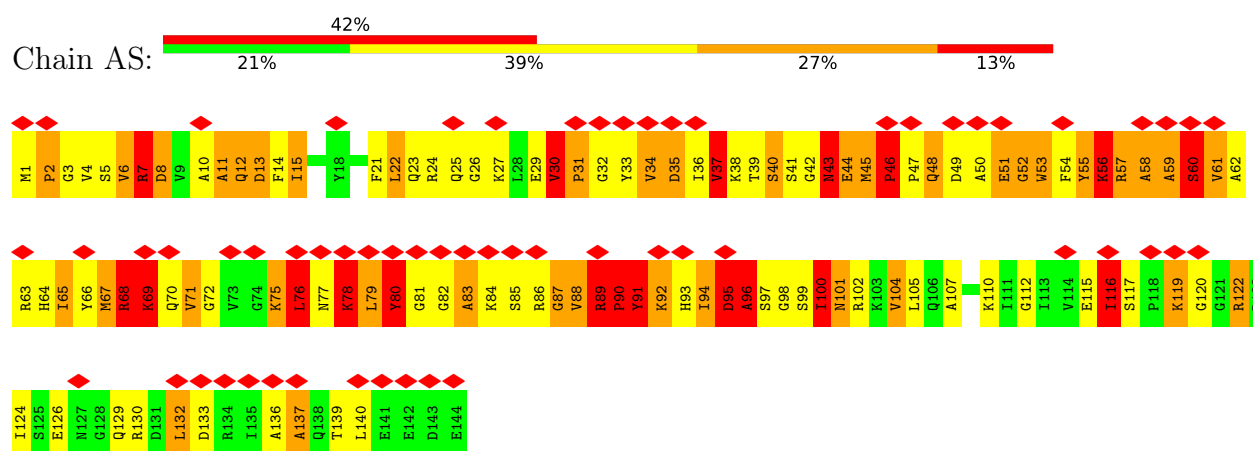


- Molecule 15: 40S ribosomal protein rpS29 (S14p)

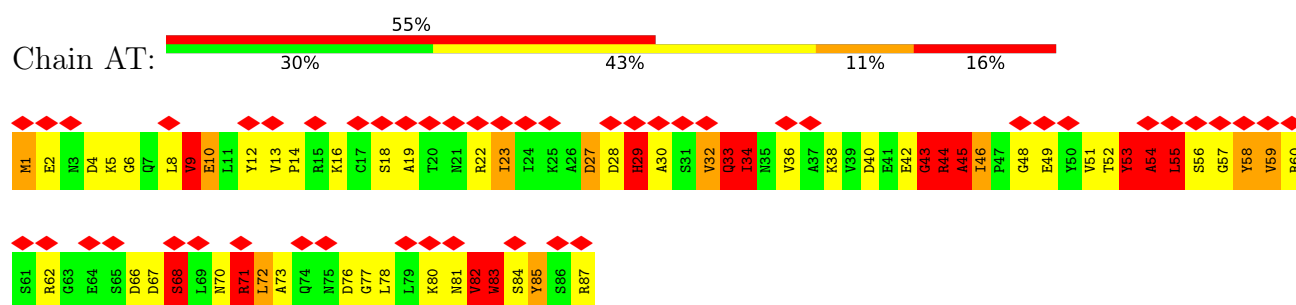




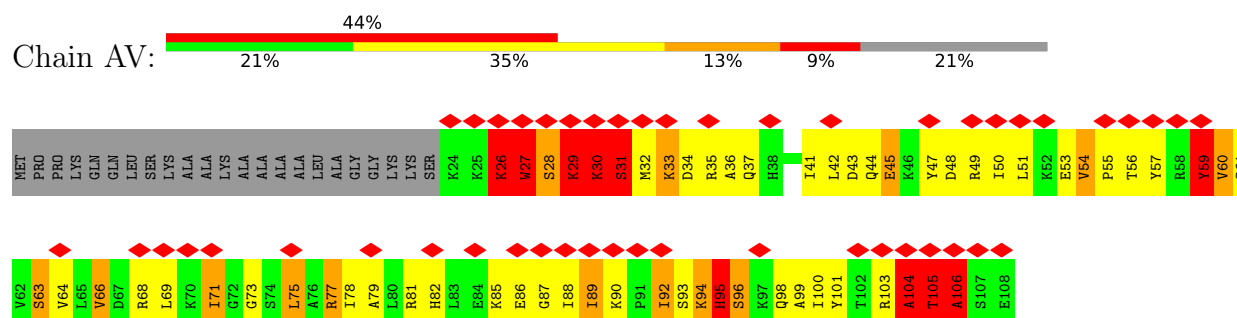
- Molecule 20: 40S ribosomal protein rpS19 (S19e)



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



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

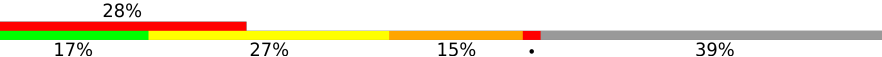


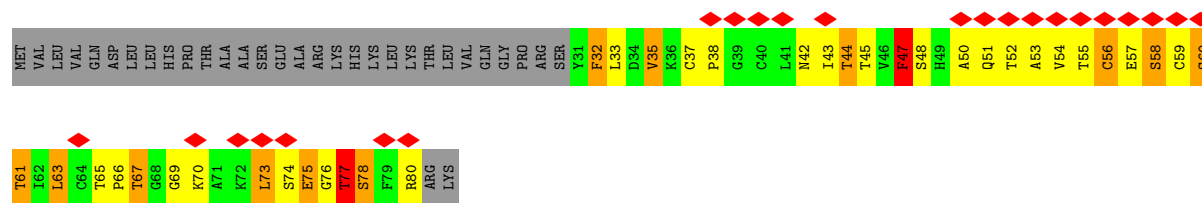
- Molecule 23: 40S ribosomal protein rpS26 (S26e)

Chain AW: 



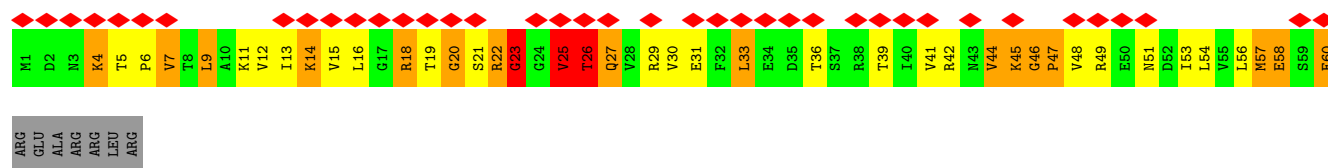
- Molecule 24: 40S ribosomal protein rpS27 (S27e)

Chain AX: 

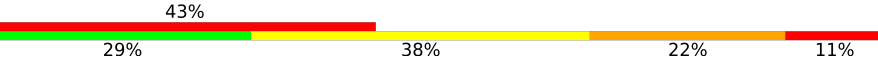


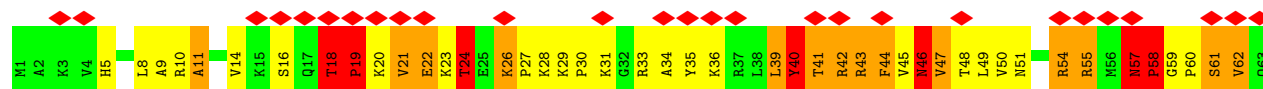
- Molecule 25: 40S ribosomal protein rpS28 (S28e)

Chain AY: 



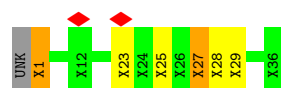
- Molecule 26: 40S ribosomal protein rpS30 (S30e)

Chain AZ: 

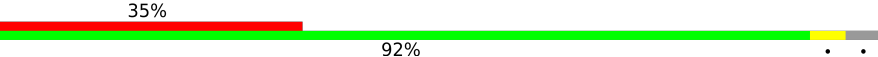


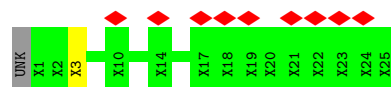
- Molecule 27: Unknown 40S ribosomal protein XS1

Chain Ab: 

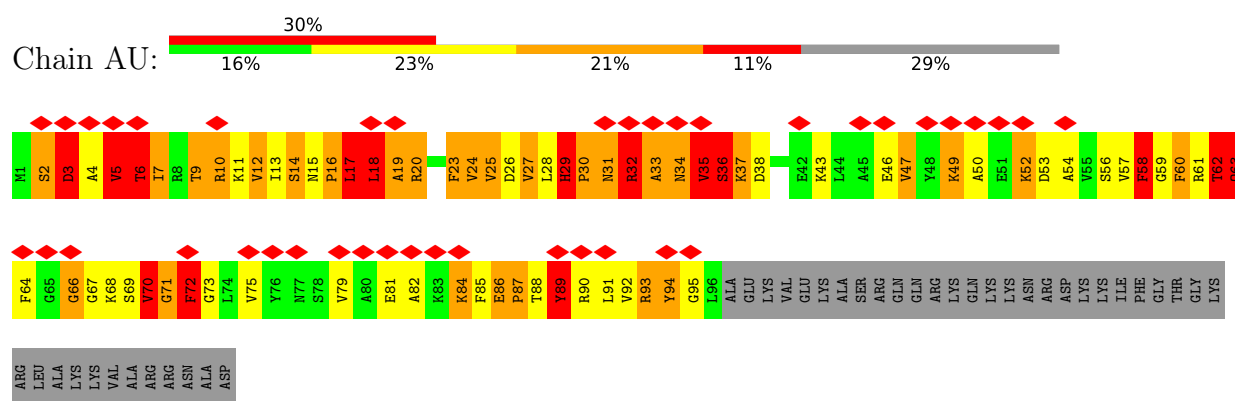


- Molecule 28: Unknown 40S ribosomal protein XS2

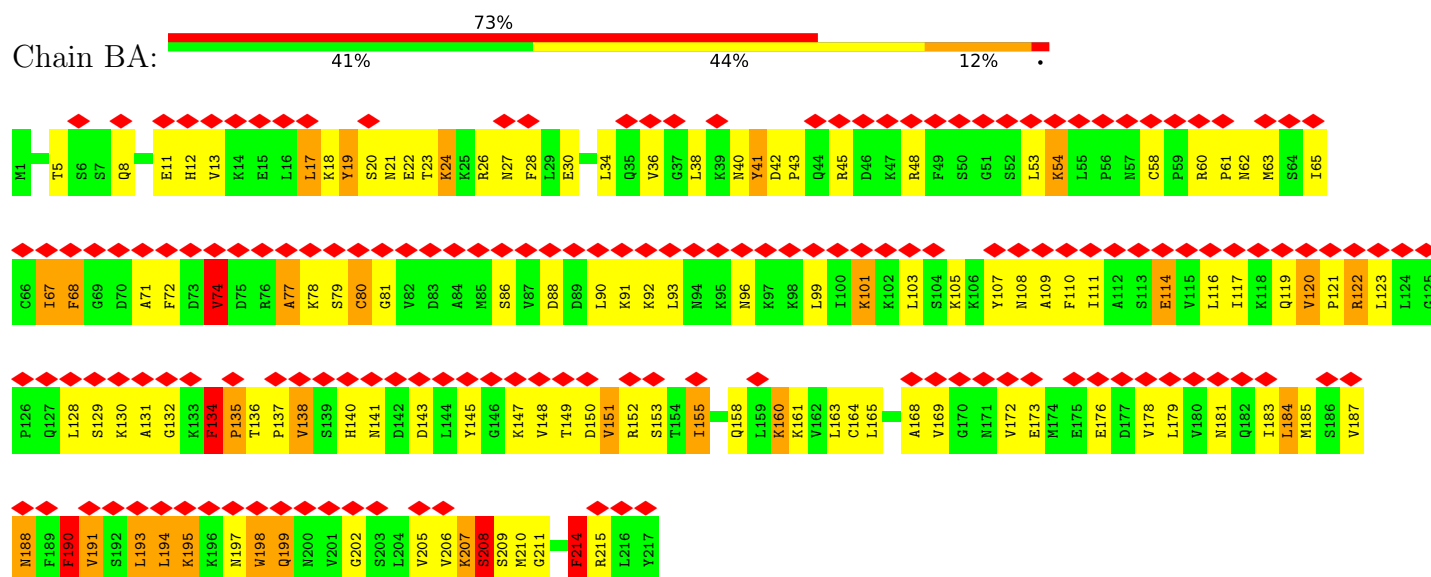
Chain Ac: 



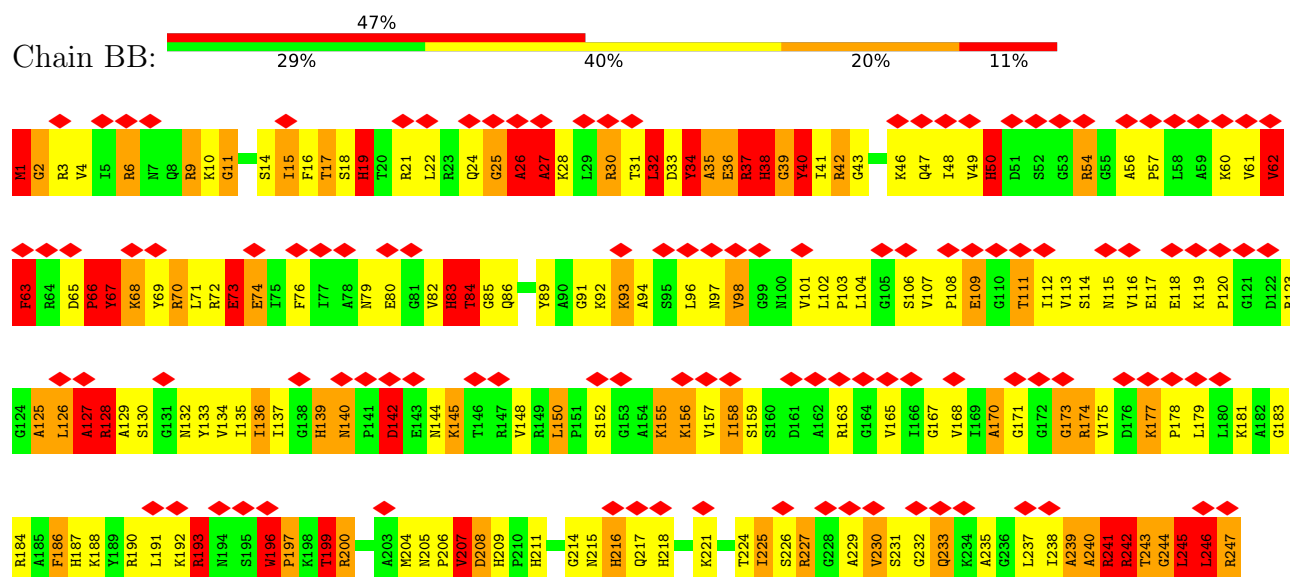
- Molecule 29: 40S ribosomal protein S24



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

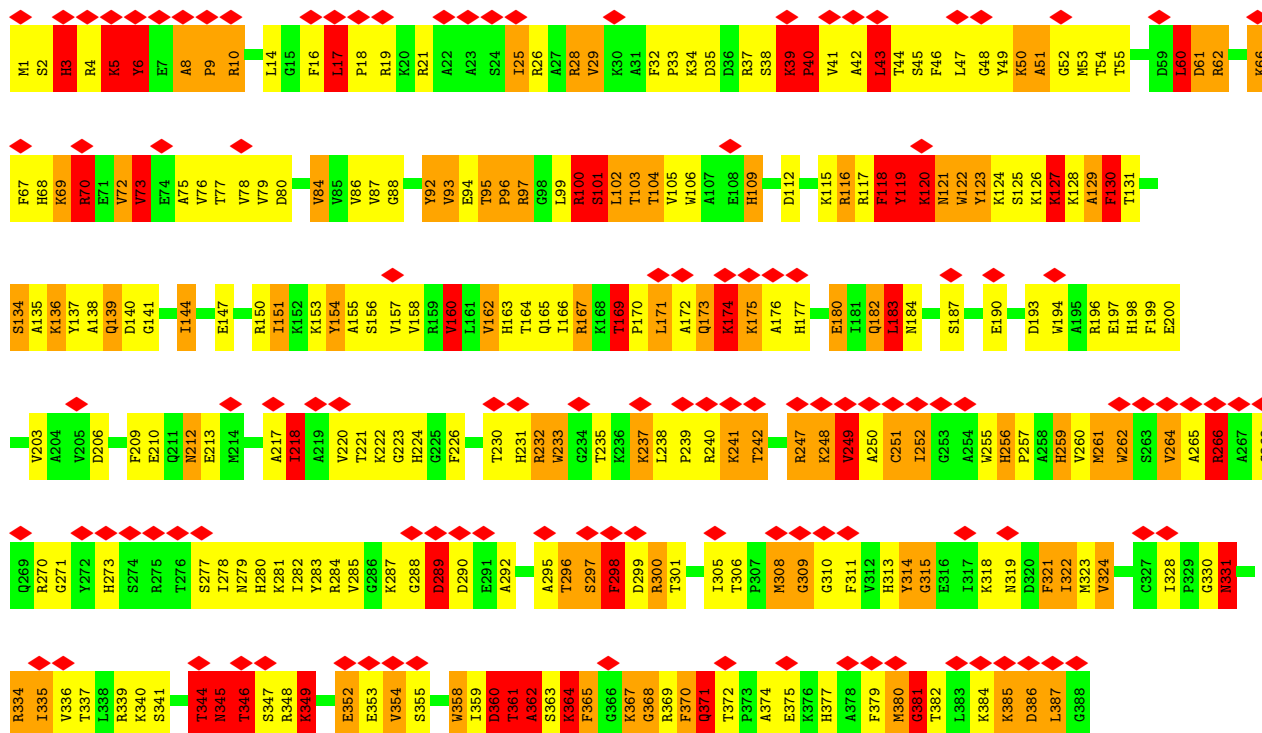


• Molecule 31: 60S ribosomal protein rpL2 (L2p)

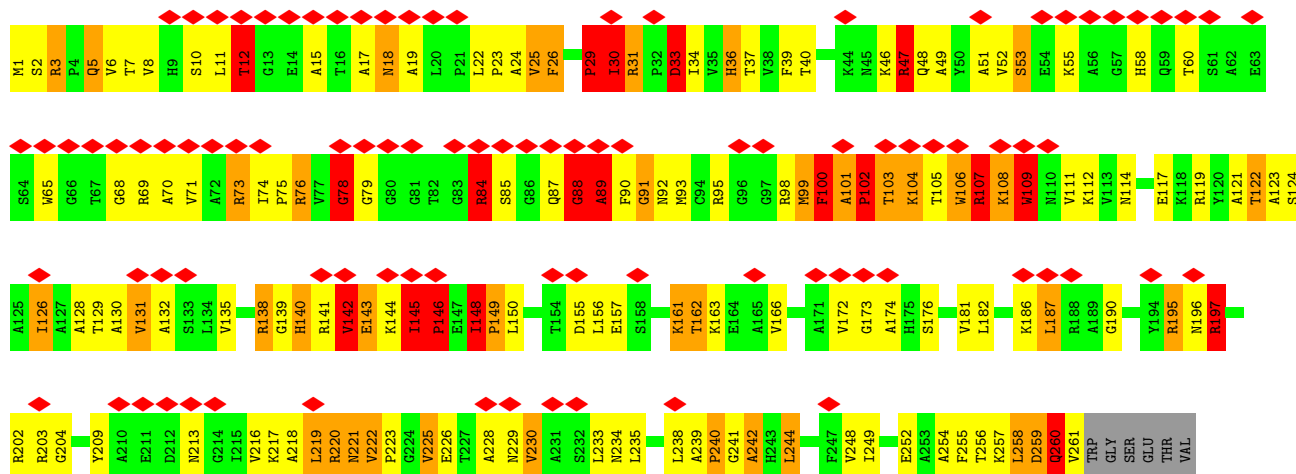


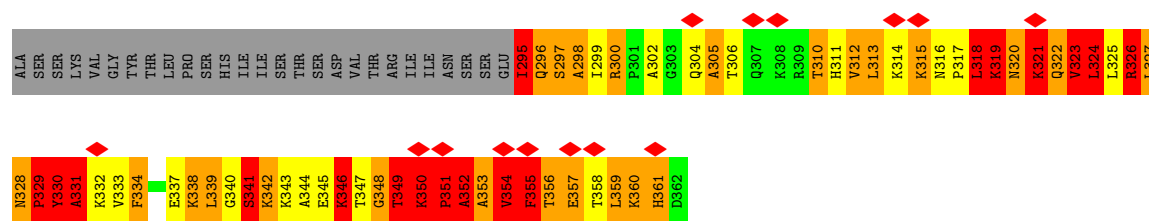


• Molecule 32: 60S ribosomal protein rpL3 (L3p)

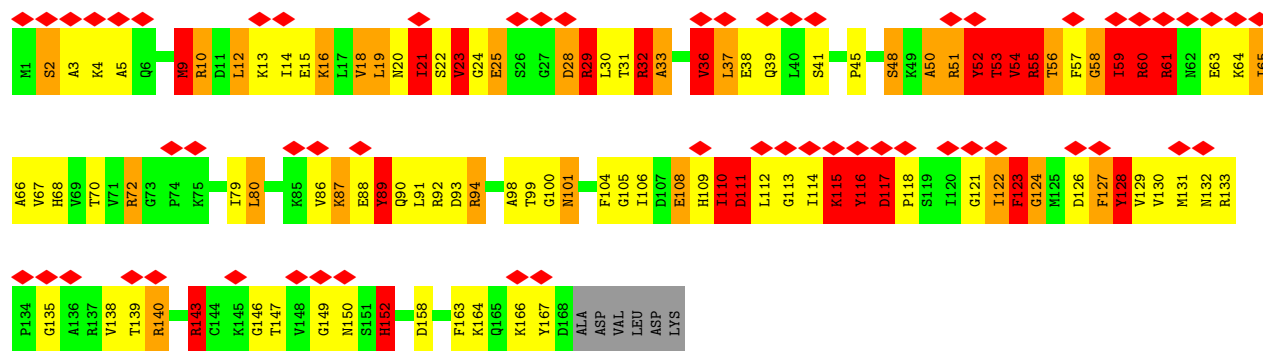


• Molecule 33: 60S ribosomal protein rpL4 (L4p)

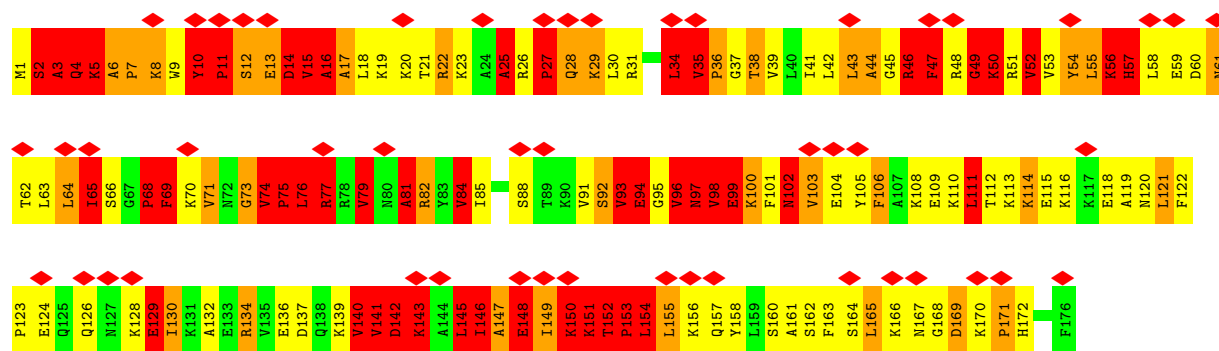




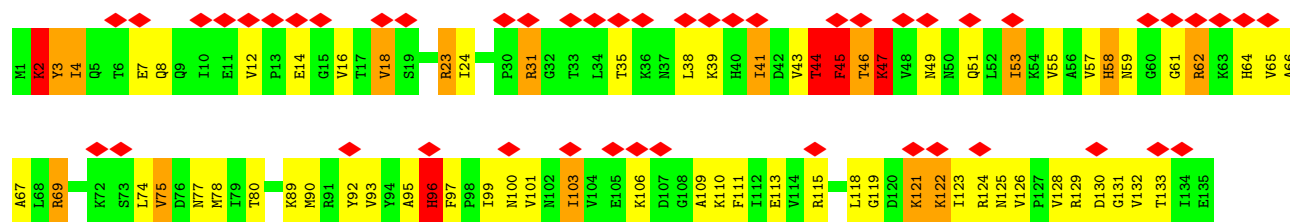
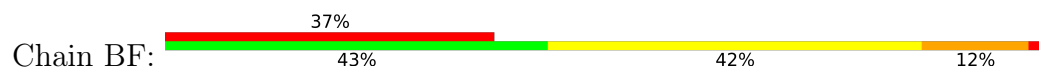
• Molecule 34: 60S ribosomal protein rpL11 (L5p)

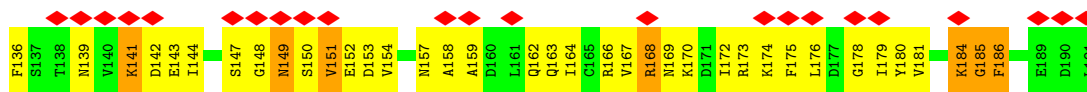


• Molecule 35: 60S ribosomal protein rpL6 (L6e)

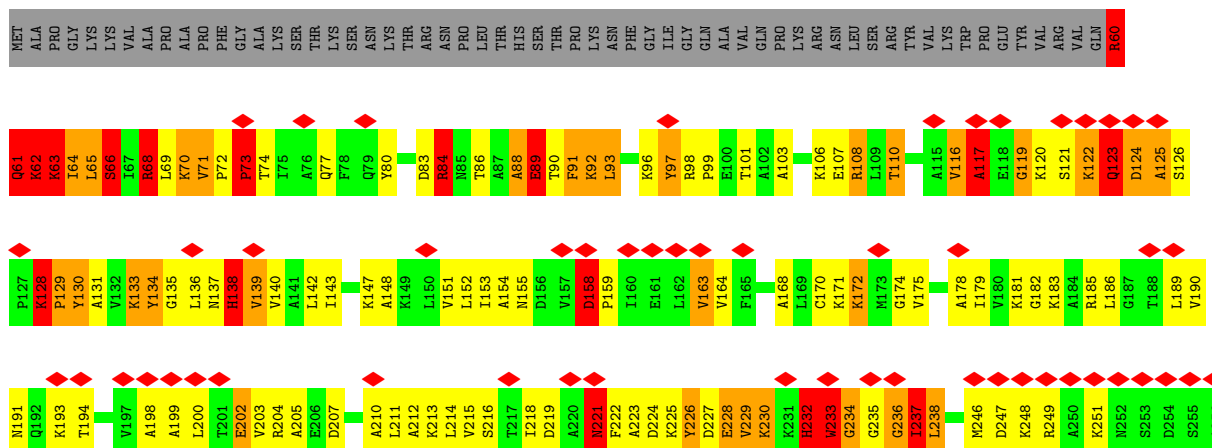
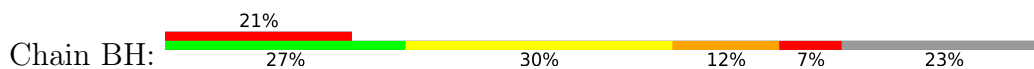


• Molecule 36: 60S ribosomal protein rpL9 (L6p)

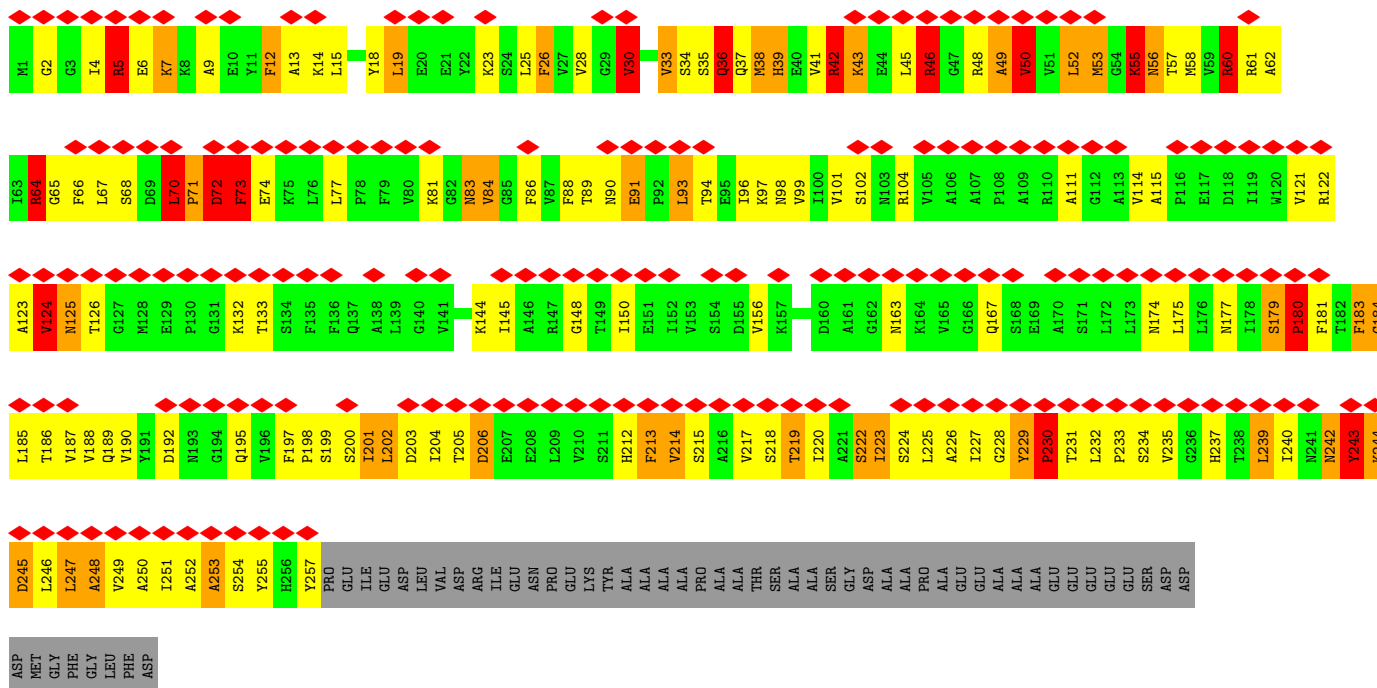




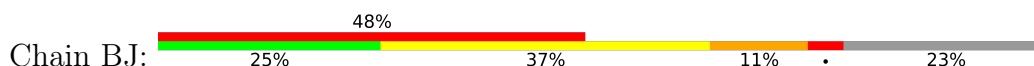
• Molecule 37: 60S ribosomal protein rpL8 (L7ae)

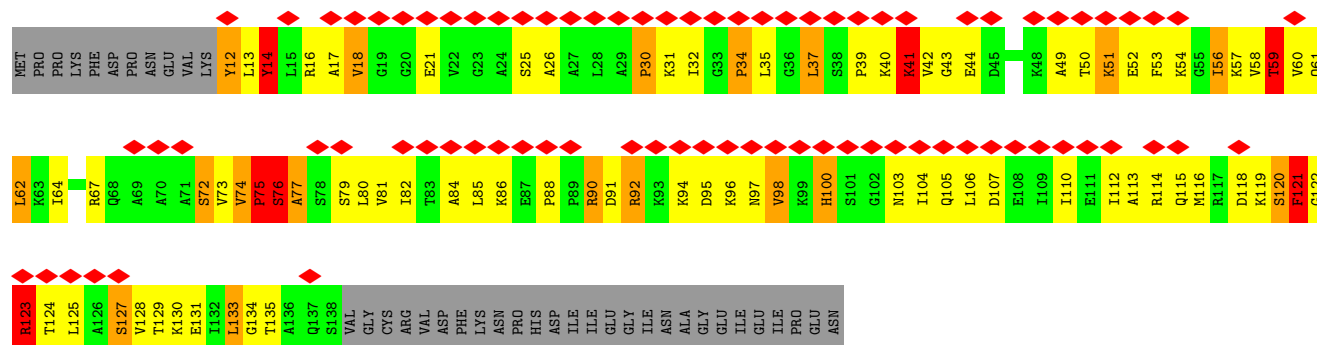


• Molecule 38: 60S acidic ribosomal protein rpP0 (L10P)

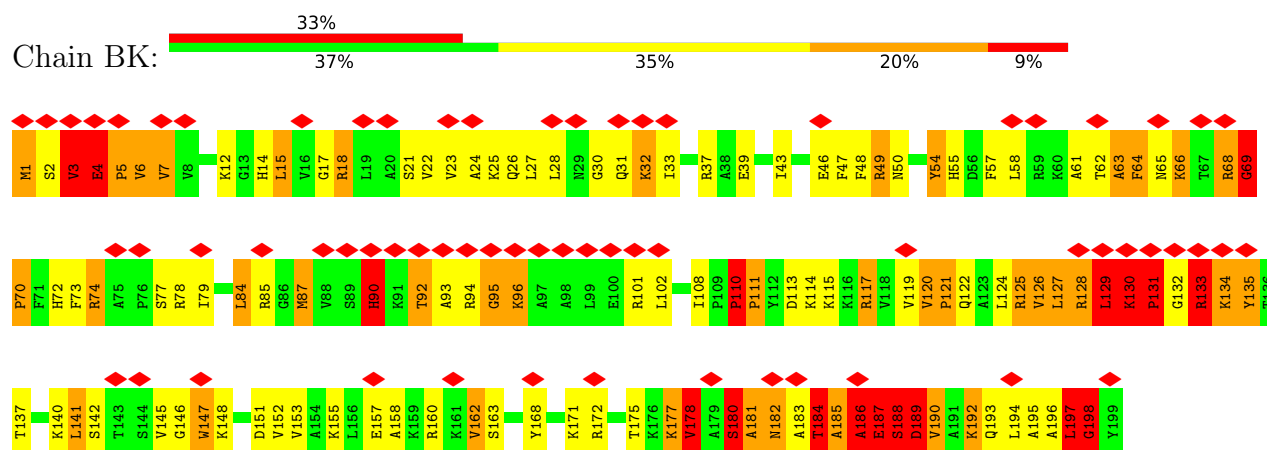


• Molecule 39: 60S ribosomal protein rpL12 (L11p)

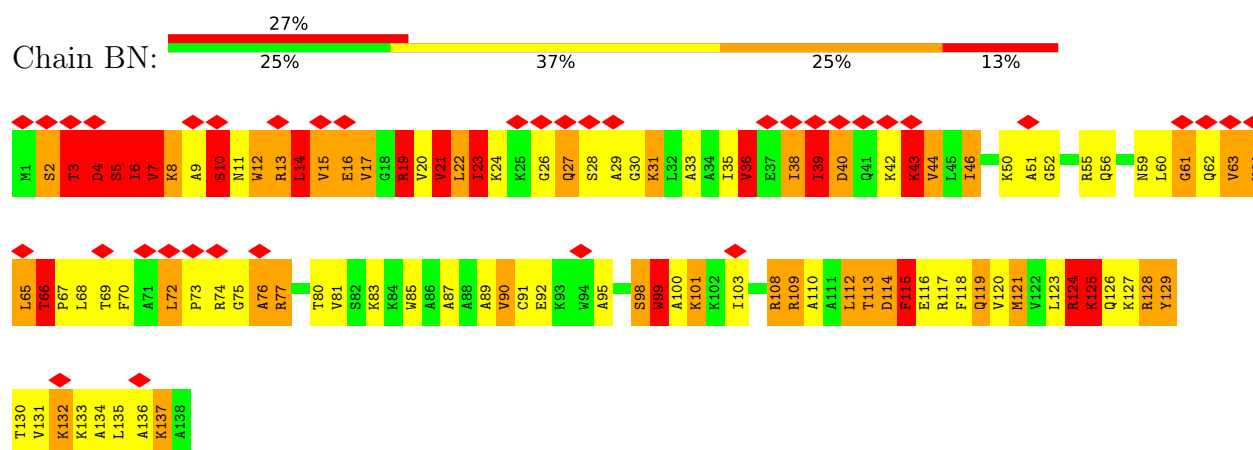




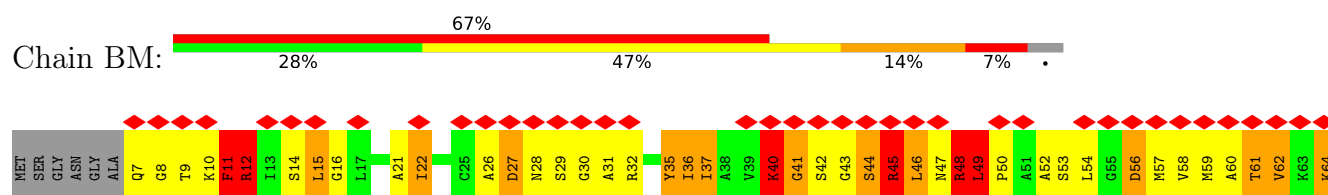
• Molecule 40: 60S ribosomal protein rpL16 (L13p)

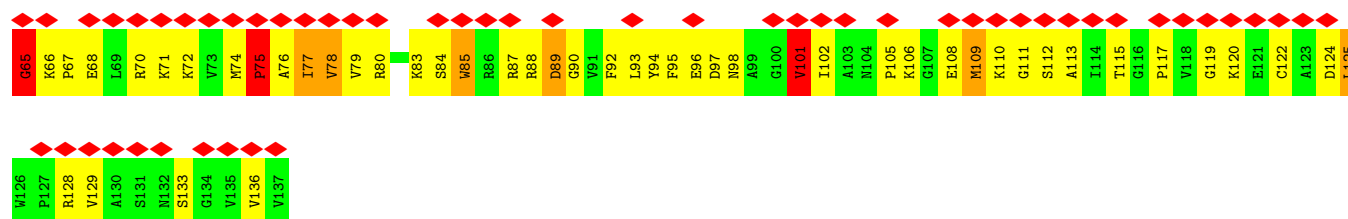


• Molecule 41: 60S ribosomal protein rpL14 (L14e)

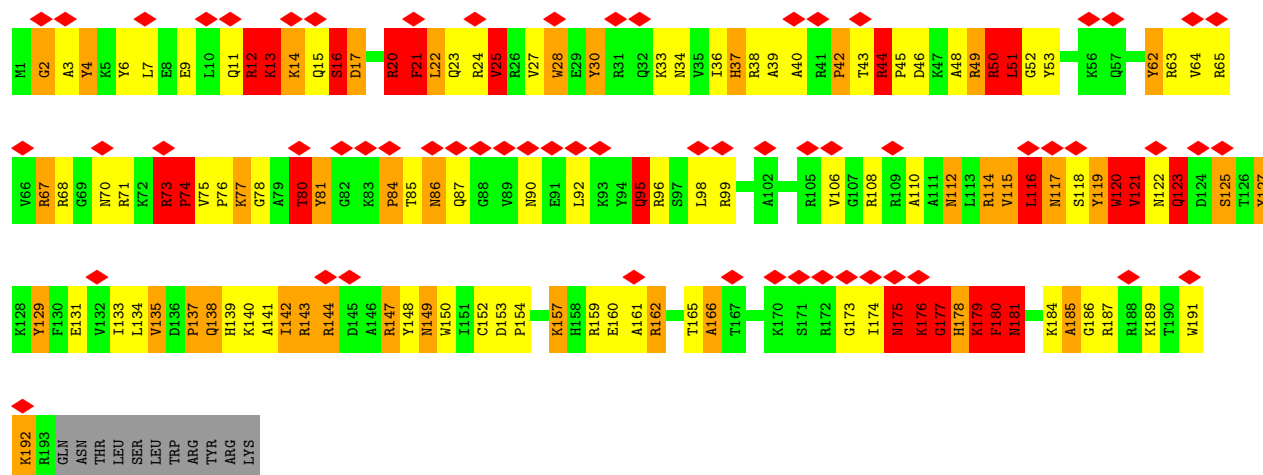


• Molecule 42: 60S ribosomal protein rpL23 (L14p)

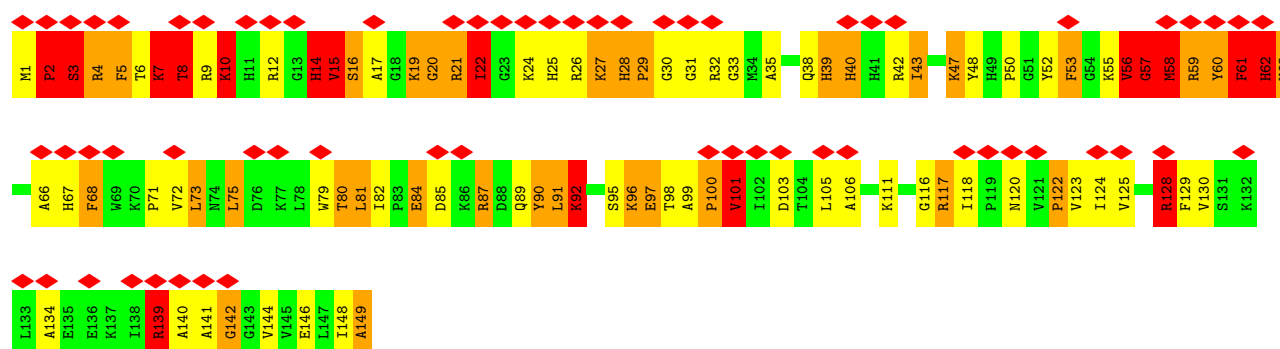




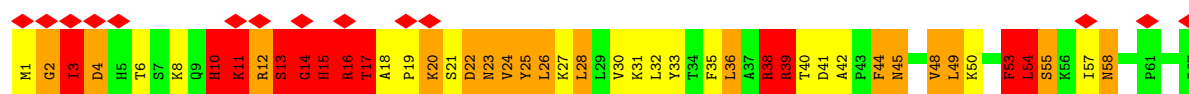
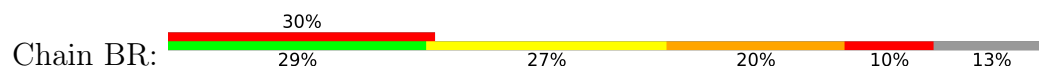
• Molecule 43: 60S ribosomal protein rpL15 (L15e)

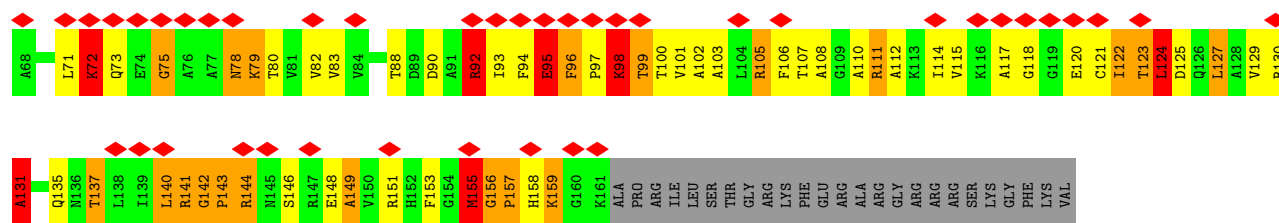


• Molecule 44: 60S ribosomal protein rpL28 (L15p)

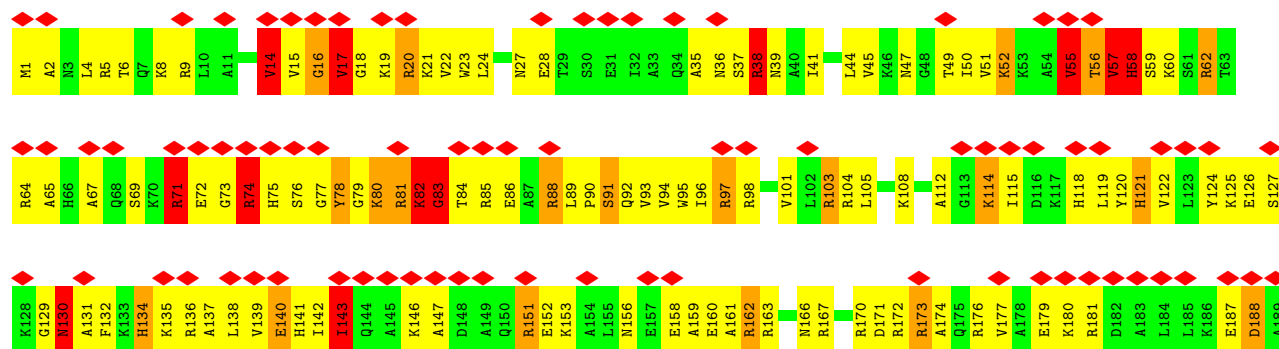


• Molecule 45: 60S ribosomal protein rpL18 (L18e)

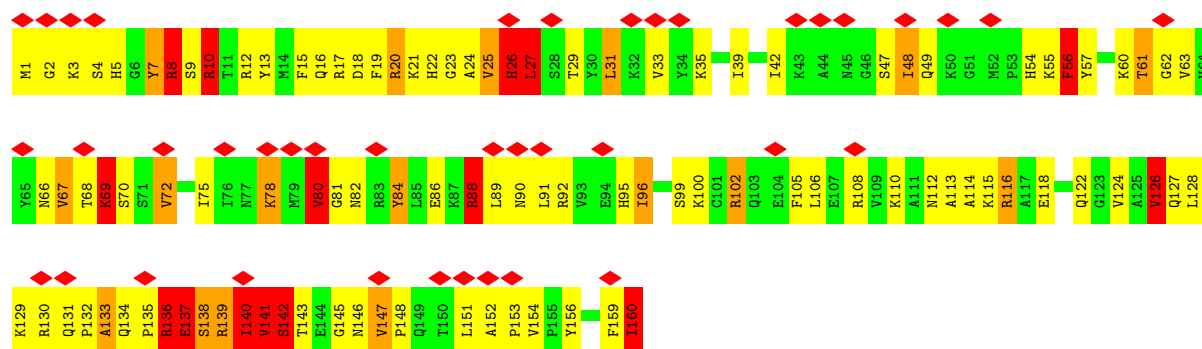




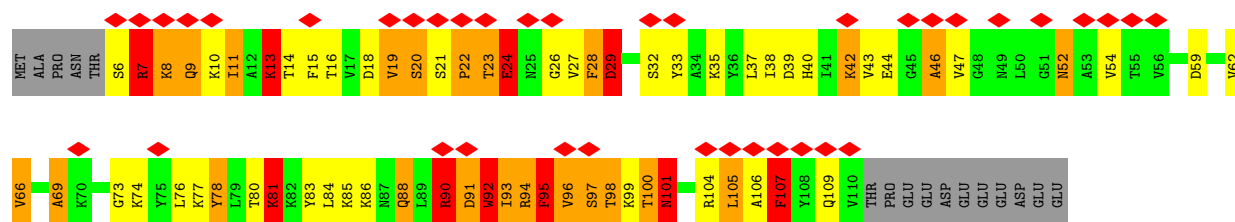
- Molecule 46: 60S ribosomal protein rpL19 (L19e)



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

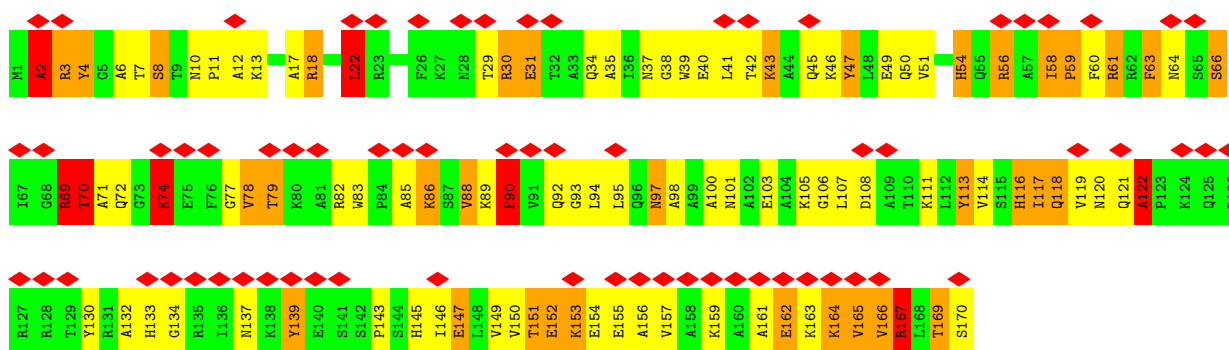


- Molecule 48: 60S ribosomal protein rpL22 (L22e)

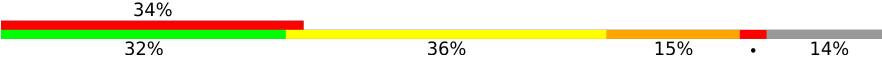


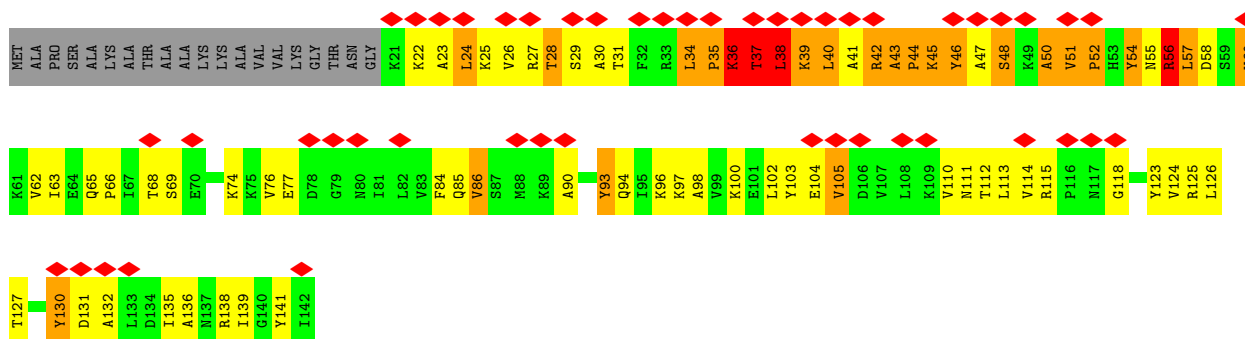
- Molecule 49: 60S ribosomal protein rpL17 (L22p)

Chain BV: 



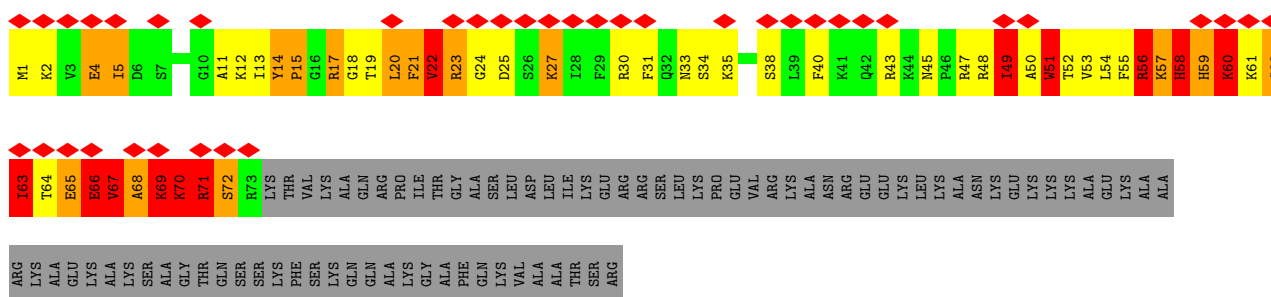
• Molecule 50: 60S ribosomal protein rpL25 (L23p)

Chain BX: 



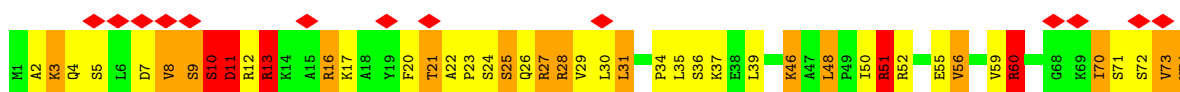
• Molecule 51: 60S ribosomal protein rpL24 (L24e)

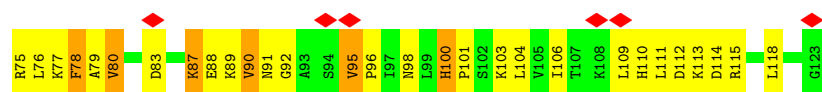
Chain BZ: 



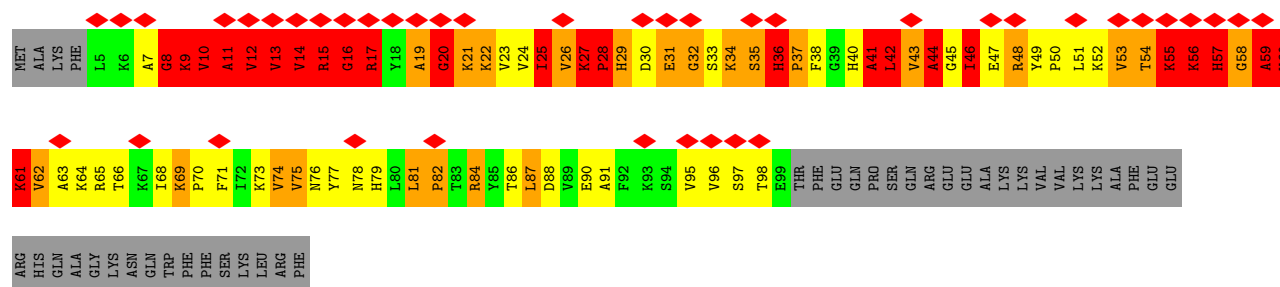
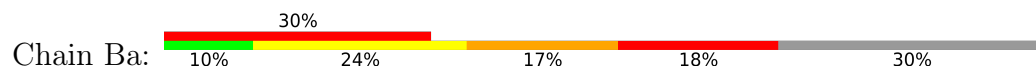
• Molecule 52: 60S ribosomal protein rpL26 (L24p)

Chain BY: 

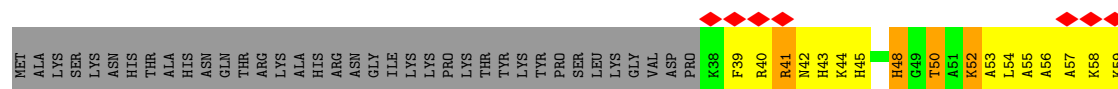




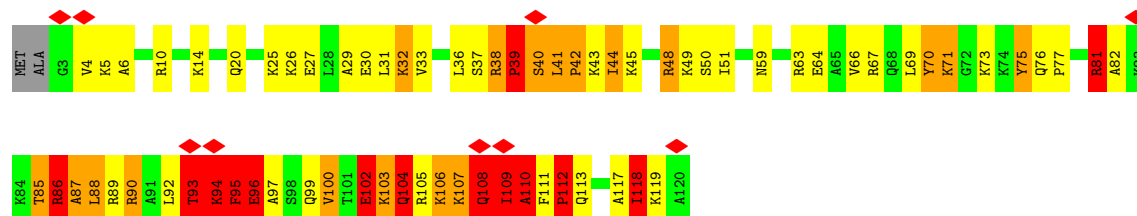
- Molecule 53: 60S ribosomal protein rpL27 (L27e)



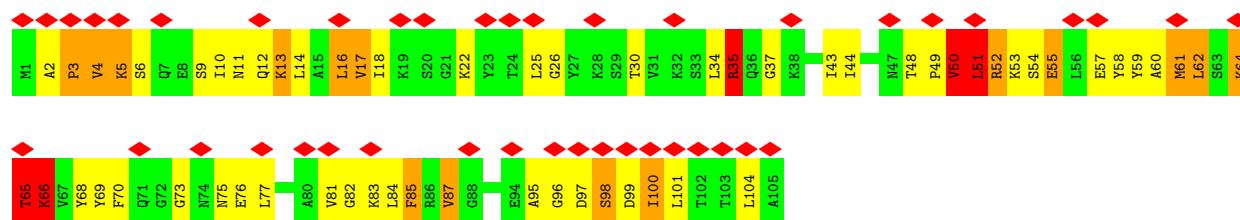
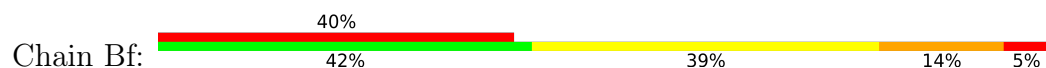
- Molecule 54: 60S ribosomal protein rpL29 (L29e)



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

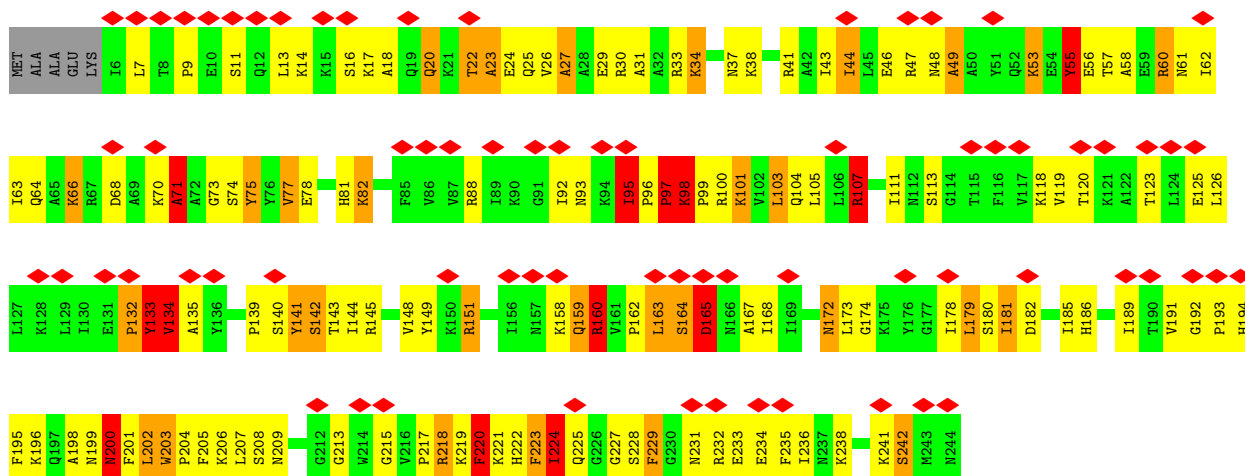


- Molecule 56: 60S ribosomal protein rpL30 (L30e)

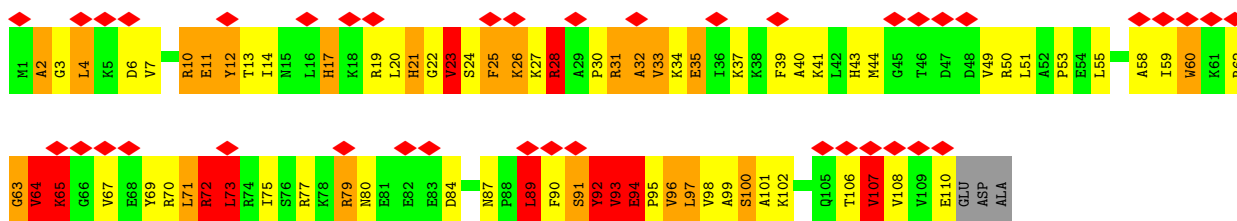


- Molecule 57: 60S ribosomal protein rpL7 (L30p)

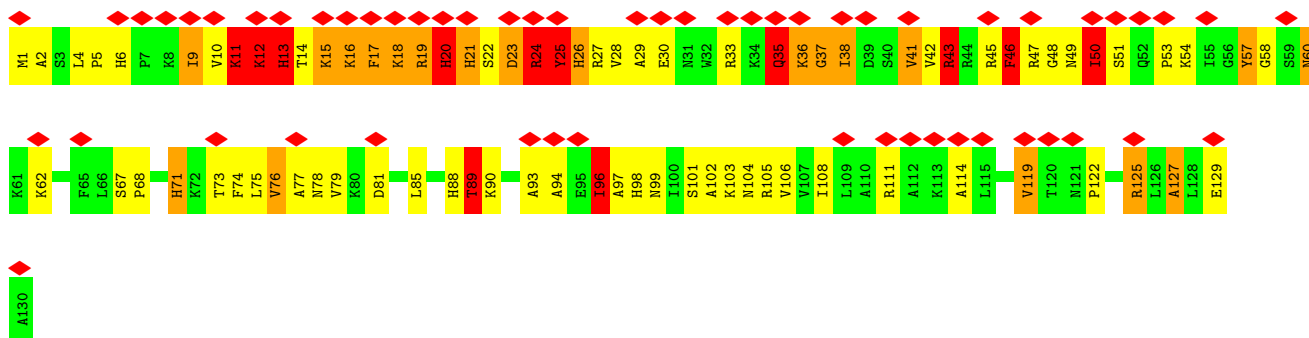
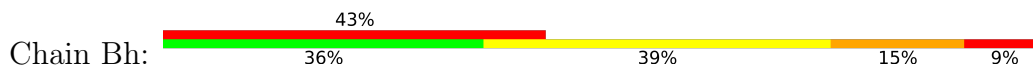




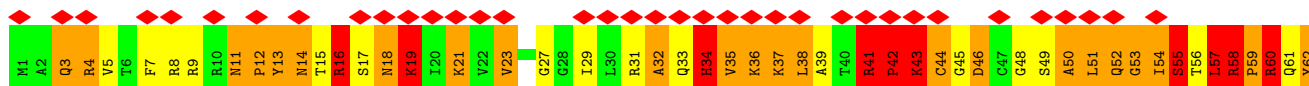
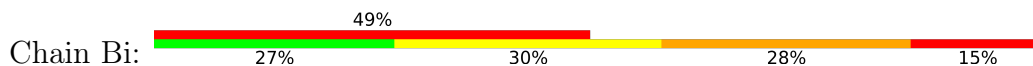
• Molecule 58: 60S ribosomal protein rpL31 (L31e)

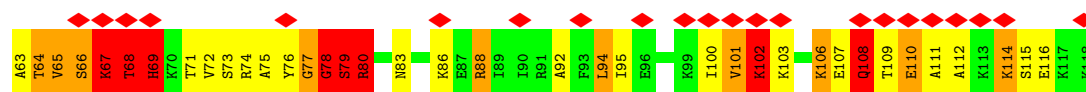


• Molecule 59: 60S ribosomal protein pL32 (L32e)

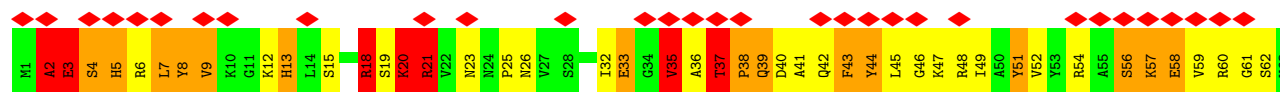
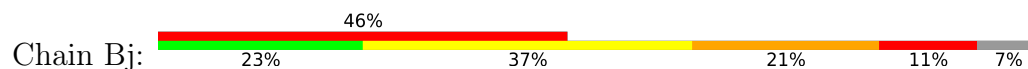


• Molecule 60: 60S ribosomal protein rpL34 (L34e)

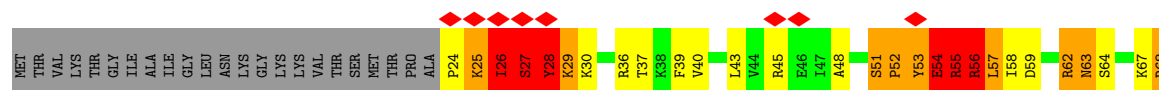
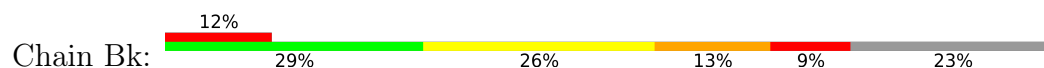




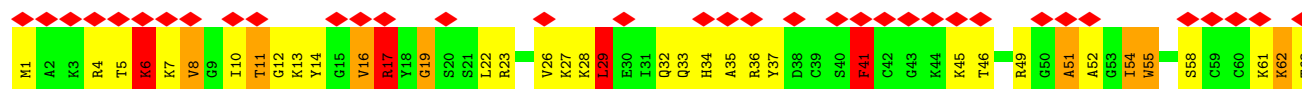
- Molecule 61: 60S ribosomal protein rpL33 (L35ae)



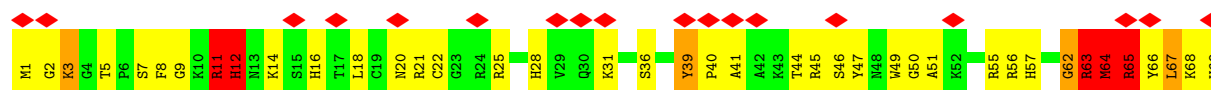
- Molecule 62: 60S ribosomal protein rpL36 (L36e)



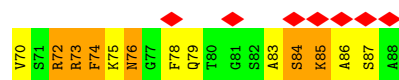
- Molecule 63: 60S ribosomal protein rpL43 (L37ae)

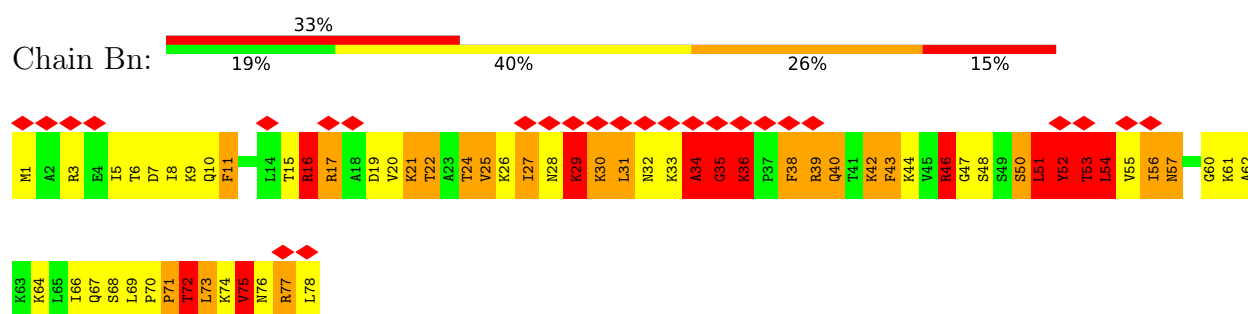


- Molecule 64: 60S ribosomal protein rpL37 (L37e)

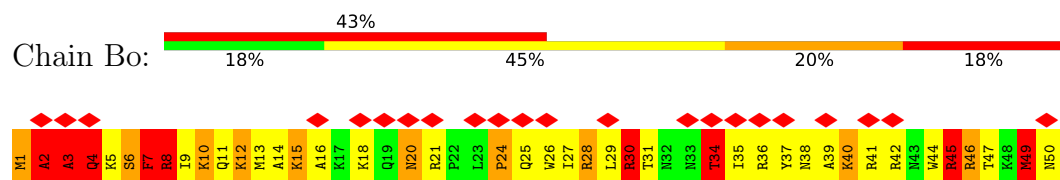


- Molecule 65: 60S ribosomal protein rpL38 (L38e)

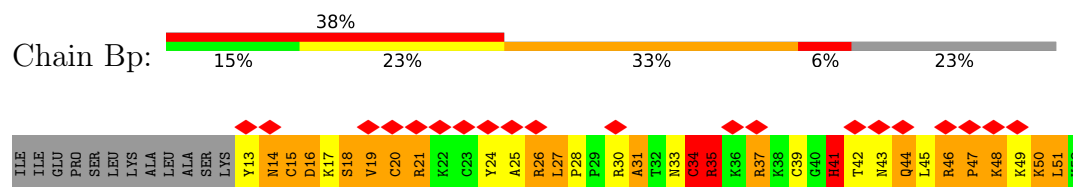




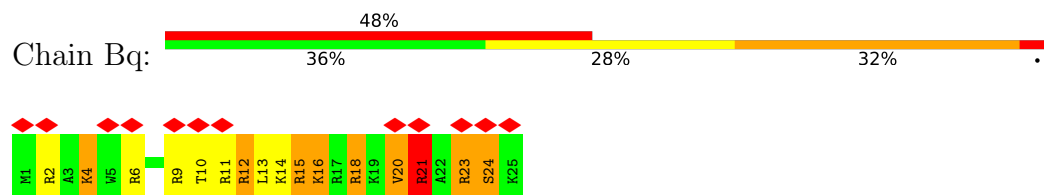
- Molecule 66: 60S ribosomal protein rpL39 (L39e)



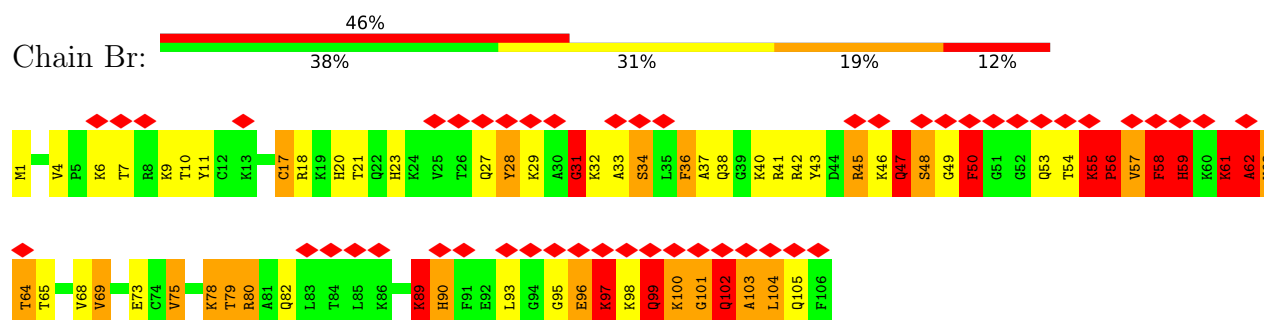
- Molecule 67: 60S ribosomal protein rpL40 (L40e)



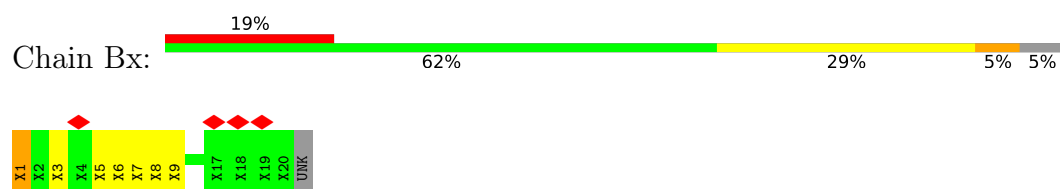
- Molecule 68: 60S ribosomal protein rpL41 (L41e)



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



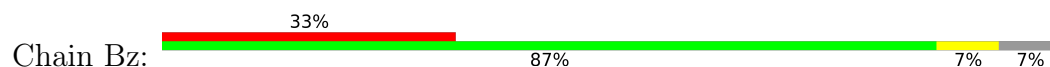
- Molecule 70: Unknown protein



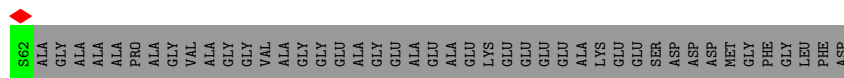
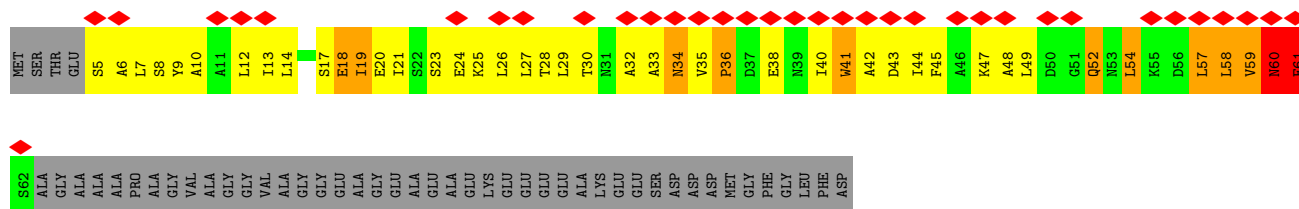
- Molecule 70: Unknown protein



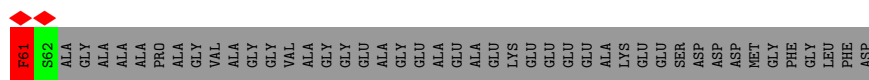
- Molecule 71: Unknown protein



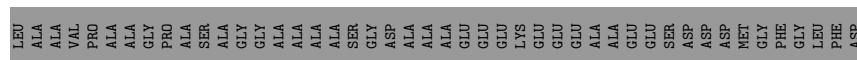
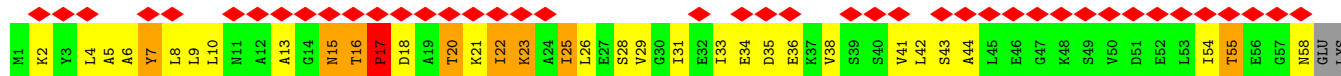
- Molecule 72: 60S acidic ribosomal protein rpP11 (P1)



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

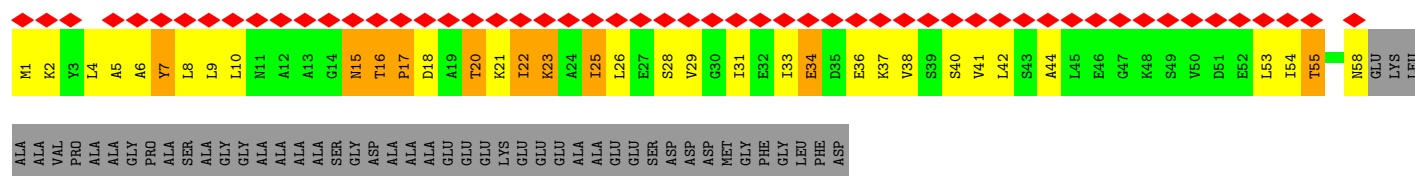


- Molecule 73: 60S acidic ribosomal protein (P2)

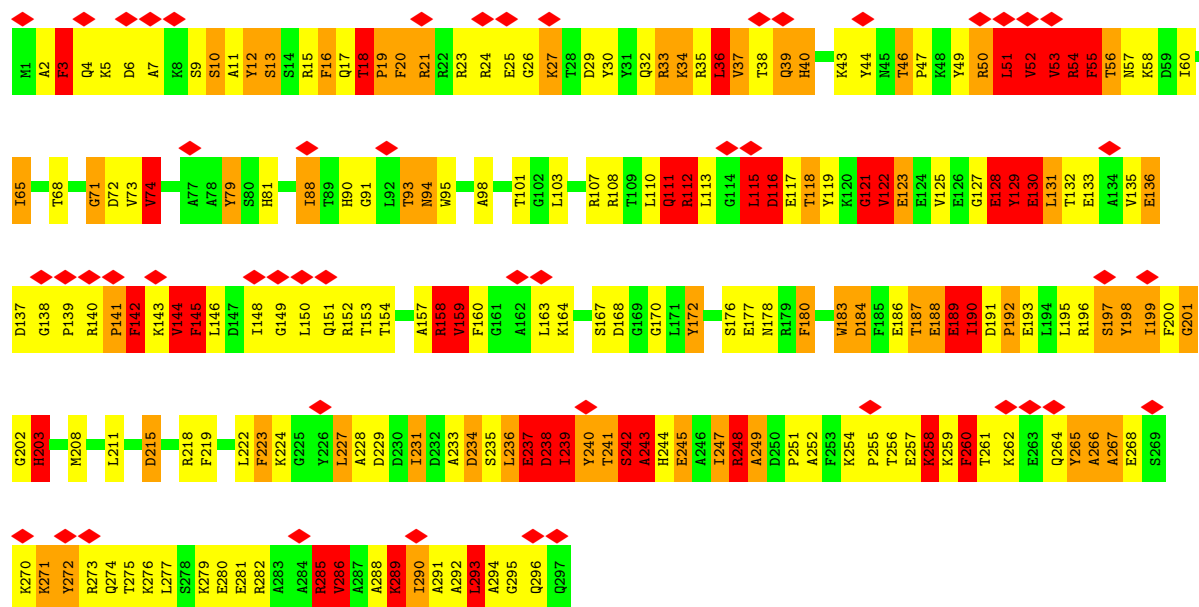


- Molecule 73: 60S acidic ribosomal protein (P2)

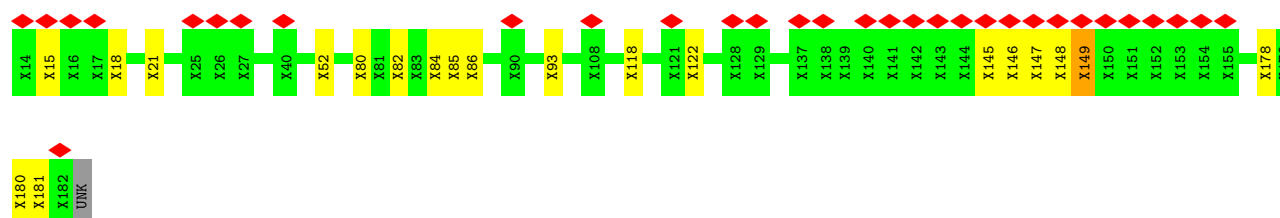




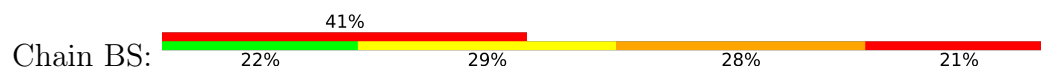
• Molecule 74: 60S ribosomal protein rpL5 (L18p)

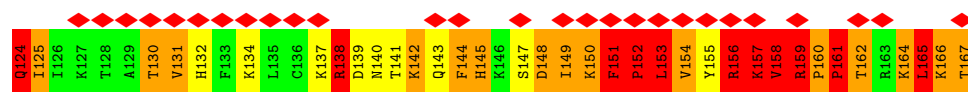


• Molecule 75: 60S ribosomal protein rpL13 (L13e)

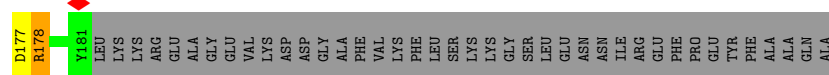
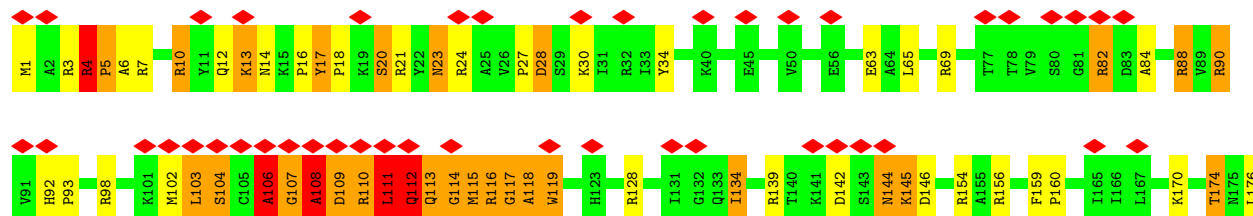


• Molecule 76: 60S ribosomal protein rpL20 (L18ae)

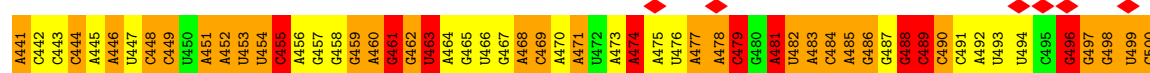
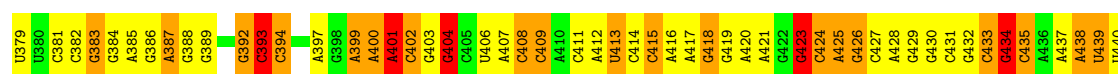
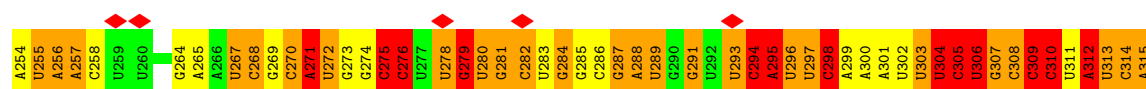
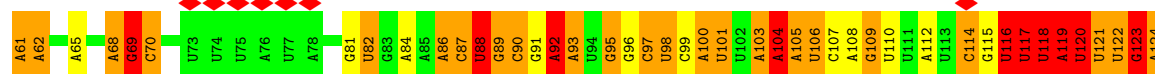
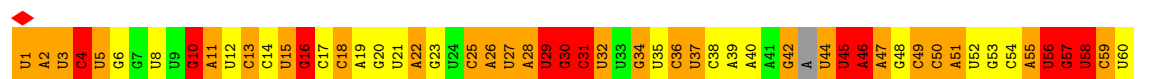


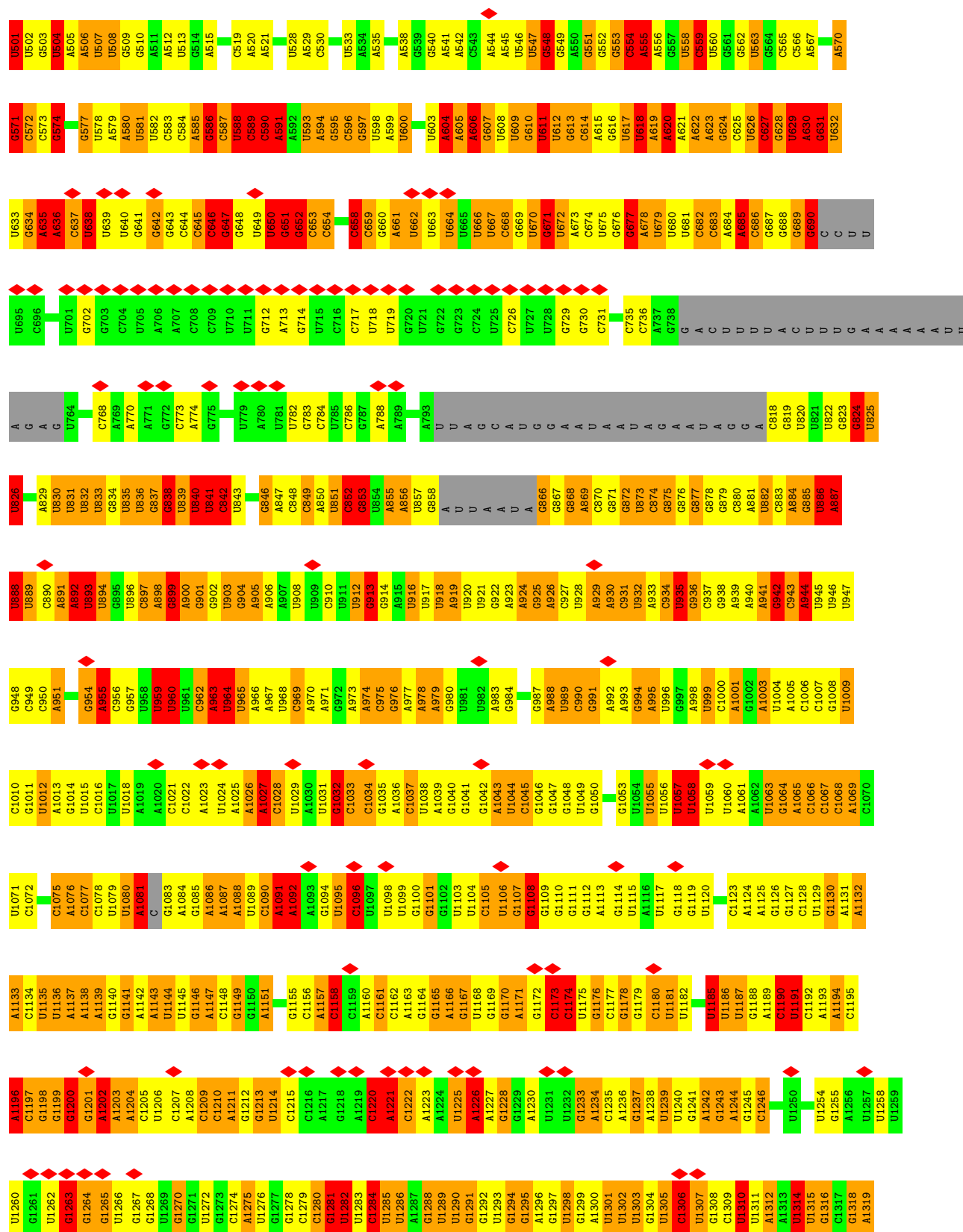


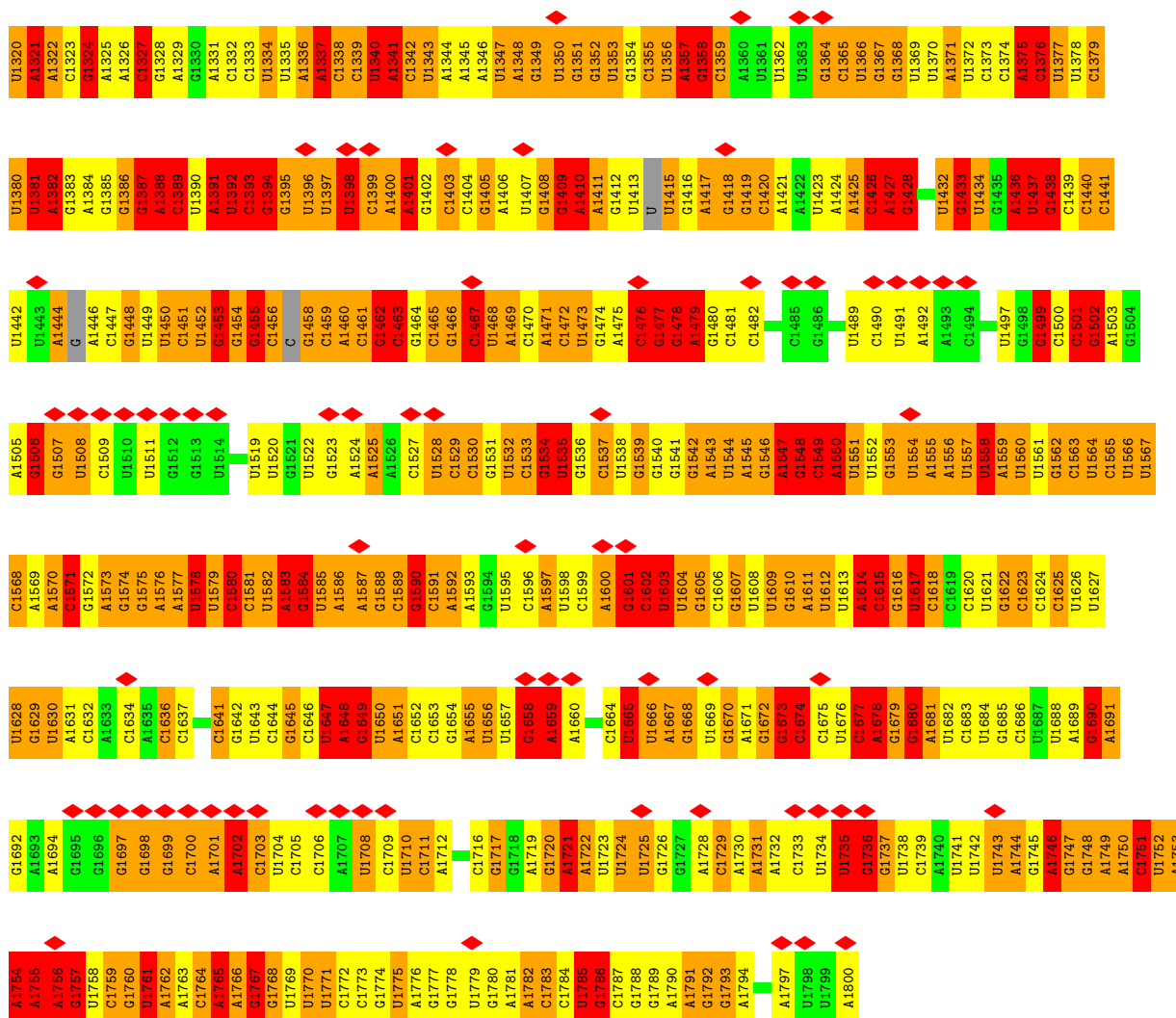
• Molecule 77: 60S ribosomal protein rpL10 (L10e)



• Molecule 78: 18S rRNA



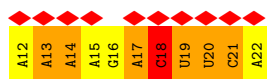




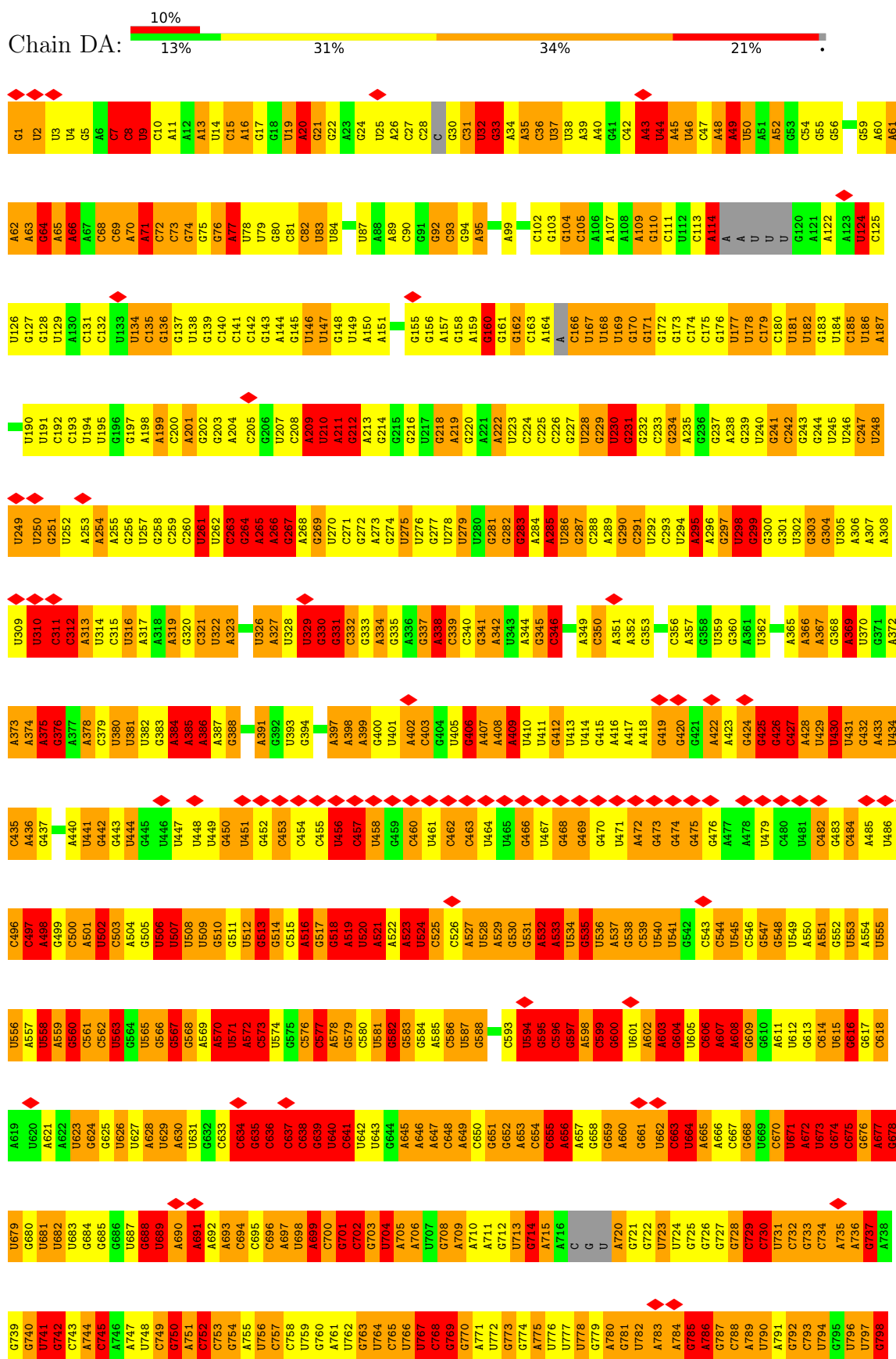
• Molecule 79: P-SITE TRNA ASP



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



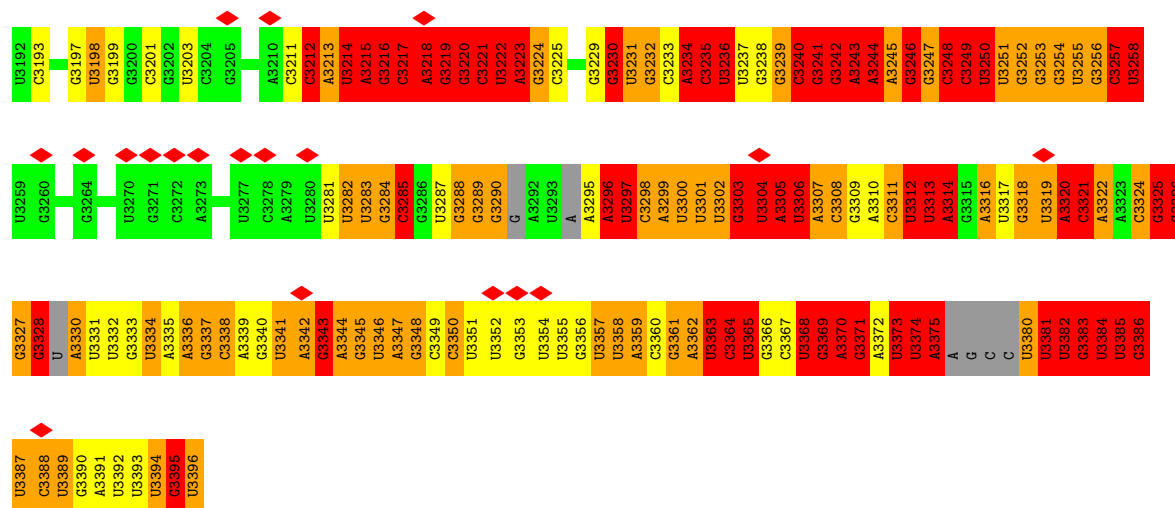
• Molecule 81: 25S rRNA



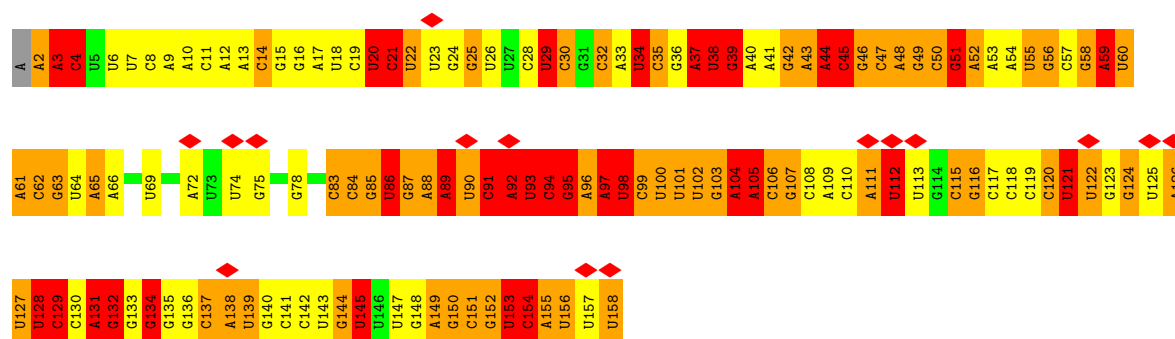




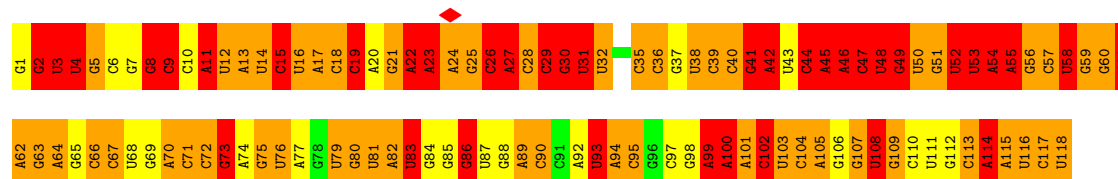




• Molecule 82: 5.8S rRNA



• 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 ($\text{\AA}$)	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 ($\text{\AA}$)	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	2.28	79/2495 (3.2%)	2.57	164/3391 (4.8%)
2	AA	2.82	69/1962 (3.5%)	3.50	210/2674 (7.9%)
3	AB	2.62	56/1530 (3.7%)	3.25	131/2049 (6.4%)
4	AD	2.72	71/1620 (4.4%)	3.76	181/2182 (8.3%)
5	AC	2.87	78/1544 (5.1%)	3.74	193/2059 (9.4%)
6	AE	2.54	66/1971 (3.3%)	3.28	202/2664 (7.6%)
8	AF	2.29	48/1561 (3.1%)	2.54	119/2103 (5.7%)
9	AH	2.55	45/1047 (4.3%)	3.01	87/1405 (6.2%)
10	AI	2.77	30/1016 (3.0%)	3.21	121/1362 (8.9%)
11	AJ	2.90	43/857 (5.0%)	3.67	110/1148 (9.6%)
12	AK	2.79	47/843 (5.6%)	3.00	105/1134 (9.3%)
13	AL	3.27	55/990 (5.6%)	4.25	127/1304 (9.7%)
14	AM	2.56	55/1175 (4.7%)	3.22	111/1577 (7.0%)
15	AN	2.41	11/358 (3.1%)	3.97	54/469 (11.5%)
16	AO	2.53	39/994 (3.9%)	3.41	136/1339 (10.2%)
17	AQ	2.96	51/1109 (4.6%)	4.07	126/1483 (8.5%)
18	AP	3.30	32/646 (5.0%)	4.88	72/867 (8.3%)
19	AR	2.19	28/691 (4.1%)	2.69	59/931 (6.3%)
20	AS	2.48	57/1138 (5.0%)	3.42	155/1527 (10.2%)
21	AT	2.88	34/694 (4.9%)	3.63	83/935 (8.9%)
22	AV	2.77	37/698 (5.3%)	3.57	95/932 (10.2%)
24	AX	2.27	18/372 (4.8%)	2.57	31/504 (6.2%)
25	AY	2.49	19/447 (4.3%)	2.78	48/601 (8.0%)
26	AZ	3.81	26/499 (5.2%)	5.03	61/660 (9.2%)
29	AU	2.58	27/725 (3.7%)	3.49	114/969 (11.8%)
30	BA	1.95	38/1745 (2.2%)	2.52	129/2342 (5.5%)
31	BB	3.05	96/1938 (5.0%)	4.03	208/2600 (8.0%)
32	BC	3.18	140/3124 (4.5%)	4.39	292/4196 (7.0%)
33	BD	3.04	127/2531 (5.0%)	3.92	286/3414 (8.4%)
34	BE	2.82	60/1362 (4.4%)	4.11	127/1824 (7.0%)
35	BG	3.70	80/1433 (5.6%)	5.07	250/1922 (13.0%)
36	BF	2.28	41/1537 (2.7%)	2.78	90/2068 (4.4%)
37	BH	3.06	66/1527 (4.3%)	3.53	152/2052 (7.4%)
38	Bs	2.48	69/2013 (3.4%)	3.19	181/2731 (6.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	BJ	2.69	62/964 (6.4%)	3.32	101/1295 (7.8%)
40	BK	2.61	52/1600 (3.2%)	3.74	181/2146 (8.4%)
41	BN	2.64	52/1083 (4.8%)	2.94	128/1456 (8.8%)
42	BM	2.30	40/987 (4.1%)	2.80	110/1326 (8.3%)
43	BP	2.85	71/1659 (4.3%)	3.39	170/2221 (7.7%)
44	BO	3.66	59/1213 (4.9%)	4.20	139/1623 (8.6%)
45	BR	3.42	59/1264 (4.7%)	4.09	137/1701 (8.1%)
46	BT	2.51	56/1547 (3.6%)	3.09	151/2060 (7.3%)
47	BU	2.47	53/1285 (4.1%)	3.49	118/1720 (6.9%)
48	BW	2.87	39/846 (4.6%)	3.74	86/1142 (7.5%)
49	BV	2.33	50/1335 (3.7%)	2.66	103/1794 (5.7%)
50	BX	2.07	24/993 (2.4%)	2.74	103/1336 (7.7%)
51	BZ	3.34	33/590 (5.6%)	3.63	68/783 (8.7%)
52	BY	2.19	30/983 (3.1%)	2.62	89/1312 (6.8%)
53	Ba	3.37	49/722 (6.8%)	4.49	144/967 (14.9%)
54	Bd	2.27	9/177 (5.1%)	3.15	24/231 (10.4%)
55	Bc	2.92	40/974 (4.1%)	3.63	127/1294 (9.8%)
56	Bf	2.14	22/793 (2.8%)	2.52	66/1062 (6.2%)
57	Be	2.53	64/1957 (3.3%)	3.04	175/2631 (6.7%)
58	Bg	2.51	39/887 (4.4%)	3.28	103/1185 (8.7%)
59	Bh	2.57	48/1064 (4.5%)	3.17	107/1423 (7.5%)
60	Bi	3.48	47/935 (5.0%)	4.81	121/1242 (9.7%)
61	Bj	3.17	47/751 (6.3%)	3.89	109/1004 (10.9%)
62	Bk	3.48	34/625 (5.4%)	5.19	84/826 (10.2%)
63	Bm	2.21	23/710 (3.2%)	2.56	59/944 (6.2%)
64	Bl	2.81	31/693 (4.5%)	3.85	65/915 (7.1%)
65	Bn	3.20	30/610 (4.9%)	4.27	78/813 (9.6%)
66	Bo	2.39	20/452 (4.4%)	3.00	49/598 (8.2%)
67	Bp	2.06	11/335 (3.3%)	2.81	35/442 (7.9%)
68	Bq	2.55	15/235 (6.4%)	2.69	22/300 (7.3%)
69	Br	2.84	37/846 (4.4%)	3.60	79/1113 (7.1%)
72	Bt	1.03	2/445 (0.4%)	2.02	22/606 (3.6%)
72	Bu	1.23	1/445 (0.2%)	2.20	27/606 (4.5%)
73	Bv	1.44	3/431 (0.7%)	2.03	19/582 (3.3%)
73	Bw	1.43	3/431 (0.7%)	2.04	19/582 (3.3%)
74	BQ	3.12	107/2404 (4.5%)	4.40	259/3236 (8.0%)
76	BS	2.59	68/1458 (4.7%)	3.35	184/1957 (9.4%)
77	BI	1.21	4/1473 (0.3%)	2.05	49/1976 (2.5%)
78	CA	2.07	1272/37406 (3.4%)	2.24	2554/57948 (4.4%)
79	CB	2.13	57/1785 (3.2%)	2.16	111/2779 (4.0%)
80	CC	2.68	10/264 (3.8%)	2.70	17/407 (4.2%)
81	DA	2.16	3026/76832 (3.9%)	2.36	6031/119578 (5.0%)
82	DB	2.11	131/3480 (3.8%)	2.28	273/5395 (5.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
83	DC	2.31	123/2808 (4.4%)	2.69	299/4372 (6.8%)
All	All	2.39	7891/202969 (3.9%)	2.82	17605/298347 (5.9%)

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 7891 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	BO	20	GLY	C-N	-57.42	0.61	1.33
35	BG	148	GLU	C-O	-51.98	0.82	1.23
32	BC	17	LEU	C-O	-46.69	0.76	1.24
38	Bs	72	ASP	C-O	-41.86	0.93	1.24
37	BH	158	ASP	C-O	-41.73	0.84	1.24

The worst 5 of 17605 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	BC	17	LEU	O-C-N	-68.52	68.11	121.55
64	Bl	39	TYR	O-C-N	-67.86	63.45	121.80
35	BG	148	GLU	O-C-N	-62.46	76.43	122.03
35	BG	148	GLU	CA-C-O	-62.34	62.61	119.34
32	BC	368	GLY	CA-C-O	-61.90	68.39	122.24

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	Peptide,Mainchain
1	Aa	54	PHE	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Aa	2442	0	2396	59	0
2	AA	1922	0	1841	39	0
3	AB	1511	0	1503	24	0
4	AD	1591	0	1653	84	0
5	AC	1521	0	1546	65	0
6	AE	1936	0	2030	89	0
7	AG	716	0	164	27	0
8	AF	1543	0	1589	40	0
9	AH	1030	0	1072	30	0
10	AI	998	0	1048	68	0
11	AJ	849	0	864	17	0
12	AK	833	0	824	79	0
13	AL	978	0	901	114	0
14	AM	1156	0	1176	155	0
15	AN	353	0	333	21	0
16	AO	978	0	1040	72	0
17	AQ	1098	0	1163	25	0
18	AP	631	0	634	93	0
19	AR	676	0	696	90	0
20	AS	1120	0	1132	88	0
21	AT	685	0	672	24	0
22	AV	688	0	734	27	0
23	AW	461	0	106	16	0
24	AX	366	0	364	19	0
25	AY	445	0	462	13	0
26	AZ	492	0	535	7	0
27	Ab	181	0	38	4	0
28	Ac	126	0	28	0	0
29	AU	714	0	711	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	BA	1718	0	1811	34	0
31	BB	1904	0	1952	175	0
32	BC	3055	0	3109	132	0
33	BD	2486	0	2587	134	0
34	BE	1341	0	1376	118	0
35	BG	1409	0	1513	119	0
36	BF	1516	0	1581	49	0
37	BH	1505	0	1582	69	0
38	Bs	1976	0	2017	219	0
39	BJ	954	0	1025	28	0
40	BK	1570	0	1676	53	0
41	BN	1068	0	1166	107	0
42	BM	972	0	1019	58	0
43	BP	1625	0	1685	75	0
44	BO	1182	0	1221	65	0
45	BR	1243	0	1327	65	0
46	BT	1530	0	1629	41	0
47	BU	1261	0	1281	36	0
48	BW	830	0	845	29	0
49	BV	1312	0	1314	23	0
50	BX	978	0	1049	4	0
51	BZ	579	0	591	55	0
52	BY	972	0	1060	17	0
53	Ba	708	0	742	114	0
54	Bd	174	0	188	5	0
55	Bc	965	0	1073	20	0
56	Bf	785	0	819	54	0
57	Be	1919	0	2013	59	0
58	Bg	873	0	913	23	0
59	Bh	1043	0	1113	47	0
60	Bi	926	0	998	131	0
61	Bj	738	0	730	33	0
62	Bk	619	0	673	13	0
63	Bm	703	0	750	48	0
64	Bl	678	0	667	14	0
65	Bn	604	0	664	28	0
66	Bo	445	0	487	14	0
67	Bp	330	0	356	18	0
68	Bq	234	0	284	3	0
69	Br	834	0	894	18	0
70	Bx	100	0	22	8	0
70	By	100	0	22	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	Bz	70	0	18	0	0
72	Bt	440	0	439	252	0
72	Bu	440	0	439	177	0
73	Bv	429	0	445	107	0
73	Bw	429	0	442	162	0
74	BQ	2356	0	2289	104	0
75	BL	845	0	192	38	0
76	BS	1420	0	1466	88	0
77	BI	1444	0	1478	32	0
78	CA	33643	0	16491	1344	0
79	CB	1599	0	807	34	0
80	CC	236	0	121	10	0
81	DA	68830	0	34361	1898	0
82	DB	3129	0	1554	81	0
83	DC	2513	0	1271	127	0
All	All	191627	0	136892	6102	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

The worst 5 of 6102 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BH:158:ASP:CA	37:BH:158:ASP:CB	1.74	1.66
14:AM:12:GLN:HG3	34:BE:116:TYR:CD1	1.28	1.65
38:Bs:229:TYR:CE1	72:Bt:44:ILE:HG22	1.19	1.64
78:CA:960:U:C2'	78:CA:960:U:C1'	1.75	1.63
69:Br:47:GLN:CA	69:Br:47:GLN:CB	1.74	1.63

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Aa	317/319 (99%)	274 (86%)	23 (7%)	20 (6%)	1	13
2	AA	250/252 (99%)	199 (80%)	21 (8%)	30 (12%)	0	4
3	AB	202/240 (84%)	137 (68%)	30 (15%)	35 (17%)	0	2
4	AD	198/261 (76%)	160 (81%)	17 (9%)	21 (11%)	0	6
5	AC	192/197 (98%)	136 (71%)	28 (15%)	28 (15%)	0	3
6	AE	252/254 (99%)	176 (70%)	36 (14%)	40 (16%)	0	2
8	AF	197/225 (88%)	170 (86%)	9 (5%)	18 (9%)	0	8
9	AH	128/130 (98%)	95 (74%)	17 (13%)	16 (12%)	0	4
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	10
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	3
14	AM	138/146 (94%)	107 (78%)	21 (15%)	10 (7%)	1	11
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	7
17	AQ	134/136 (98%)	90 (67%)	22 (16%)	22 (16%)	0	2
18	AP	83/156 (53%)	65 (78%)	12 (14%)	6 (7%)	1	11
19	AR	86/142 (61%)	64 (74%)	10 (12%)	12 (14%)	0	3
20	AS	142/144 (99%)	118 (83%)	8 (6%)	16 (11%)	0	5
21	AT	85/87 (98%)	66 (78%)	10 (12%)	9 (11%)	0	6
22	AV	83/108 (77%)	66 (80%)	7 (8%)	10 (12%)	0	4
24	AX	48/82 (58%)	37 (77%)	7 (15%)	4 (8%)	0	9
25	AY	58/67 (87%)	46 (79%)	7 (12%)	5 (9%)	0	9
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	16
31	BB	252/254 (99%)	208 (82%)	18 (7%)	26 (10%)	0	6
32	BC	386/388 (100%)	316 (82%)	33 (8%)	37 (10%)	0	7
33	BD	325/362 (90%)	250 (77%)	34 (10%)	41 (13%)	0	4
34	BE	166/174 (95%)	136 (82%)	11 (7%)	19 (11%)	0	5
35	BG	174/176 (99%)	108 (62%)	15 (9%)	51 (29%)	0	0
36	BF	189/191 (99%)	173 (92%)	13 (7%)	3 (2%)	7	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	BH	195/256 (76%)	156 (80%)	18 (9%)	21 (11%)	0	6
38	Bs	255/312 (82%)	224 (88%)	16 (6%)	15 (6%)	1	13
39	BJ	125/165 (76%)	107 (86%)	11 (9%)	7 (6%)	1	14
40	BK	197/199 (99%)	161 (82%)	15 (8%)	21 (11%)	0	6
41	BN	136/138 (99%)	104 (76%)	14 (10%)	18 (13%)	0	4
42	BM	129/137 (94%)	124 (96%)	5 (4%)	0	100	100
43	BP	191/204 (94%)	168 (88%)	14 (7%)	9 (5%)	2	16
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	4
46	BT	187/189 (99%)	163 (87%)	14 (8%)	10 (5%)	1	15
47	BU	158/160 (99%)	144 (91%)	7 (4%)	7 (4%)	2	17
48	BW	103/121 (85%)	79 (77%)	15 (15%)	9 (9%)	0	9
49	BV	168/170 (99%)	135 (80%)	20 (12%)	13 (8%)	1	10
50	BX	120/142 (84%)	95 (79%)	11 (9%)	14 (12%)	0	4
51	BZ	71/155 (46%)	48 (68%)	13 (18%)	10 (14%)	0	3
52	BY	121/123 (98%)	115 (95%)	2 (2%)	4 (3%)	3	21
53	Ba	93/136 (68%)	62 (67%)	15 (16%)	16 (17%)	0	2
54	Bd	20/59 (34%)	19 (95%)	1 (5%)	0	100	100
55	Bc	116/120 (97%)	92 (79%)	11 (10%)	13 (11%)	0	5
56	Bf	103/105 (98%)	91 (88%)	7 (7%)	5 (5%)	1	16
57	Be	237/244 (97%)	213 (90%)	14 (6%)	10 (4%)	2	17
58	Bg	108/113 (96%)	95 (88%)	4 (4%)	9 (8%)	0	9
59	Bh	128/130 (98%)	115 (90%)	7 (6%)	6 (5%)	2	16
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	2
62	Bk	75/100 (75%)	61 (81%)	6 (8%)	8 (11%)	0	6
63	Bm	90/92 (98%)	78 (87%)	10 (11%)	2 (2%)	5	29
64	Bl	86/88 (98%)	65 (76%)	14 (16%)	7 (8%)	1	9
65	Bn	76/78 (97%)	56 (74%)	10 (13%)	10 (13%)	0	4
66	Bo	49/51 (96%)	38 (78%)	3 (6%)	8 (16%)	0	2
67	Bp	38/52 (73%)	28 (74%)	7 (18%)	3 (8%)	1	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	Bq	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	2	17
69	Br	104/106 (98%)	71 (68%)	14 (14%)	19 (18%)	0	2
72	Bt	56/106 (53%)	53 (95%)	0	3 (5%)	1	15
72	Bu	56/106 (53%)	53 (95%)	0	3 (5%)	1	15
73	Bv	56/106 (53%)	53 (95%)	1 (2%)	2 (4%)	2	20
73	Bw	56/106 (53%)	53 (95%)	1 (2%)	2 (4%)	2	20
74	BQ	295/297 (99%)	232 (79%)	27 (9%)	36 (12%)	0	4
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	4
All	All	9997/11298 (88%)	7958 (80%)	949 (10%)	1090 (11%)	1	6

5 of 1090 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Aa	29	GLN
1	Aa	51	ASP
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%)	235 (91%)	24 (9%)	8	26
2	AA	198/210 (94%)	177 (89%)	21 (11%)	6	21
3	AB	148/195 (76%)	135 (91%)	13 (9%)	9	28
4	AD	173/222 (78%)	157 (91%)	16 (9%)	8	27
5	AC	153/166 (92%)	131 (86%)	22 (14%)	3	13
6	AE	205/205 (100%)	180 (88%)	25 (12%)	5	17
8	AF	163/191 (85%)	144 (88%)	19 (12%)	5	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	AH	111/111 (100%)	98 (88%)	13 (12%)	5	18
10	AI	105/119 (88%)	93 (89%)	12 (11%)	5	18
11	AJ	93/114 (82%)	85 (91%)	8 (9%)	10	29
12	AK	82/105 (78%)	76 (93%)	6 (7%)	13	34
13	AL	87/120 (72%)	75 (86%)	12 (14%)	3	14
14	AM	123/129 (95%)	107 (87%)	16 (13%)	4	15
15	AN	34/49 (69%)	30 (88%)	4 (12%)	5	18
16	AO	105/128 (82%)	89 (85%)	16 (15%)	3	12
17	AQ	122/124 (98%)	113 (93%)	9 (7%)	13	33
18	AP	63/137 (46%)	57 (90%)	6 (10%)	8	25
19	AR	71/118 (60%)	62 (87%)	9 (13%)	4	16
20	AS	115/116 (99%)	100 (87%)	15 (13%)	4	15
21	AT	74/74 (100%)	66 (89%)	8 (11%)	6	21
22	AV	74/89 (83%)	64 (86%)	10 (14%)	4	14
24	AX	43/71 (61%)	34 (79%)	9 (21%)	1	6
25	AY	50/60 (83%)	45 (90%)	5 (10%)	7	24
26	AZ	51/54 (94%)	47 (92%)	4 (8%)	11	32
29	AU	72/113 (64%)	58 (81%)	14 (19%)	1	7
30	BA	198/198 (100%)	179 (90%)	19 (10%)	8	25
31	BB	189/196 (96%)	173 (92%)	16 (8%)	10	29
32	BC	315/323 (98%)	258 (82%)	57 (18%)	2	9
33	BD	253/289 (88%)	219 (87%)	34 (13%)	4	14
34	BE	145/150 (97%)	118 (81%)	27 (19%)	1	8
35	BG	153/153 (100%)	124 (81%)	29 (19%)	1	8
36	BF	170/171 (99%)	156 (92%)	14 (8%)	10	31
37	BH	154/208 (74%)	136 (88%)	18 (12%)	5	18
38	Bs	216/254 (85%)	210 (97%)	6 (3%)	38	60
39	BJ	102/136 (75%)	93 (91%)	9 (9%)	9	28
40	BK	162/162 (100%)	139 (86%)	23 (14%)	3	13
41	BN	109/109 (100%)	88 (81%)	21 (19%)	1	7
42	BM	101/105 (96%)	86 (85%)	15 (15%)	3	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	BP	165/176 (94%)	141 (86%)	24 (14%)	3	13
44	BO	119/119 (100%)	104 (87%)	15 (13%)	4	16
45	BR	131/151 (87%)	107 (82%)	24 (18%)	2	8
46	BT	154/154 (100%)	140 (91%)	14 (9%)	9	27
47	BU	132/137 (96%)	111 (84%)	21 (16%)	2	11
48	BW	90/107 (84%)	76 (84%)	14 (16%)	2	12
49	BV	131/137 (96%)	116 (88%)	15 (12%)	5	18
50	BX	106/118 (90%)	97 (92%)	9 (8%)	10	29
51	BZ	59/129 (46%)	49 (83%)	10 (17%)	2	10
52	BY	107/107 (100%)	93 (87%)	14 (13%)	4	15
53	Ba	73/116 (63%)	60 (82%)	13 (18%)	2	9
54	Bd	15/47 (32%)	13 (87%)	2 (13%)	4	14
55	Bc	104/105 (99%)	90 (86%)	14 (14%)	4	14
56	Bf	83/88 (94%)	74 (89%)	9 (11%)	6	21
57	Be	202/205 (98%)	180 (89%)	22 (11%)	6	21
58	Bg	90/97 (93%)	77 (86%)	13 (14%)	3	13
59	Bh	111/111 (100%)	94 (85%)	17 (15%)	3	12
60	Bi	99/101 (98%)	84 (85%)	15 (15%)	3	12
61	Bj	71/91 (78%)	61 (86%)	10 (14%)	3	13
62	Bk	64/82 (78%)	58 (91%)	6 (9%)	8	26
63	Bm	72/72 (100%)	69 (96%)	3 (4%)	26	48
64	Bl	68/71 (96%)	60 (88%)	8 (12%)	5	18
65	Bn	66/69 (96%)	51 (77%)	15 (23%)	1	6
66	Bo	46/46 (100%)	38 (83%)	8 (17%)	2	9
67	Bp	37/47 (79%)	35 (95%)	2 (5%)	20	41
68	Bq	23/23 (100%)	22 (96%)	1 (4%)	26	47
69	Br	87/91 (96%)	77 (88%)	10 (12%)	5	18
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%)	26	47
73	Bw	47/74 (64%)	46 (98%)	1 (2%)	47	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
74	BQ	238/245 (97%)	201 (84%)	37 (16%)	2	12
76	BS	153/153 (100%)	116 (76%)	37 (24%)	1	4
77	BI	151/187 (81%)	134 (89%)	17 (11%)	5	19
All	All	8278/9418 (88%)	7252 (88%)	1026 (12%)	7	17

5 of 1026 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
69	Br	50	PHE
74	BQ	144	VAL
69	Br	47	GLN
32	BC	249	VAL
32	BC	160	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 219 such sidechains are listed below:

Mol	Chain	Res	Type
37	BH	155	ASN
44	BO	49	HIS
60	Bi	52	GLN
38	Bs	32	ASN
41	BN	56	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
78	CA	1471/1800 (81%)	511 (34%)	209 (14%)
79	CB	74/75 (98%)	26 (35%)	10 (13%)
80	CC	10/11 (90%)	7 (70%)	1 (10%)
81	DA	3140/3396 (92%)	1252 (39%)	607 (19%)
82	DB	141/158 (89%)	65 (46%)	36 (25%)
83	DC	117/118 (99%)	60 (51%)	26 (22%)
All	All	4953/5558 (89%)	1921 (38%)	889 (17%)

5 of 1921 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
78	CA	3	U
78	CA	4	C

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Mol	Chain	Res	Type
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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
78	CA	4
44	BO	3
23	AW	1
80	CC	1

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Mol	Chain	Number of breaks
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

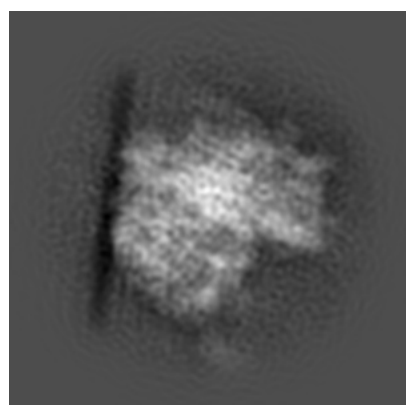
6 Map visualisation [i](#)

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.

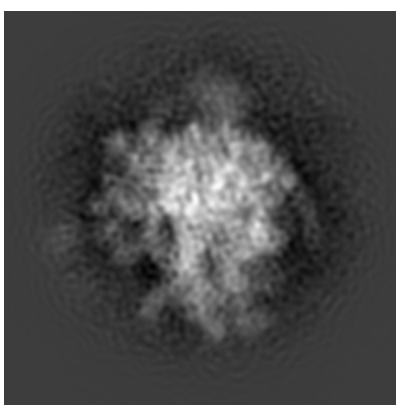
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

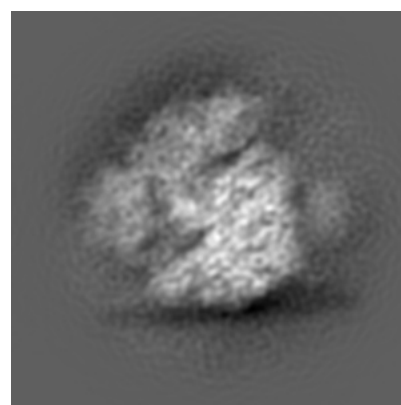
6.1.1 Primary map



X



Y

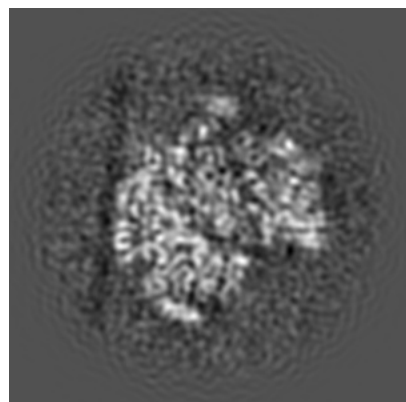


Z

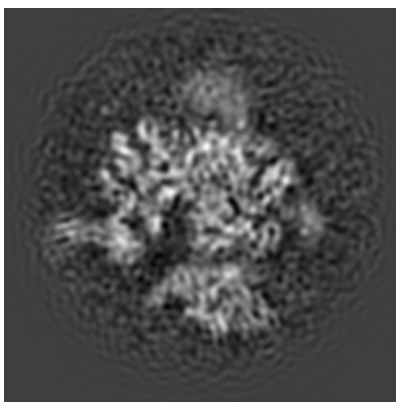
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

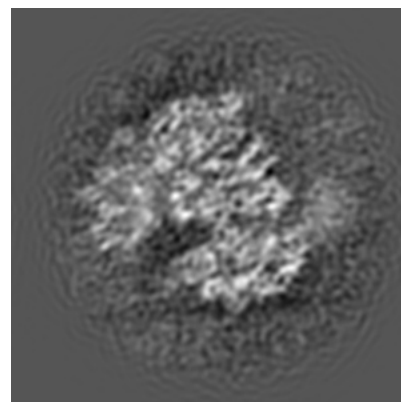
6.2.1 Primary map



X Index: 184



Y Index: 184

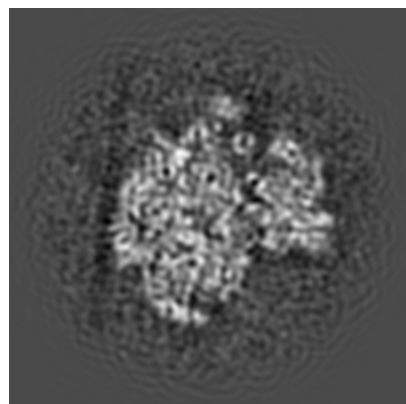


Z Index: 184

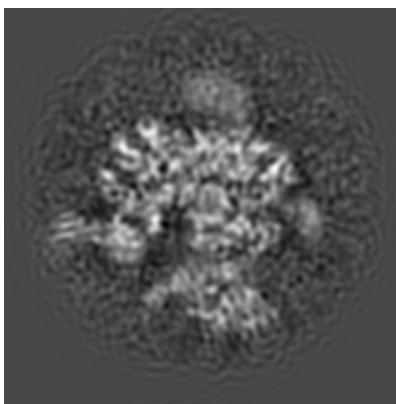
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

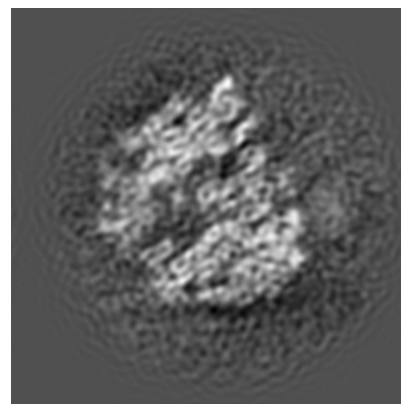
6.3.1 Primary map



X Index: 188



Y Index: 187

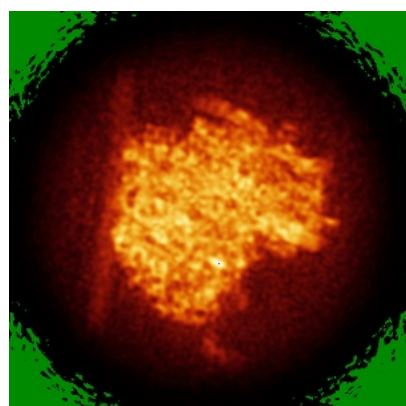


Z Index: 172

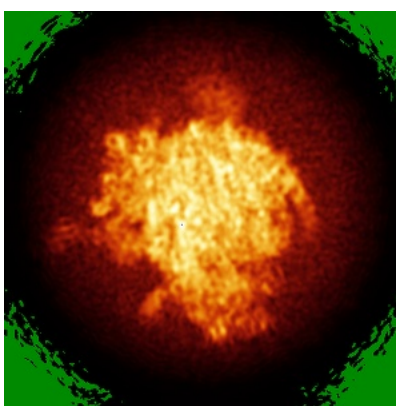
The images above show the largest variance slices of the map in three orthogonal directions.

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

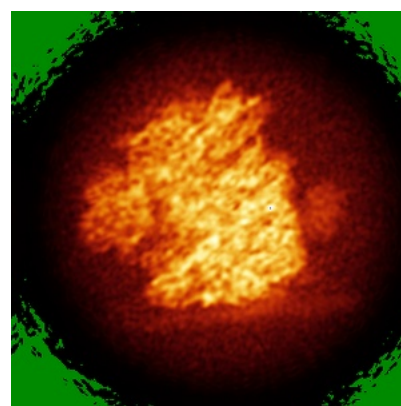
6.4.1 Primary map



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 1.75. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

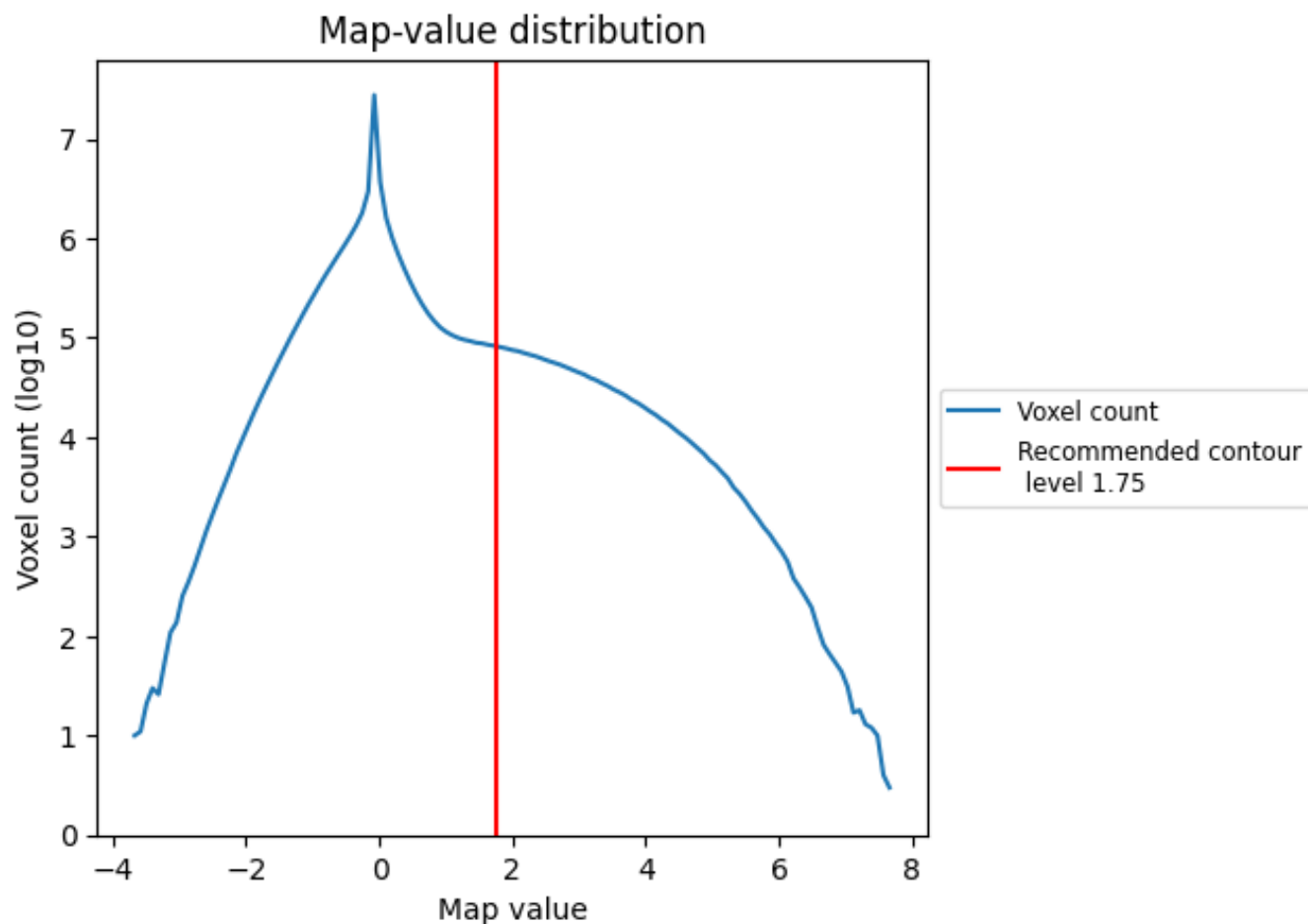
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

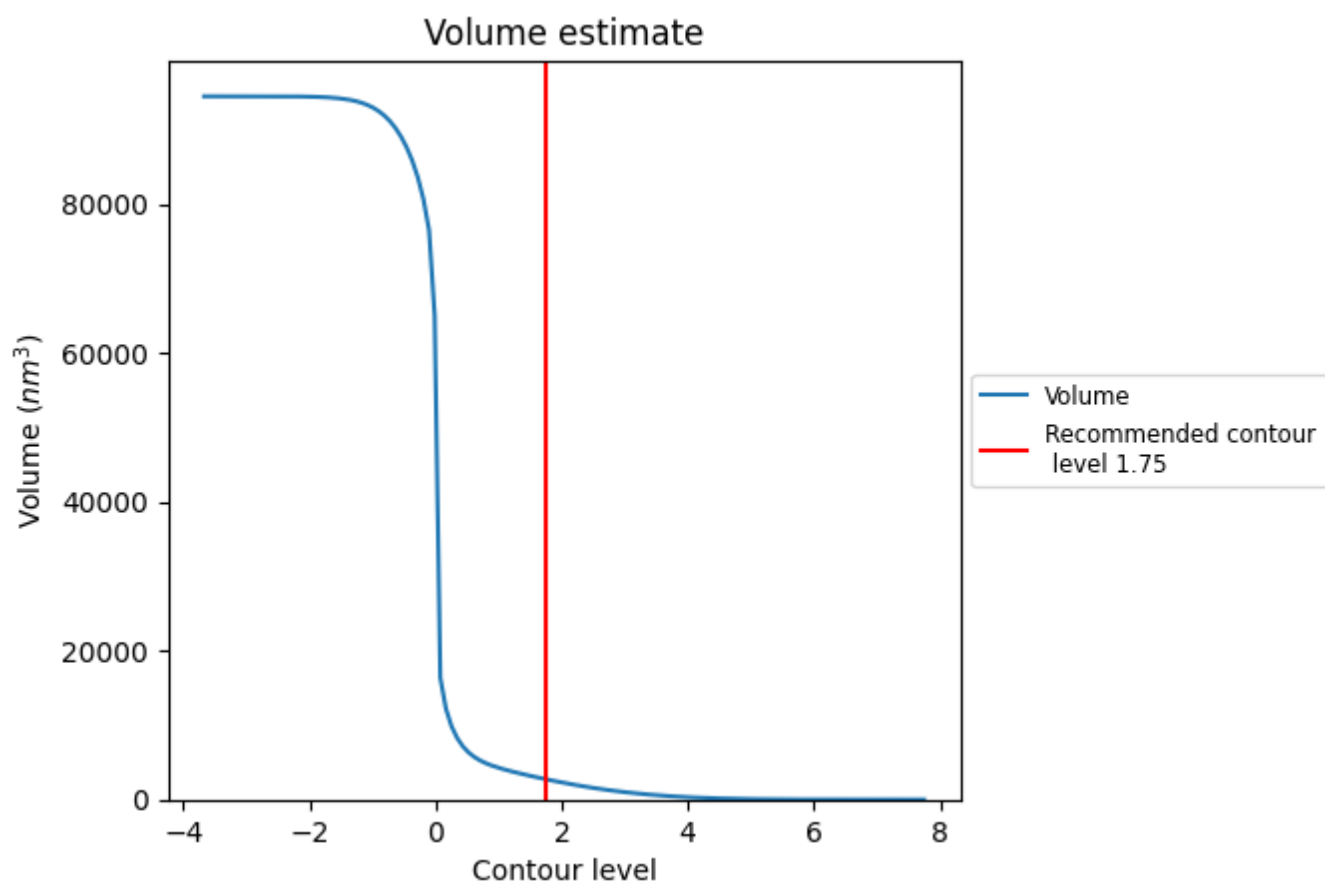
This section contains the results of statistical analysis of the map.

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.

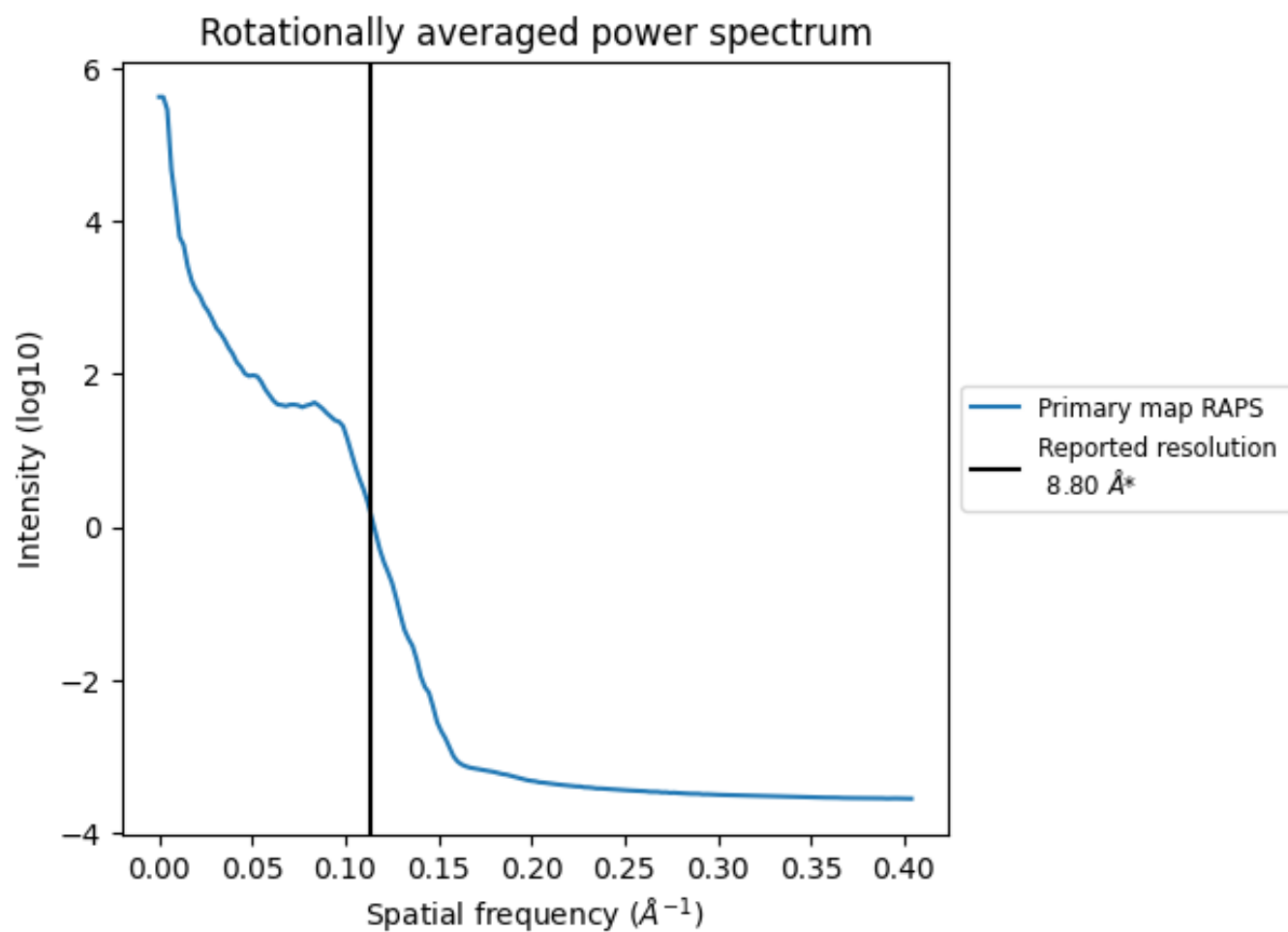
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 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

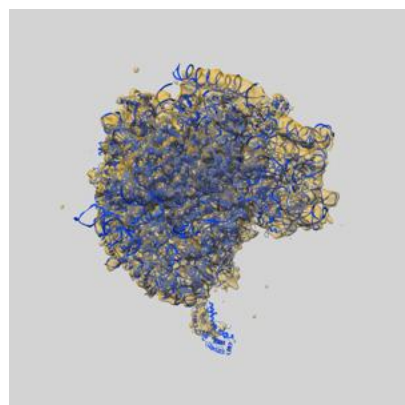
8 Fourier-Shell correlation

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

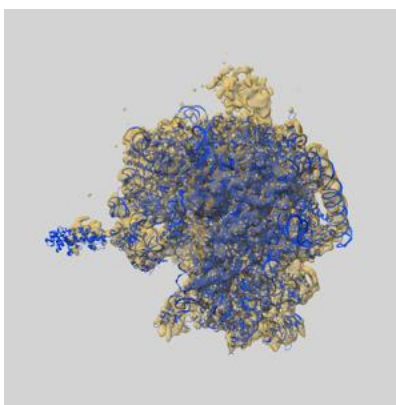
9 Map-model fit [i](#)

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.

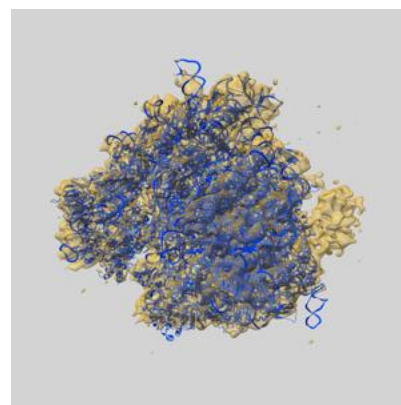
9.1 Map-model overlay [i](#)



X



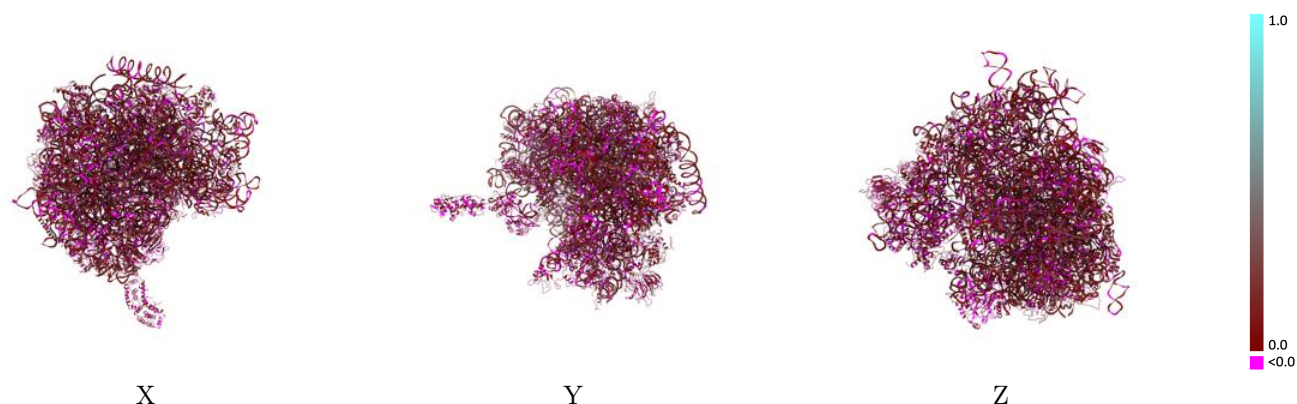
Y



Z

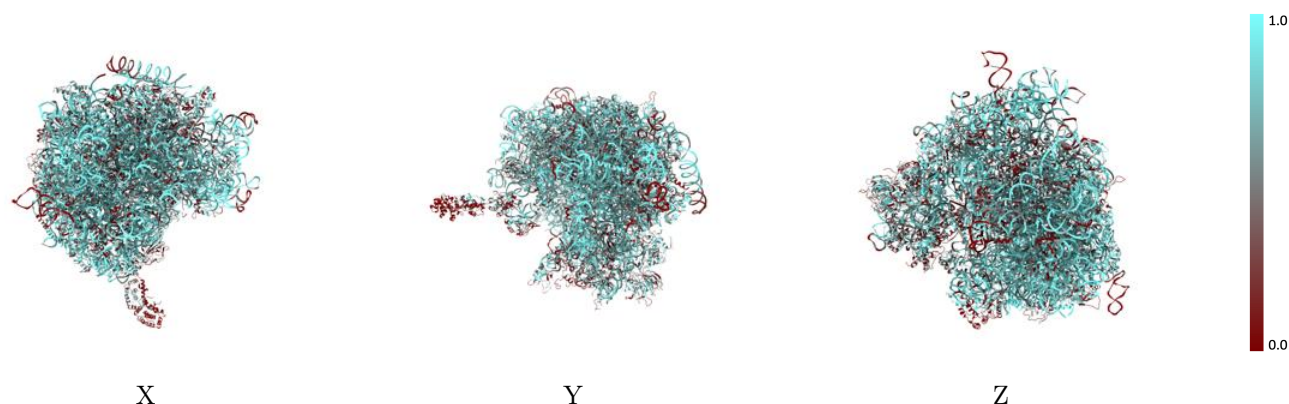
The images above show the 3D surface view of the map at the recommended contour level 1.75 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



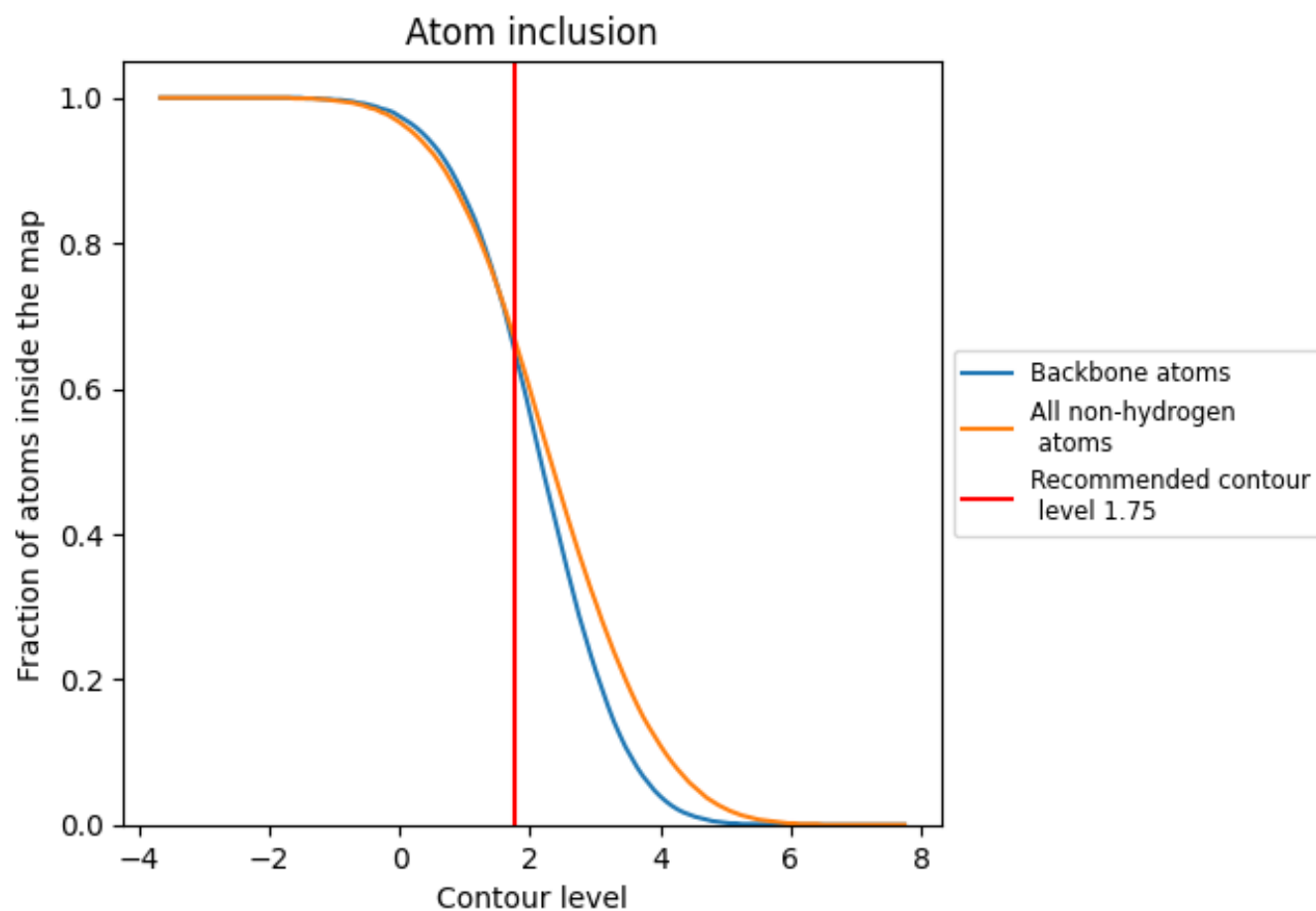
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.6070	 0.1010
AB	 0.4530	 0.0770
AC	 0.5850	 0.0770
AD	 0.5780	 0.0860
AE	 0.5530	 0.0920
AF	 0.5030	 0.0710
AG	 0.6840	 0.1610
AH	 0.5130	 0.0870
AI	 0.5430	 0.0530
AJ	 0.5000	 0.0680
AK	 0.5770	 0.0700
AL	 0.6540	 0.0570
AM	 0.2950	 0.0500
AN	 0.3770	 0.0420
AO	 0.4520	 0.0830
AP	 0.4140	 0.0750
AQ	 0.3000	 0.0670
AR	 0.3300	 0.0730
AS	 0.5260	 0.0540
AT	 0.4160	 0.1050
AU	 0.5370	 0.0730
AV	 0.3770	 0.0800
AW	 0.7200	 0.1670
AX	 0.4820	 0.0650
AY	 0.3320	 0.0120
AZ	 0.4960	 0.0540
Aa	 0.4650	 0.0690
Ab	 0.8670	 0.2310
Ac	 0.6350	 0.2370
BA	 0.2180	 0.0010
BB	 0.4620	 0.0460
BC	 0.5830	 0.0580
BD	 0.5840	 0.0660
BE	 0.5590	 0.0870



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Chain	Atom inclusion	Q-score
BF	 0.5300	 0.0860
BG	 0.5860	 0.0780
BH	 0.6210	 0.0830
BI	 0.6600	 0.0620
BJ	 0.3380	 0.0300
BK	 0.5740	 0.0870
BL	 0.7800	 0.1700
BM	 0.2620	 0.0860
BN	 0.6400	 0.0980
BO	 0.4910	 0.0400
BP	 0.5560	 0.0370
BQ	 0.7450	 0.0620
BR	 0.5520	 0.1000
BS	 0.5020	 0.0650
BT	 0.4790	 0.0960
BU	 0.6290	 0.0650
BV	 0.5070	 0.0570
BW	 0.6070	 0.0800
BX	 0.5130	 0.0770
BY	 0.6950	 0.0860
BZ	 0.3940	 0.0600
Ba	 0.4830	 0.0350
Bc	 0.7380	 0.1170
Bd	 0.6180	 0.0590
Be	 0.5650	 0.0900
Bf	 0.4790	 0.1190
Bg	 0.5580	 0.0760
Bh	 0.4620	 0.0730
Bi	 0.4370	 0.0580
Bj	 0.4450	 0.0490
Bk	 0.6900	 0.0950
Bl	 0.6730	 0.0500
Bm	 0.3920	 0.0810
Bn	 0.5630	 0.0860
Bo	 0.4720	 0.0500
Bp	 0.4370	 -0.0300
Bq	 0.4880	 0.1170
Br	 0.4650	 0.0650
Bs	 0.2770	 0.0350
Bt	 0.3560	 0.0260
Bu	 0.0000	 0.0530
Bv	 0.2740	 0.0480

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Chain	Atom inclusion	Q-score
Bw	 0.0370	 0.0100
Bx	 0.7900	 0.1580
By	 0.9100	 0.2380
Bz	 0.6140	 0.2150
CA	 0.7890	 0.1050
CB	 0.0690	 0.0440
CC	 0.1440	 -0.0370
DA	 0.7960	 0.1160
DB	 0.8120	 0.1140
DC	 0.9130	 0.1250