wwPDB EM Validation Summary Report

Oct 13, 2024 – 10:49 pm BST

PDB ID	:	4V8M
EMDB ID	:	EMD-2239
Title	:	High-resolution cryo-electron microscopy structure of the Trypanosoma brucei ribosome
Authors	:	Hashem, Y.; des Georges, A.; Fu, J.; Buss, S.N.; Jossinet, F.; Jobe, A.; Zhang, Q.; Liao, H.Y.; Grassucci, R.A.; Bajaj, C.; Westhof, E.; Madison-Antenucci, S.; Frank, J.
Deposited on	:	2012-12-09
Resolution	:	5.57 Å(reported)
Based on initial models	:	3U5G, 2XZM, 4A1B, 4A1A, 4A19, 3U5B, 3U5I, 3U5F, 3IZ6, 4A1E, 3IZR, 2XZN, 3U5C, 3U5E, 4A1C, 3IZ7, 3IZ9, 4A17, 4A18, 4A1D, 3U5D, 3U5H

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 (i) 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 (i)) were used in the production of this report:

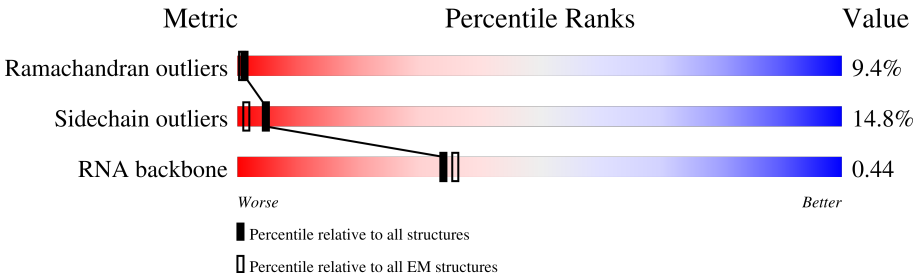
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 5.57 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	A0	256	30% 55% 22% 7% • 14%
2	A1	273	24% 58% 26% 5% • 9%
3	A2	190	62% 69% 18% 10% • •
4	A3	250	25% 64% 26% 8% •
5	A4	202	17% 52% 29% 11% • 5%
6	A5	220	35% 60% 20% 6% • 11%
7	A6	190	17% 61% 25% 9% • •
8	A7	318	68% 74% 21% • •

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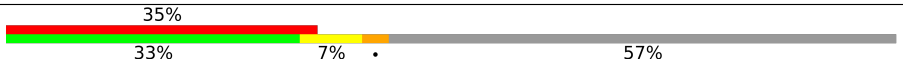
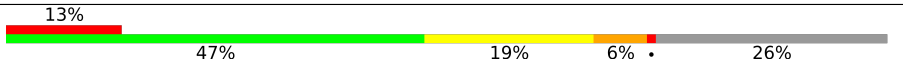
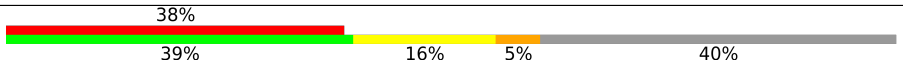
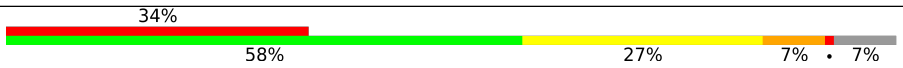
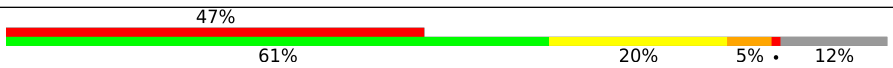
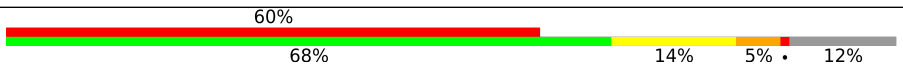
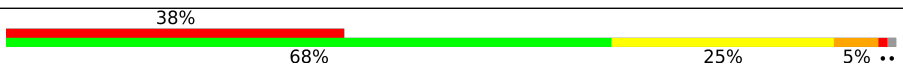
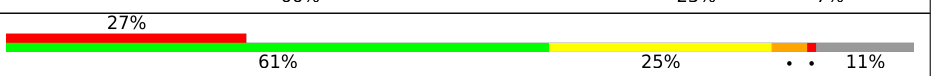
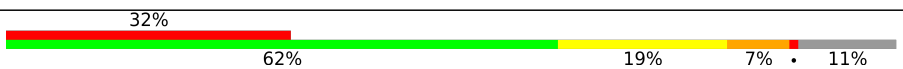
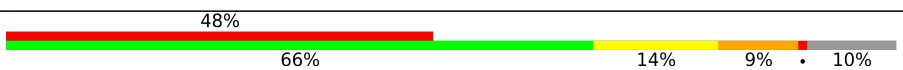
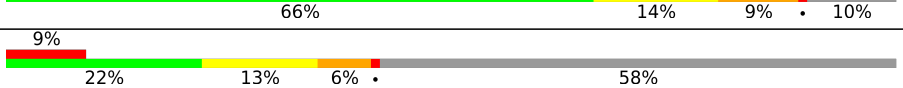
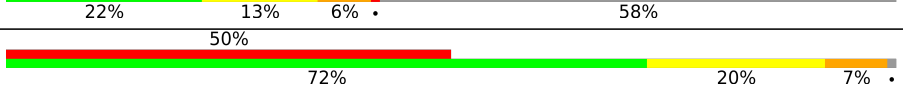
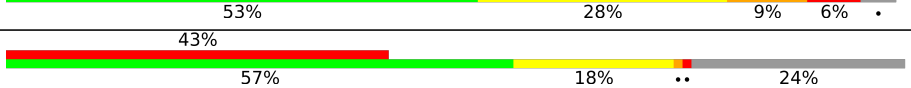
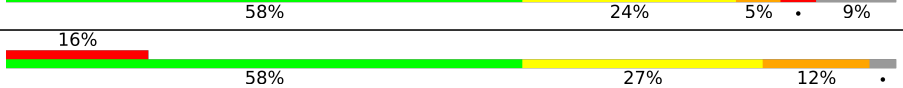
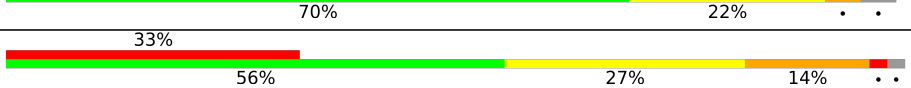
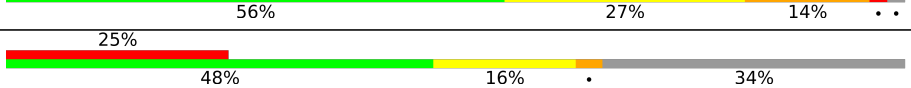
Mol	Chain	Length	Quality of chain
9	A8	57	
10	A9	153	
11	AC	277	
12	AD	172	
13	AE	174	
14	AF	144	
15	AG	151	
16	AH	144	
17	AI	152	
18	AJ	130	
19	AK	149	
20	AL	142	
21	AM	153	
22	AO	167	
23	AP	266	
24	AQ	117	
25	AR	194	
26	AS	143	
27	AT	137	
28	AU	113	
29	AV	111	
30	AW	86	
31	AX	214	
32	AY	66	
33	AZ	103	

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Mol	Chain	Length	Quality of chain
34	BA	1847	6% 17% 54% 29%
35	BB	1465	16% 23% 52% 23%
36	BC	169	19% 56% 25%
37	BD	119	18% 60% 23%
38	BE	210	9% 12% 54% 34%
39	BF	73	7% 30% 63%
40	BG	182	17% 64% 19%
41	BH	135	14% 24% 47% 29%
42	BI	193	27% 51% 37% 9%
43	BJ	214	100% 87% 11%
44	BK	213	24% 60% 28% 9%
45	BL	194	8% 58% 23% 12%
46	BM	164	84% 74% 10% 15%
47	BN	218	16% 50% 28% 16% 6%
48	BO	222	20% 59% 23% 7% 9%
49	BP	189	9% 62% 27% 5%
50	BQ	221	26% 54% 28% 8% 8%
51	BR	166	27% 54% 30% 8% 7%
52	BS	179	30% 54% 31% 11%
53	BT	260	13% 49% 18% 8% 23%
54	BU	159	33% 62% 24% 9%
55	BV	130	75% 61% 15% 20%
56	BW	139	17% 62% 26% 9%
57	BX	164	14% 49% 18% 26%
58	BY	125	46% 50% 22% 6% 20%

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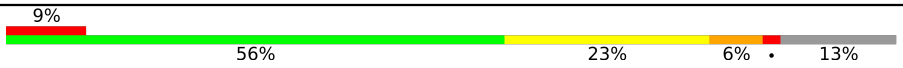
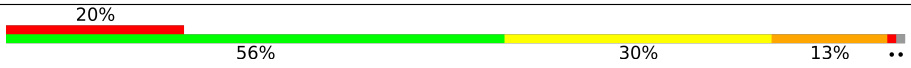
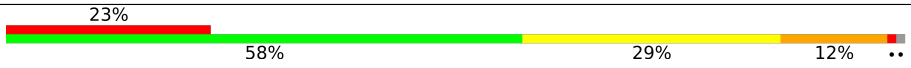
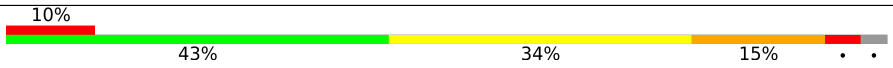
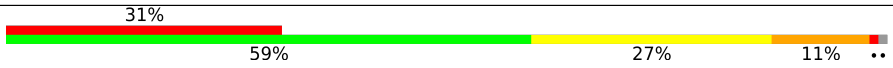
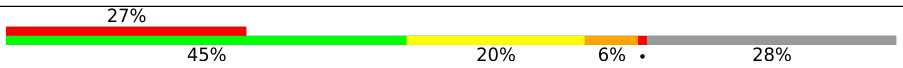
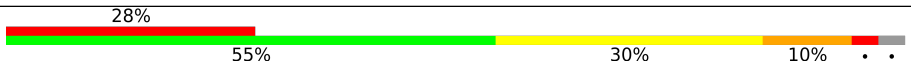
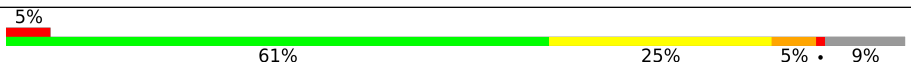
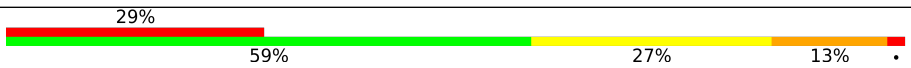
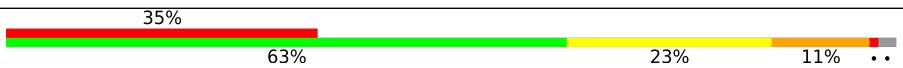
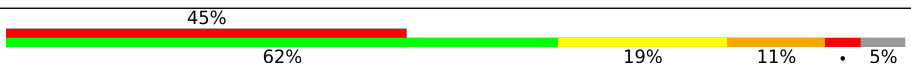
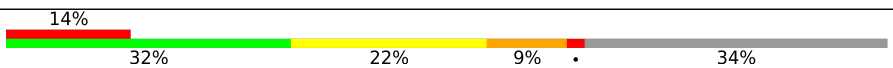
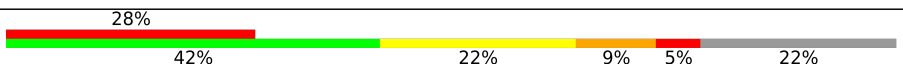
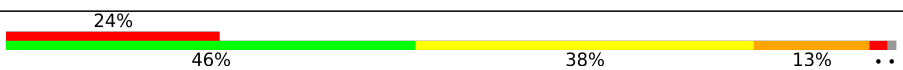
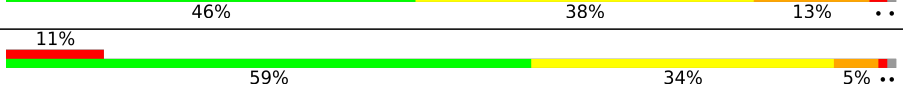
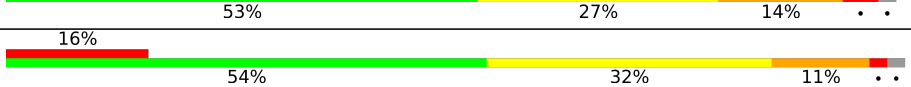
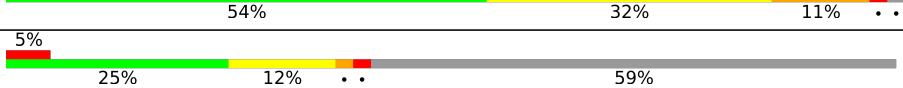
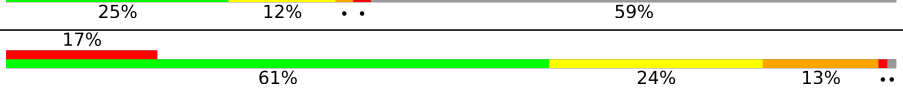
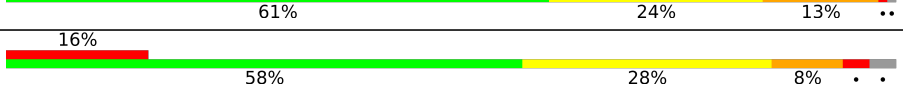
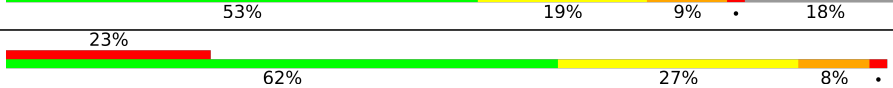
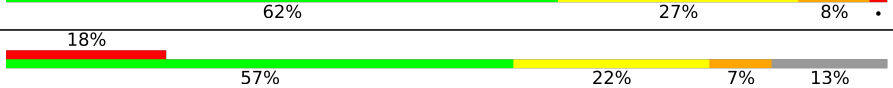
Mol	Chain	Length	Quality of chain
59	BZ	143	
60	Ba	133	
61	Bb	145	
62	Bc	146	
63	Bd	71	
64	Be	260	
65	Bf	429	
66	Bg	105	
67	Bh	188	
68	Bi	132	
69	Bj	170	
70	Bk	127	
71	Bl	149	
72	Bm	109	
73	Bn	84	
74	Bo	93	
75	Bp	82	
76	Bq	51	
77	Br	374	
78	Bs	128	
79	Bt	106	
80	Bu	308	
81	Bv	192	
82	Bw	257	
83	Bx	276	

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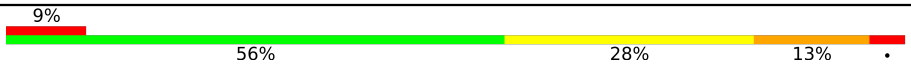
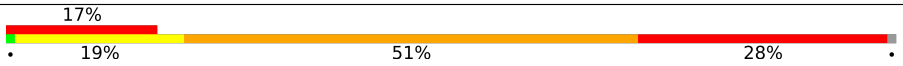
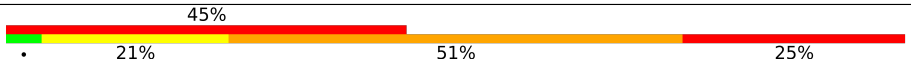
Mol	Chain	Length	Quality of chain
84	By	189	
85	AA	2251	
86	AB	73	

2 Entry composition (i)

There are 86 unique types of molecules in this entry. The entry contains 232955 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 S3A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A0	219	1782	1124	337	313	8	0	1

- Molecule 2 is a protein called 40S RIBOSOMAL PROTEIN S4, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A1	248	1940	1232	360	339	9	0	1

- Molecule 3 is a protein called 40S RIBOSOMAL PROTEIN S5, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	A2	187	1484	928	286	265	5	0	0

- Molecule 4 is a protein called 40S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A3	250	2003	1243	415	341	4	0	0

- Molecule 5 is a protein called RIBOSOMAL PROTEIN S7, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A4	192	1592	1014	310	263	5	0	1

- Molecule 6 is a protein called 40S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	A5	195	1551	975	315	259	2	0	1

- Molecule 7 is a protein called 40S RIBOSOMAL PROTEIN S9, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A6	187	Total	C	N	O	S	0	1
			1518	951	307	253	7		

- Molecule 8 is a protein called GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A7	315	Total	C	N	O	S	0	1
			2412	1508	429	462	13		

- Molecule 9 is a protein called RIBOSOMAL PROTEIN S29, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A8	42	Total	C	N	O	S	0	0
			334	204	69	57	4		

- Molecule 10 is a protein called UBIQUITIN/RIBOSOMAL PROTEIN S27A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A9	66	Total	C	N	O	S	0	1
			530	330	102	91	7		

- Molecule 11 is a protein called 40S RIBOSOMAL PROTEIN SA, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AC	204	Total	C	N	O	S	0	1
			1620	1034	293	282	11		

- Molecule 12 is a protein called 40S RIBOSOMAL PROTEIN S10, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AD	104	Total	C	N	O	S	0	1
			853	553	148	147	5		

- Molecule 13 is a protein called 40S RIBOSOMAL PROTEINS S11, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AE	160	Total	C	N	O	S	0	0
			1300	812	262	220	6		

- Molecule 14 is a protein called 40S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AF	121	Total	C	N	O	S	0	0
			940	578	169	184	9		

- Molecule 15 is a protein called 40S RIBOSOMAL PROTEIN S13, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AG	141	Total	C	N	O	S	0	0
			1148	724	227	190	7		

- Molecule 16 is a protein called 40S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AH	126	Total	C	N	O	S	0	1
			922	572	167	174	9		

- Molecule 17 is a protein called 40S RIBOSOMAL PROTEIN S15, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AI	134	Total	C	N	O	S	0	1
			1074	679	211	181	3		

- Molecule 18 is a protein called 40S RIBOSOMAL PROTEIN S15A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AJ	129	Total	C	N	O	S	0	0
			1018	645	191	174	8		

- Molecule 19 is a protein called 40S RIBOSOMAL PROTEIN S16, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AK	148	Total	C	N	O	S	0	0
			1190	757	225	205	3		

- Molecule 20 is a protein called 40S RIBOSOMAL PROTEIN S17, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AL	127	Total	C	N	O	S	0	1
			1021	641	198	177	5		

- Molecule 21 is a protein called 40S RIBOSOMAL PROTEIN S18, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AM	153	Total	C	N	O	S	0	0
			1229	764	244	215	6		

- Molecule 22 is a protein called RIBOSOMAL PROTEIN S19, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AO	149	Total	C	N	O	S	0	0
			1181	746	230	196	9		

- Molecule 23 is a protein called 40S RIBOSOMAL PROTEIN S2, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AP	224	Total	C	N	O	S	0	1
			1731	1103	309	310	9		

- Molecule 24 is a protein called RIBOSOMAL PROTEIN S20, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AQ	105	Total	C	N	O	S	0	1
			827	522	153	149	3		

- Molecule 25 is a protein called 40S RIBOSOMAL PROTEIN S21, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AR	81	Total	C	N	O	S	0	1
			603	374	108	118	3		

- Molecule 26 is a protein called 40S RIBOSOMAL PROTEIN S23, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AS	142	Total	C	N	O	S	0	0
			1116	706	219	189	2		

- Molecule 27 is a protein called 40S RIBOSOMAL PROTEIN S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AT	131	Total	C	N	O	S	0	0
			1050	666	206	174	4		

- Molecule 28 is a protein called 40S RIBOSOMAL PROTEIN S25, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AU	86	Total	C	N	O	S	0	1
			673	427	127	114	5		

- Molecule 29 is a protein called RIBOSOMAL PROTEIN S26, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AV	101	Total	C	N	O	S	0	1
			809	498	172	131	8		

- Molecule 30 is a protein called 40S RIBOSOMAL PROTEIN S27, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AW	83	Total	C	N	O	S	0	1
			636	396	120	111	9		

- Molecule 31 is a protein called 40S RIBOSOMAL PROTEIN S3, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AX	206	Total	C	N	O	S	0	1
			1628	1020	307	289	12		

- Molecule 32 is a protein called 40S RIBOSOMAL PROTEIN S30, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AY	65	Total	C	N	O	S	0	0
			514	322	107	84	1		

- Molecule 33 is a protein called 40S RIBOSOMAL PROTEIN S33, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AZ	68	Total	C	N	O	S	0	0
			526	315	107	100	4		

- Molecule 34 is a RNA chain called ALPHA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT 28S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BA	1847	Total	C	N	O	P	0	0
			39395	17589	7008	12952	1846		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BA	?	-	C	deletion	GB X14553
BA	?	-	U	deletion	GB X14553
BA	?	-	U	deletion	GB X14553
BA	?	-	C	deletion	GB X14553
BA	?	-	C	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	?	-	C	deletion	GB X14553
BA	?	-	C	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	?	-	U	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	799	A	-	insertion	GB X14553

- Molecule 35 is a RNA chain called BETA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT 28S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BB	1465	Total	C	N	O	P	0	0
			31164	13918	5476	10306	1464		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BB	484	G	-	insertion	GB X14553
BB	485	U	-	insertion	GB X14553
BB	486	G	-	insertion	GB X14553
BB	487	A	-	insertion	GB X14553

- Molecule 36 is a RNA chain called 5.8S RRNA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BC	169	Total	C	N	O	P	0	0
			3584	1604	629	1183	168		

- Molecule 37 is a RNA chain called 5S RRNA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BD	119	Total	C	N	O	P	0	0
			2533	1131	449	835	118		

- Molecule 38 is a RNA chain called SHORT RRNA-I OF THE LARGE RIBOSOMAL SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BE	210	Total	C	N	O	P	0	0
			4441	1986	768	1478	209		

- Molecule 39 is a RNA chain called SHORT RRNA-II OF THE LARGE RIBOSOMAL SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BF	73	Total	C	N	O	P	0	0
			1521	682	247	520	72		

- Molecule 40 is a RNA chain called SHORT RRNA-III OF THE LARGE RIBOSOMAL SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BG	182	Total	C	N	O	P	0	0
			3896	1737	706	1272	181		

- Molecule 41 is a RNA chain called SHORT RRNA-IV OF THE LARGE RIBOSOMAL SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BH	135	Total	C	N	O	P	0	0
			2867	1280	502	951	134		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BI	192	Total	C	N	O	S	0	0
			1527	956	315	248	8		

- Molecule 43 is a protein called RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BJ	214	Total	C	N	O	S	0	0
			1717	1086	308	307	16		

- Molecule 44 is a protein called 60S RIBOSOMAL PROTEIN L10, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BK	212	Total	C	N	O	S	0	0
			1725	1086	338	287	14		

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L11, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BL	170	Total	C	N	O	S	0	1
			1363	859	258	239	7		

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L12, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BM	139	Total	C	N	O	S	0	1
			1022	642	187	188	5		

- Molecule 47 is a protein called 60S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BN	216	Total	C	N	O	S	0	1
			1762	1097	366	292	7		

- Molecule 48 is a protein called 60S RIBOSOMAL PROTEIN L13A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BO	201	Total	C	N	O	S	0	1
			1627	1035	323	262	7		

- Molecule 49 is a protein called PROBABLE 60S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BP	184	Total	C	N	O	S	0	1
			1484	934	299	247	4		

- Molecule 50 is a protein called RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BQ	203	Total	C	N	O	S	0	0
			1716	1077	370	264	5		

- Molecule 51 is a protein called 60S RIBOSOMAL PROTEIN L17, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BR	155	Total	C	N	O	S	0	1
			1245	782	247	208	8		

- Molecule 52 is a protein called 60S RIBOSOMAL PROTEIN L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BS	179	Total	C	N	O	S	0	0
			1473	931	290	244	8		

- Molecule 53 is a protein called 60S RIBOSOMAL PROTEIN L19, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BT	200	Total	C	N	O	S	0	1
			1672	1025	366	273	8		

- Molecule 54 is a protein called 60S RIBOSOMAL PROTEIN L21E, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BU	158	Total	C	N	O	S	0	0
			1260	802	246	206	6		

- Molecule 55 is a protein called 60S RIBOSOMAL PROTEIN L22, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BV	104	Total	C	N	O	S	0	1
			863	558	152	150	3		

- Molecule 56 is a protein called 60S RIBOSOMAL PROTEIN L23, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BW	138	Total	C	N	O	S	0	0
			1042	659	198	180	5		

- Molecule 57 is a protein called 60S RIBOSOMAL PROTEIN L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BX	121	Total	C	N	O	S	0	0
			990	629	186	173	2		

- Molecule 58 is a protein called 60S RIBOSOMAL PROTEIN L24, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BY	100	Total	C	N	O	S	0	0
			836	530	171	130	5		

- Molecule 59 is a protein called 60S RIBOSOMAL PROTEIN L26, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BZ	125	Total	C	N	O	S	0	1
			1008	623	213	167	5		

- Molecule 60 is a protein called 60S RIBOSOMAL PROTEIN L27, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Ba	132	Total	C	N	O	S	0	0
			1091	691	222	175	3		

- Molecule 61 is a protein called 60S RIBOSOMAL PROTEIN L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Bb	144	Total	C	N	O	S	0	0
			1137	717	228	186	6		

- Molecule 62 is a protein called 60S RIBOSOMAL PROTEIN L28, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Bc	141	Total	C	N	O	S	0	1
			1129	704	226	191	8		

- Molecule 63 is a protein called 60S RIBOSOMAL PROTEIN L29, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Bd	70	Total	C	N	O	S	0	0
			571	349	128	93	1		

- Molecule 64 is a protein called 60S RIBOSOMAL PROTEIN L2, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Be	186	Total	C	N	O	S	0	1
			1390	859	284	237	10		

- Molecule 65 is a protein called RIBOSOMAL PROTEIN L3, MITOCHONDRIAL, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Bf	414	Total	C	N	O	S	0	1
			3317	2084	661	559	13		

- Molecule 66 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bg	96	Total	C	N	O	S	0	0
			735	457	132	141	5		

- Molecule 67 is a protein called 60S RIBOSOMAL SUBUNIT PROTEIN L31, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Bh	188	Total	C	N	O	S	0	0
			1526	961	309	250	6		

- Molecule 68 is a protein called 60S RIBOSOMAL PROTEIN L32, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Bi	129	Total	C	N	O	S	0	1
			1054	664	215	171	4		

- Molecule 69 is a protein called 60S RIBOSOMAL PROTEIN L34, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Bj	162	Total	C	N	O	S	0	1
			1293	801	286	202	4		

- Molecule 70 is a protein called 60S RIBOSOMAL PROTEIN L35, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bk	84	Total	C	N	O	S	0	0
			719	448	161	108	2		

- Molecule 71 is a protein called 60S RIBOSOMAL PROTEIN L35A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Bl	116	Total	C	N	O	S	0	0
			936	589	189	155	3		

- Molecule 72 is a protein called RIBOSOMAL PROTEIN L36, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bm	107	Total	C	N	O	S	0	1
			849	530	178	139	2		

- Molecule 73 is a protein called RIBOSOMAL PROTEIN L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bn	83	Total	C	N	O	S	0	0
			699	425	161	107	6		

- Molecule 74 is a protein called 60S RIBOSOMAL PROTEIN L37A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bo	92	Total	C	N	O	S	0	1
			715	442	148	119	6		

- Molecule 75 is a protein called 60S RIBOSOMAL PROTEIN L38, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Bp	81	Total	C	N	O	S	0	0
			656	411	130	111	4		

- Molecule 76 is a protein called 60S RIBOSOMAL PROTEIN L39, PUTATIVE.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	Bq	50	Total	C	N	O	0	0
			457	297	98	62		

- Molecule 77 is a protein called 60S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Br	368	Total	C	N	O	S	0	1
			2883	1802	576	488	17		

- Molecule 78 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bs	52	Total	C	N	O	S	0	0
			427	265	88	67	7		

- Molecule 79 is a protein called 60S RIBOSOMAL PROTEIN L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Bt	105	Total	C	N	O	S	0	0
			866	547	170	144	5		

- Molecule 80 is a protein called 60S RIBOSOMAL PROTEIN L5, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Bu	299	Total	C	N	O	S	0	1
			2354	1485	447	416	6		

- Molecule 81 is a protein called 60S RIBOSOMAL PROTEIN L6, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Bv	158	Total	C	N	O	S	0	1
			1222	776	228	215	3		

- Molecule 82 is a protein called 60S RIBOSOMAL PROTEIN L7, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Bw	257	Total	C	N	O	S	0	0
			2066	1316	394	345	11		

- Molecule 83 is a protein called 60S RIBOSOMAL PROTEIN L7A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Bx	240	Total	C	N	O	S	0	0
			1908	1198	375	329	6		

- Molecule 84 is a protein called 60S RIBOSOMAL PROTEIN L9, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	By	189	Total	C	N	O	S	0	0
			1540	975	284	277	4		

- Molecule 85 is a RNA chain called 18S RRNA OF THE SMALL RIBOSOMAL SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	AA	2227	Total	C	N	O	P	0	0
			47370	21162	8354	15629	2225		

- Molecule 86 is a RNA chain called E-SITE TRNA.

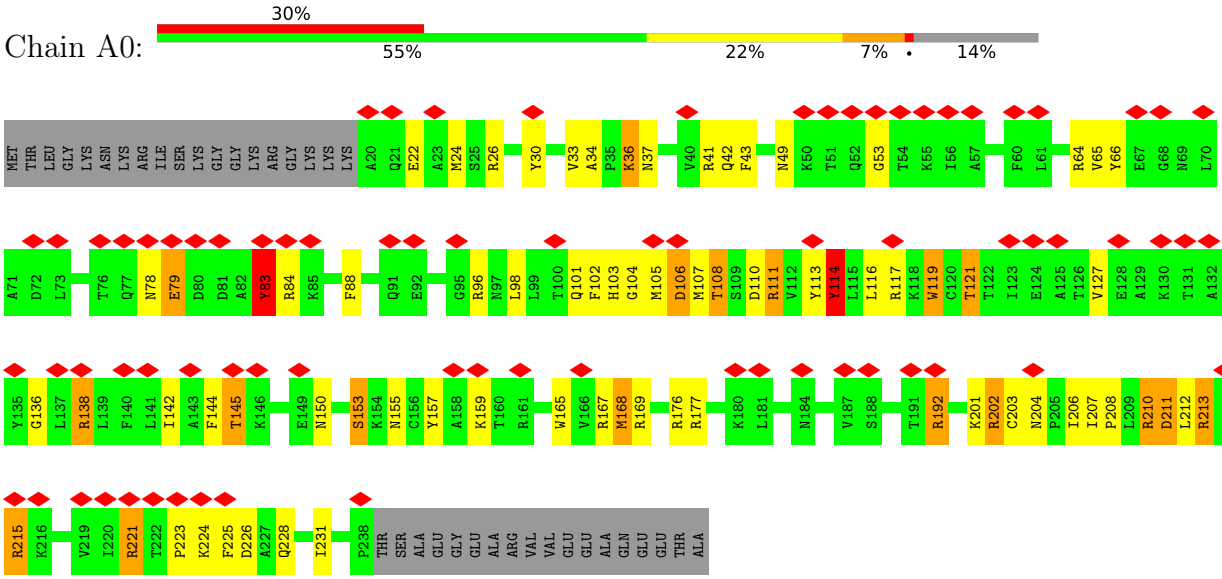
Mol	Chain	Residues	Atoms					AltConf	Trace
86	AB	73	Total	C	N	O	P	0	0
			1557	695	279	511	72		

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.

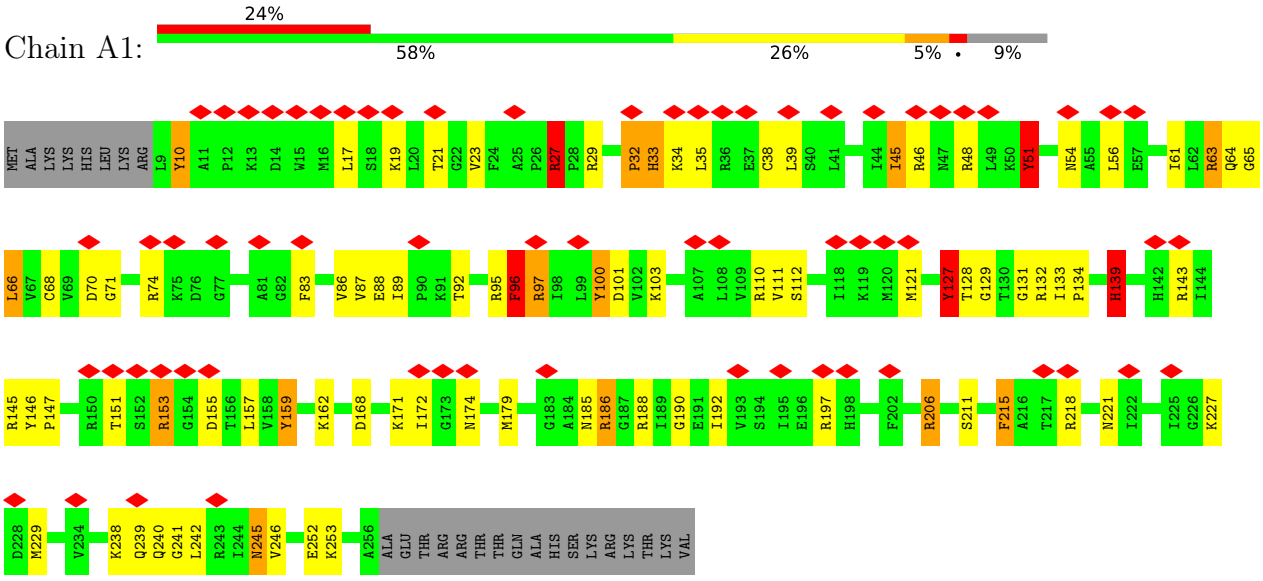
• Molecule 1: 40S RIBOSOMAL PROTEIN S3A, PUTATIVE

Chain A0:



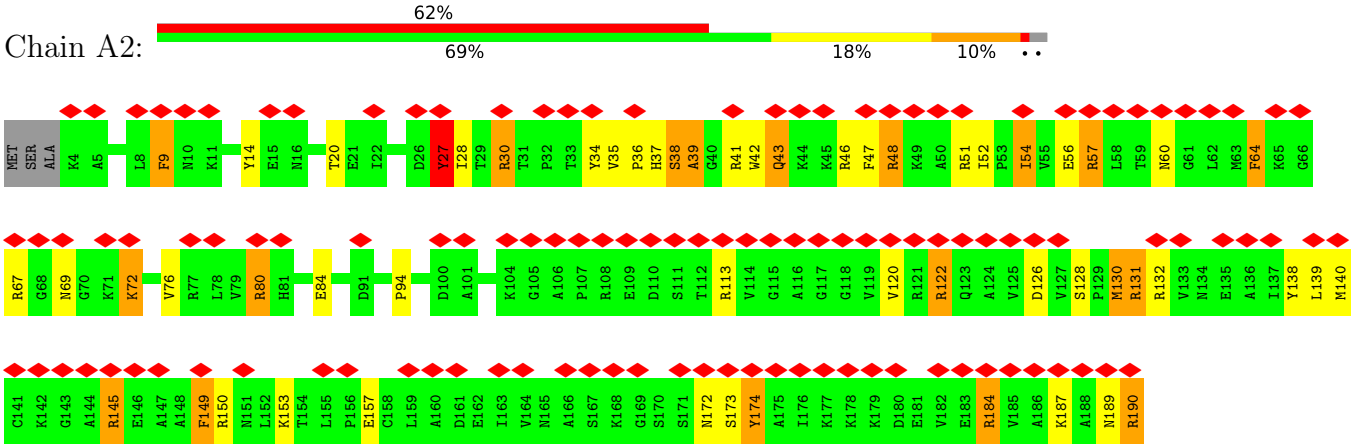
• Molecule 2: 40S RIBOSOMAL PROTEIN S4, PUTATIVE

Chain A1:



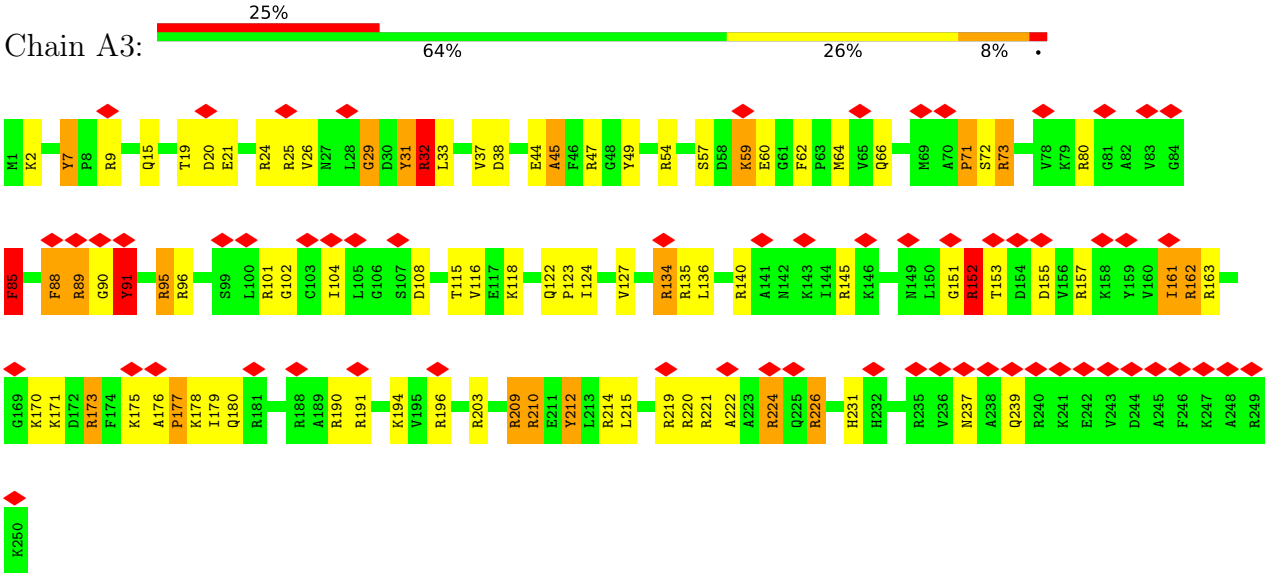
• Molecule 3: 40S RIBOSOMAL PROTEIN S5, PUTATIVE

Chain A2:



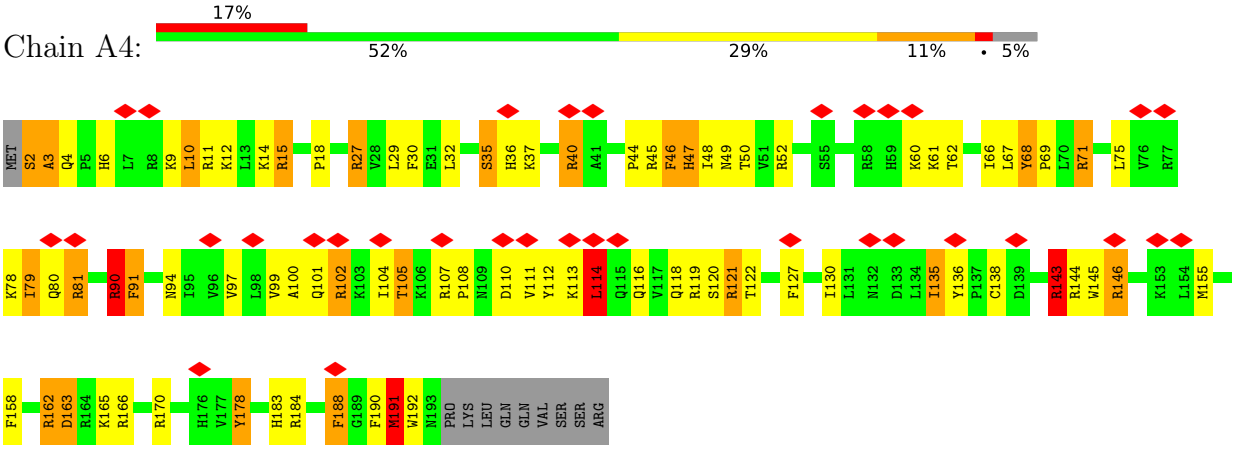
• Molecule 4: 40S RIBOSOMAL PROTEIN S6

Chain A3:



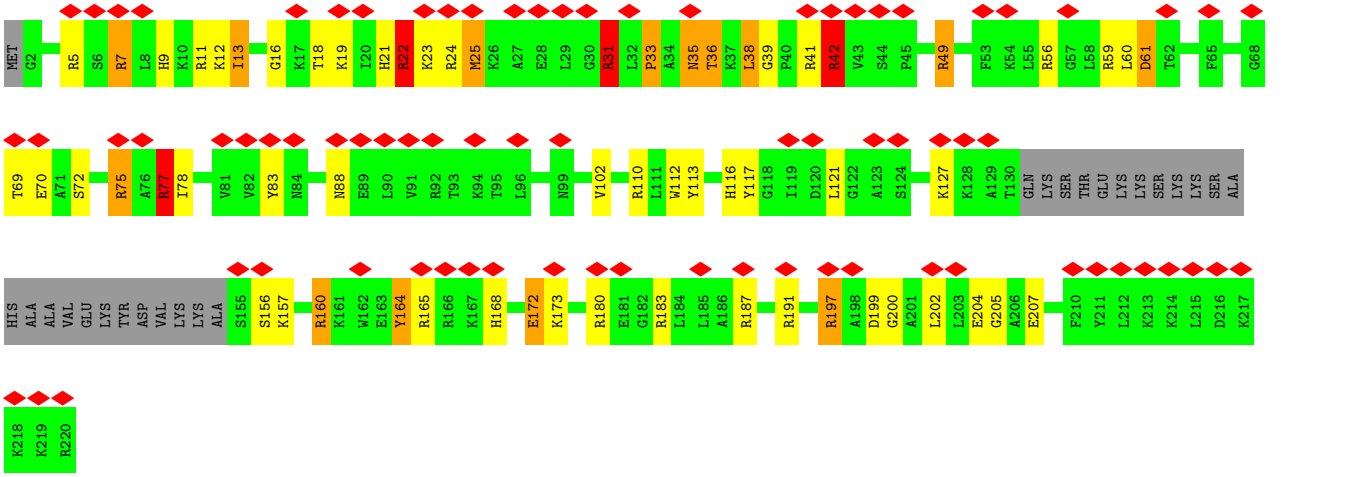
• Molecule 5: RIBOSOMAL PROTEIN S7, PUTATIVE

Chain A4:



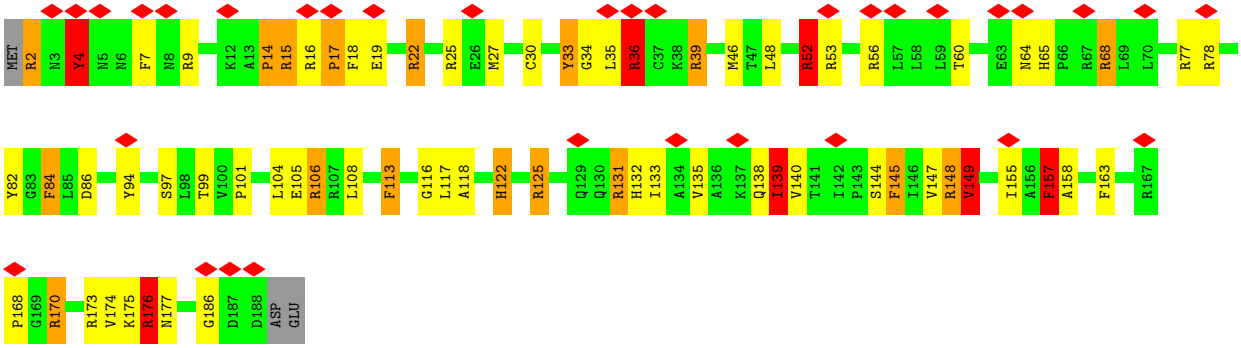
• Molecule 6: 40S RIBOSOMAL PROTEIN S8

Chain A5:



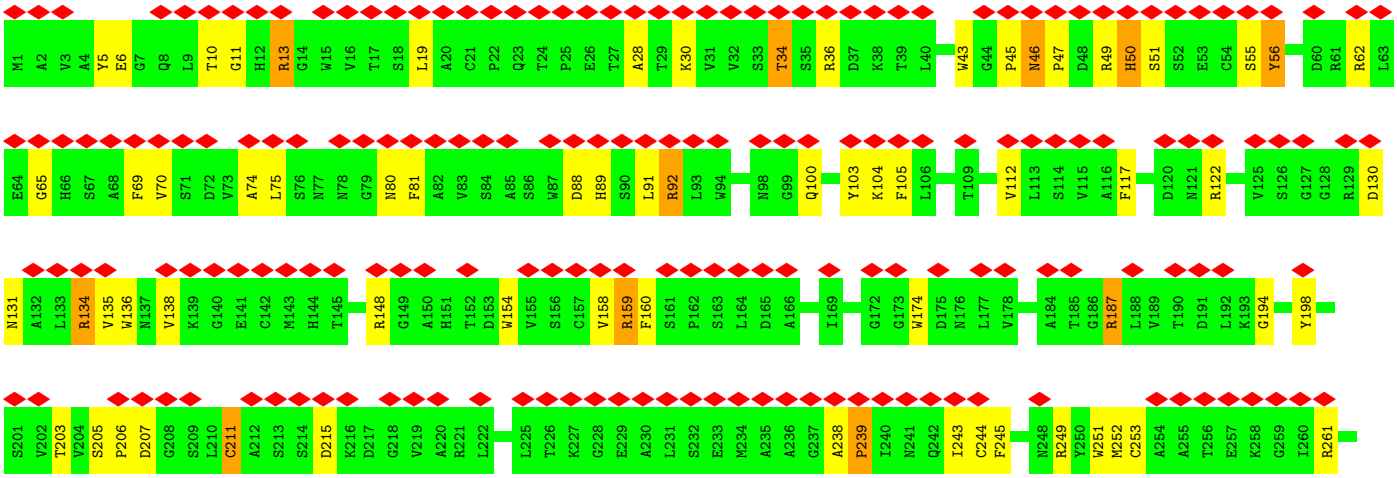
• Molecule 7: 40S RIBOSOMAL PROTEIN S9, PUTATIVE

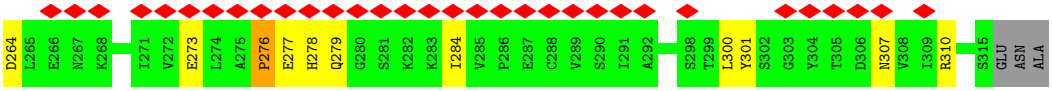
Chain A6:



• Molecule 8: GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN

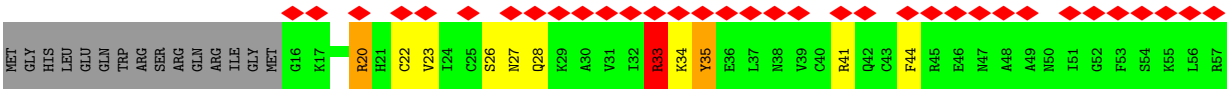
Chain A7:





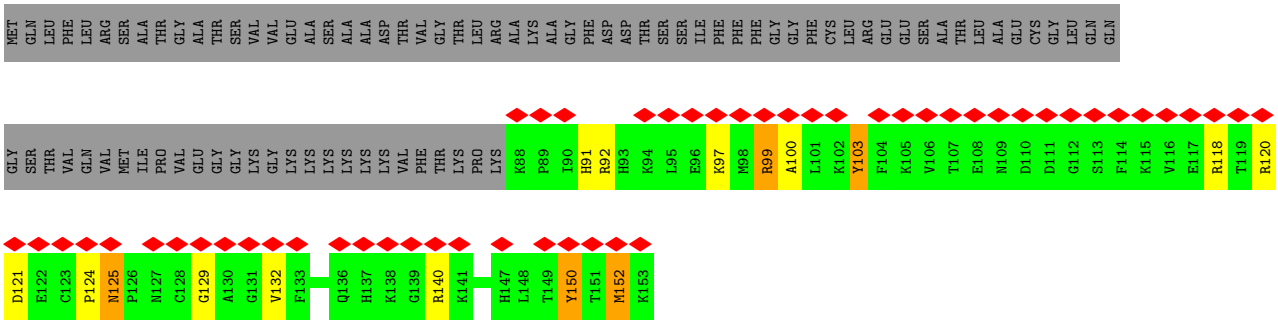
• Molecule 9: RIBOSOMAL PROTEIN S29, PUTATIVE

Chain A8:



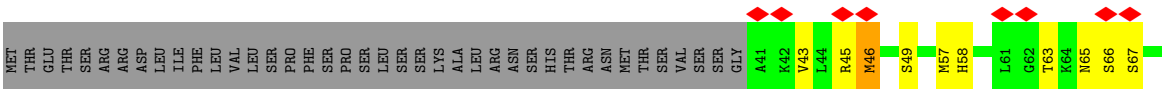
• Molecule 10: UBIQUITIN/RIBOSOMAL PROTEIN S27A, PUTATIVE

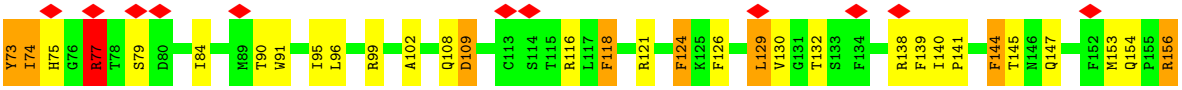
Chain A9:

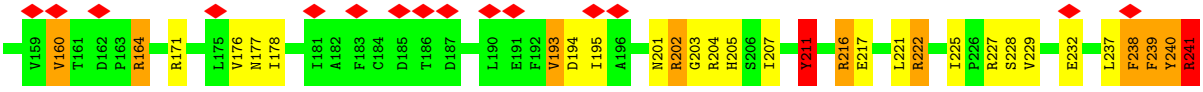


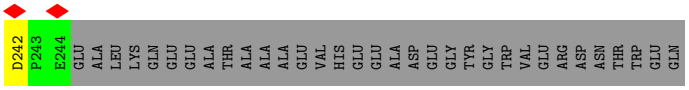
• Molecule 11: 40S RIBOSOMAL PROTEIN SA, PUTATIVE

Chain AC:



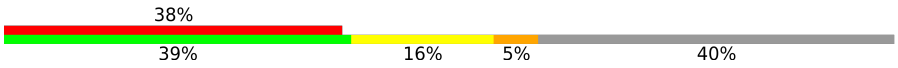


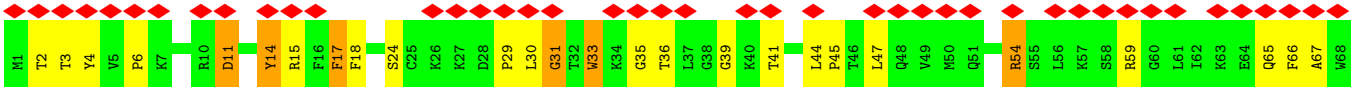


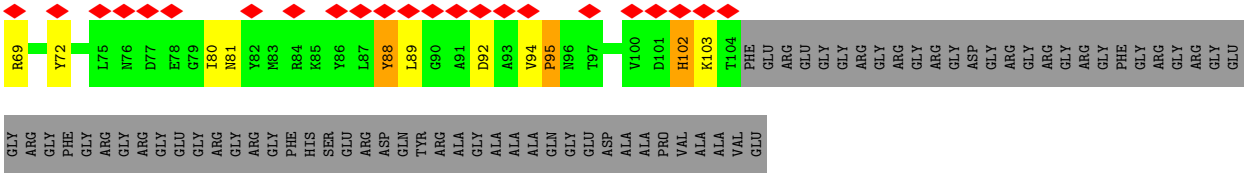


• Molecule 12: 40S RIBOSOMAL PROTEIN S10, PUTATIVE

Chain AD:

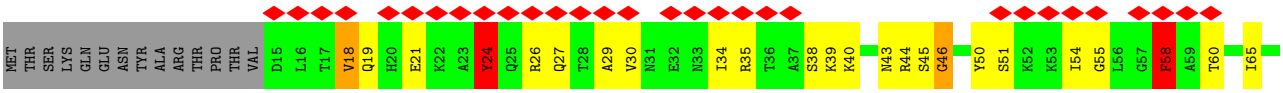


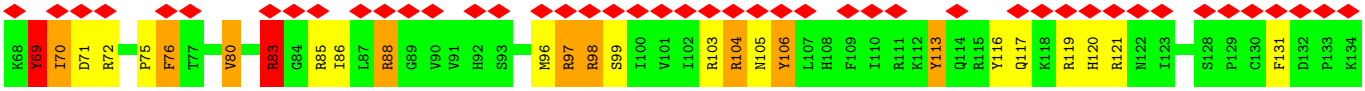


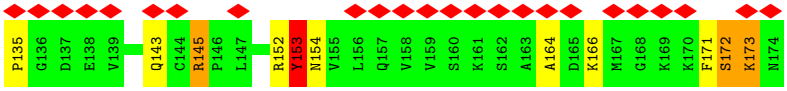


• Molecule 13: 40S RIBOSOMAL PROTEINS S11, PUTATIVE

Chain AE:

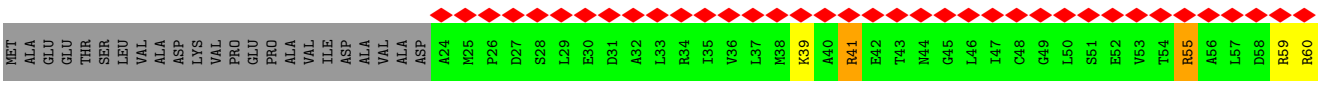


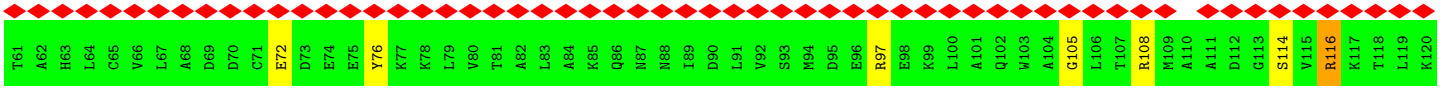


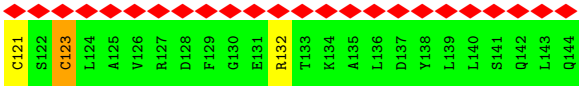


• Molecule 14: 40S RIBOSOMAL PROTEIN S12

Chain AF:

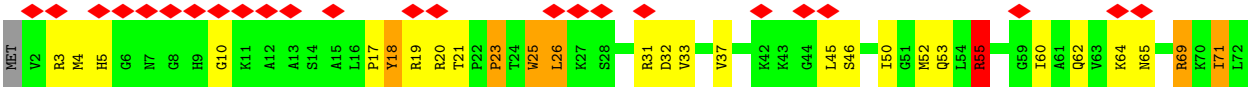


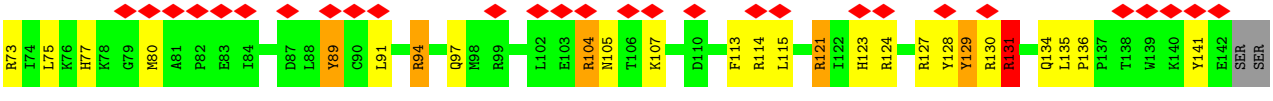




• Molecule 15: 40S RIBOSOMAL PROTEIN S13, PUTATIVE

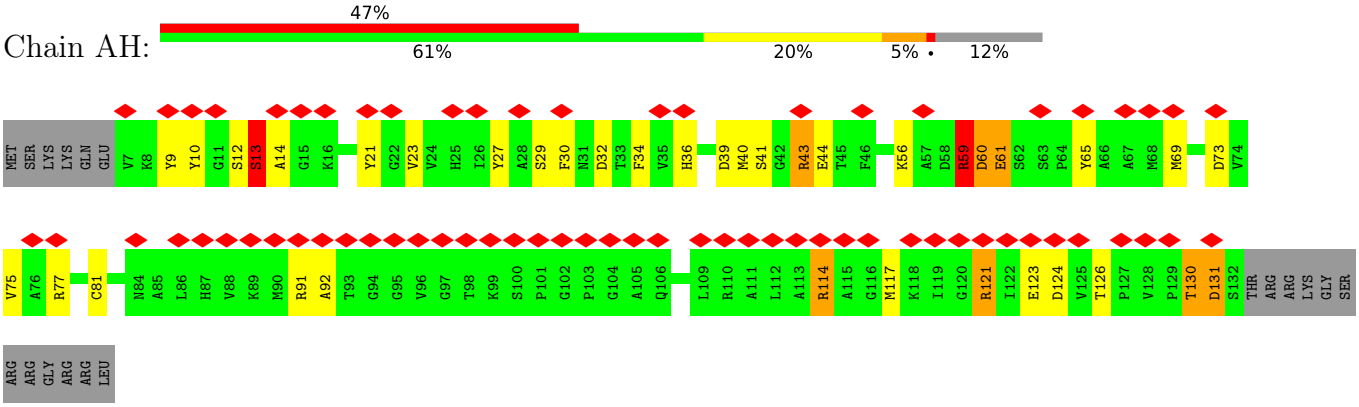
Chain AG:





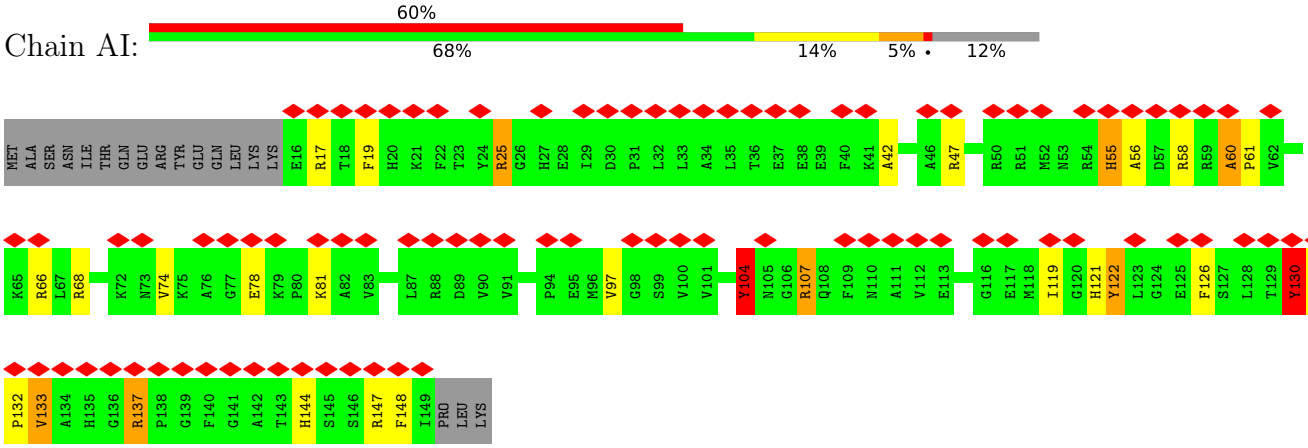
• Molecule 16: 40S RIBOSOMAL PROTEIN S14

Chain AH:



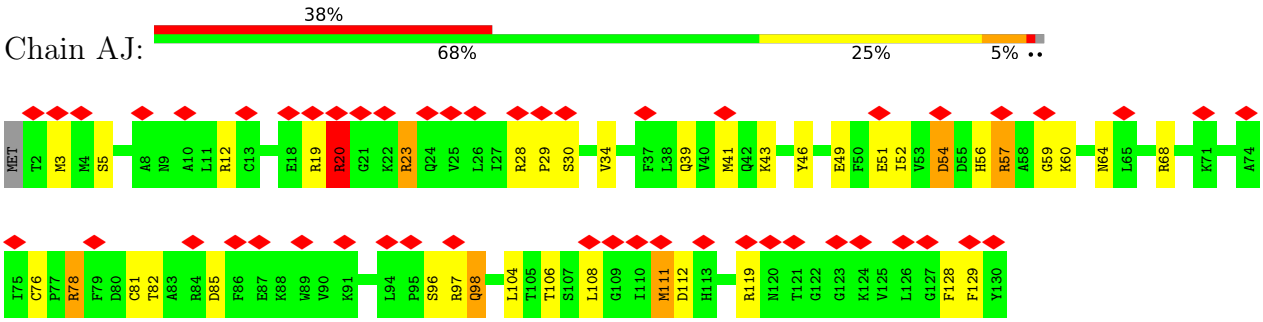
• Molecule 17: 40S RIBOSOMAL PROTEIN S15, PUTATIVE

Chain AI:



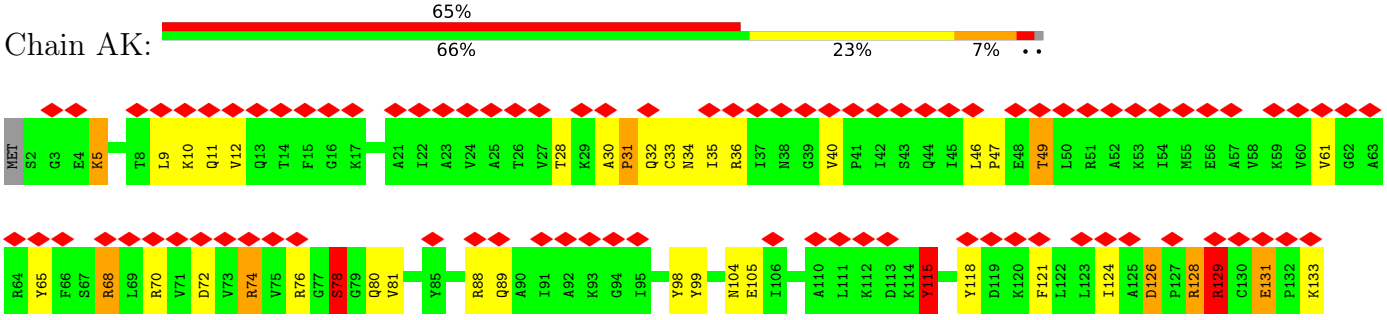
• Molecule 18: 40S RIBOSOMAL PROTEIN S15A, PUTATIVE

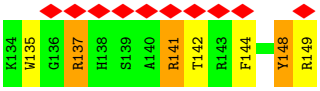
Chain AJ:



• Molecule 19: 40S RIBOSOMAL PROTEIN S16, PUTATIVE

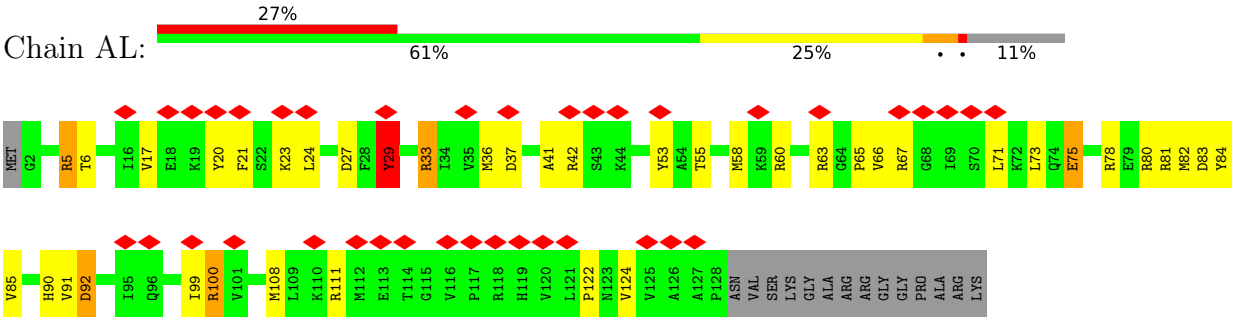
Chain AK:





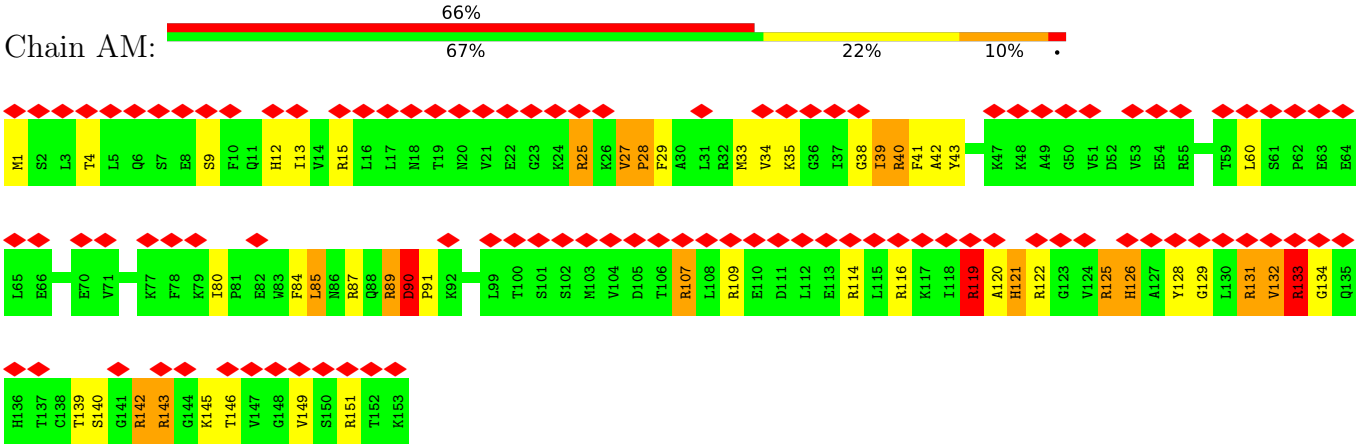
• Molecule 20: 40S RIBOSOMAL PROTEIN S17, PUTATIVE

Chain AL:



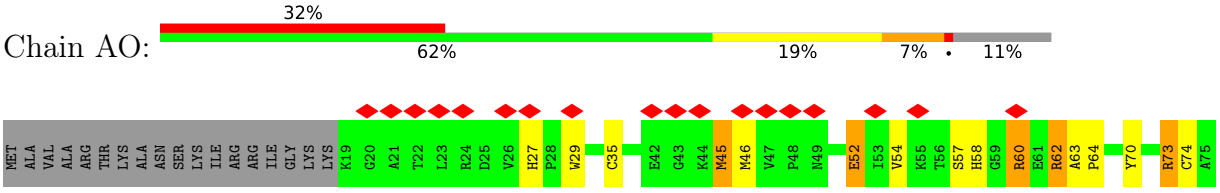
• Molecule 21: 40S RIBOSOMAL PROTEIN S18, PUTATIVE

Chain AM:



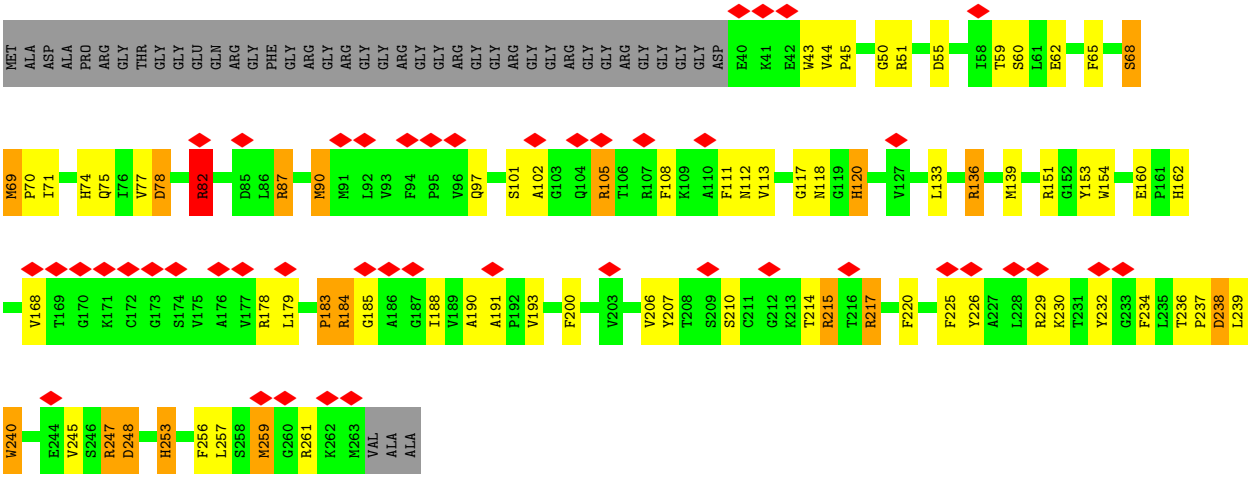
• Molecule 22: RIBOSOMAL PROTEIN S19, PUTATIVE

Chain AO:



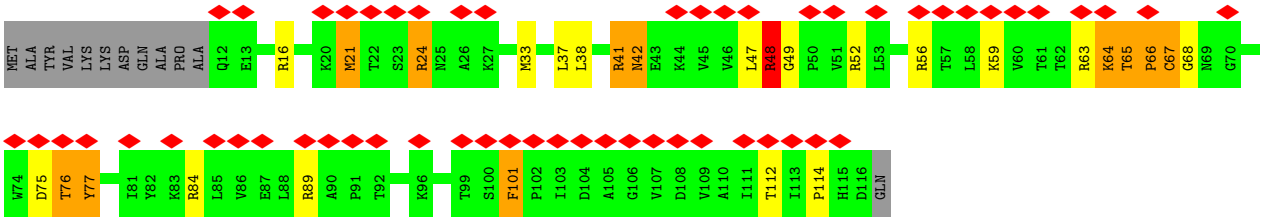
• Molecule 23: 40S RIBOSOMAL PROTEIN S2, PUTATIVE

Chain AP:



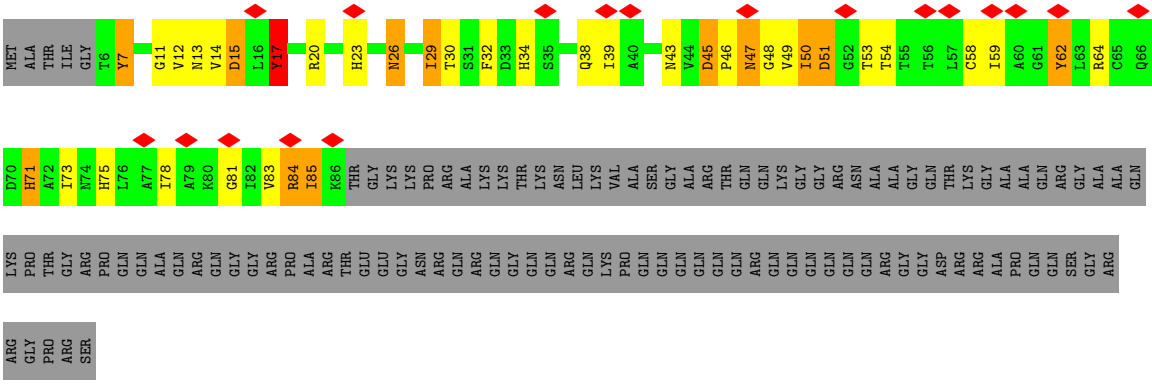
• Molecule 24: RIBOSOMAL PROTEIN S20, PUTATIVE

Chain AQ:



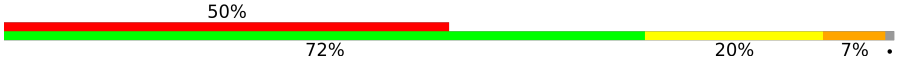
• Molecule 25: 40S RIBOSOMAL PROTEIN S21, PUTATIVE

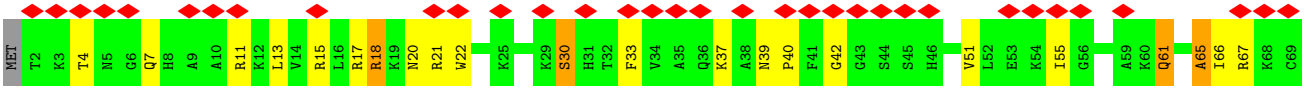
Chain AR:

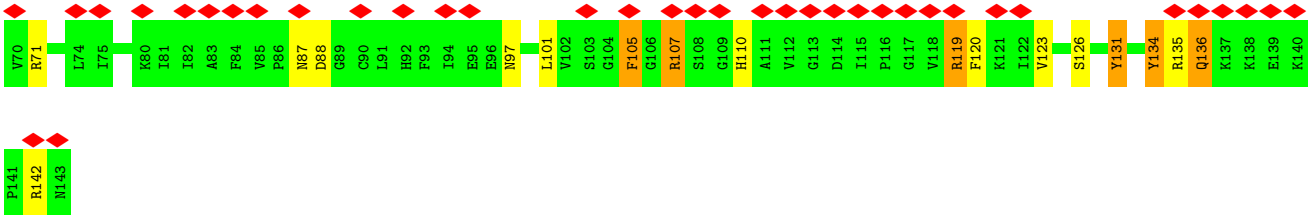


• Molecule 26: 40S RIBOSOMAL PROTEIN S23, PUTATIVE

Chain AS:

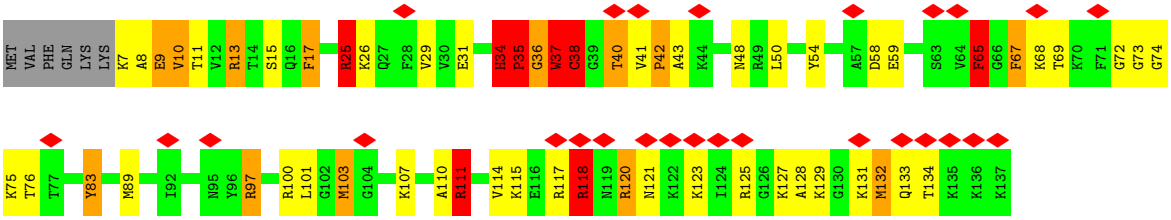






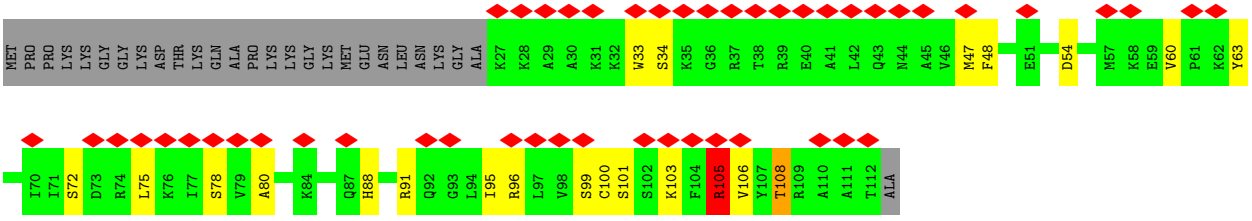
• Molecule 27: 40S RIBOSOMAL PROTEIN S24

Chain AT:



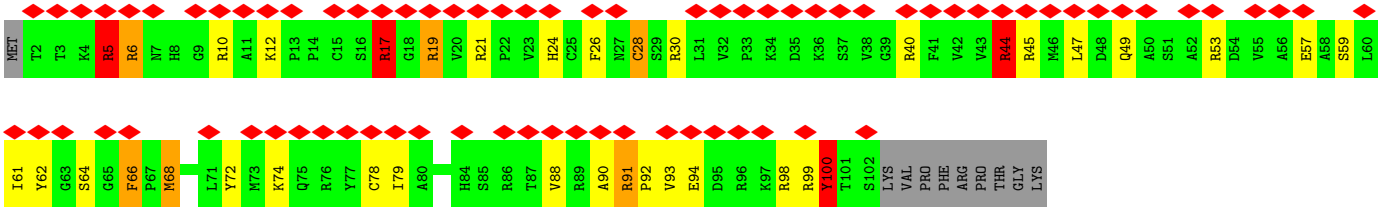
• Molecule 28: 40S RIBOSOMAL PROTEIN S25, PUTATIVE

Chain AU:



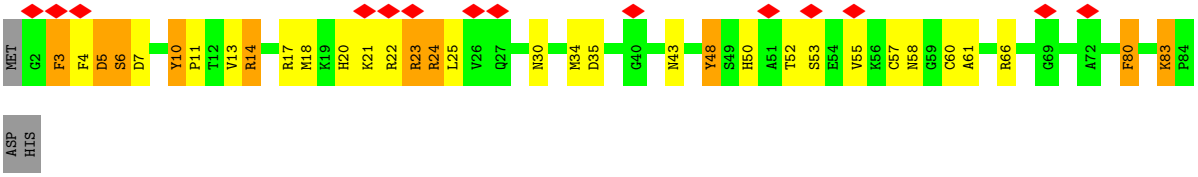
• Molecule 29: RIBOSOMAL PROTEIN S26, PUTATIVE

Chain AV:



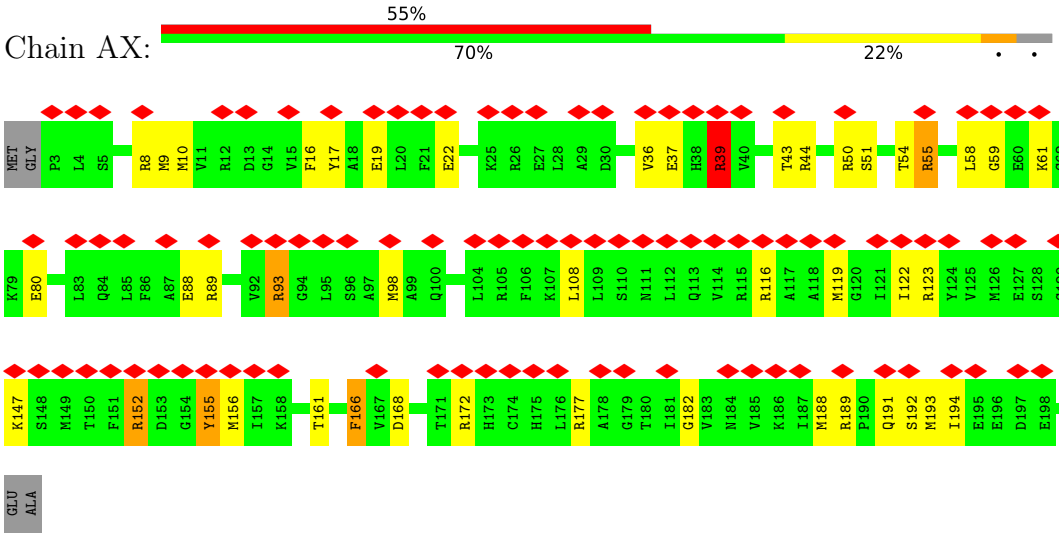
• Molecule 30: 40S RIBOSOMAL PROTEIN S27, PUTATIVE

Chain AW:



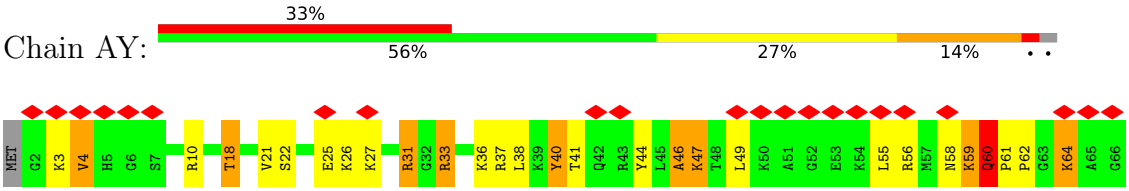
• Molecule 31: 40S RIBOSOMAL PROTEIN S3, PUTATIVE

Chain AX:



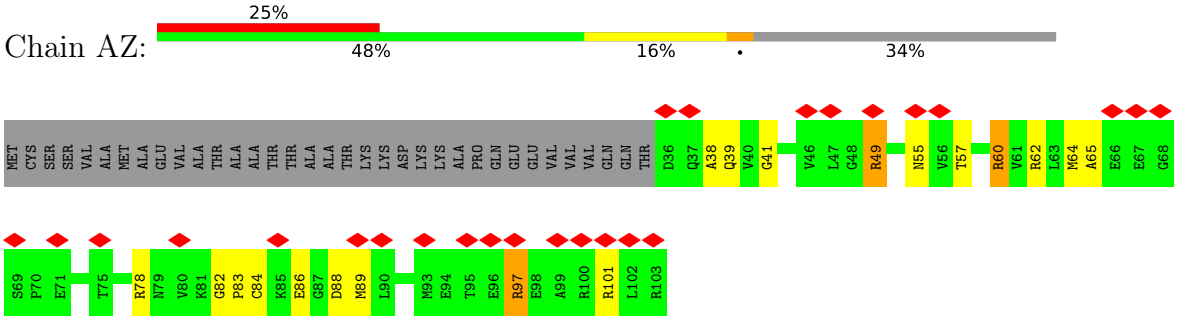
• Molecule 32: 40S RIBOSOMAL PROTEIN S30, PUTATIVE

Chain AY:



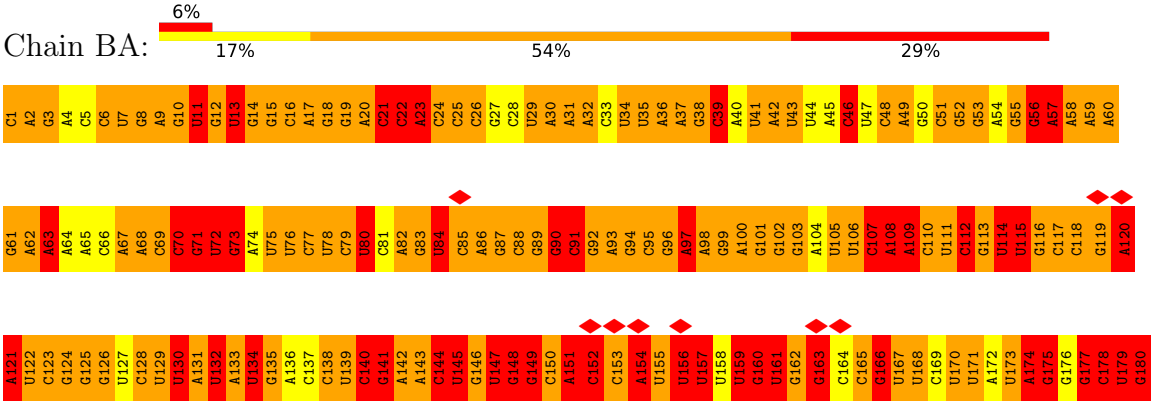
• Molecule 33: 40S RIBOSOMAL PROTEIN S33, PUTATIVE

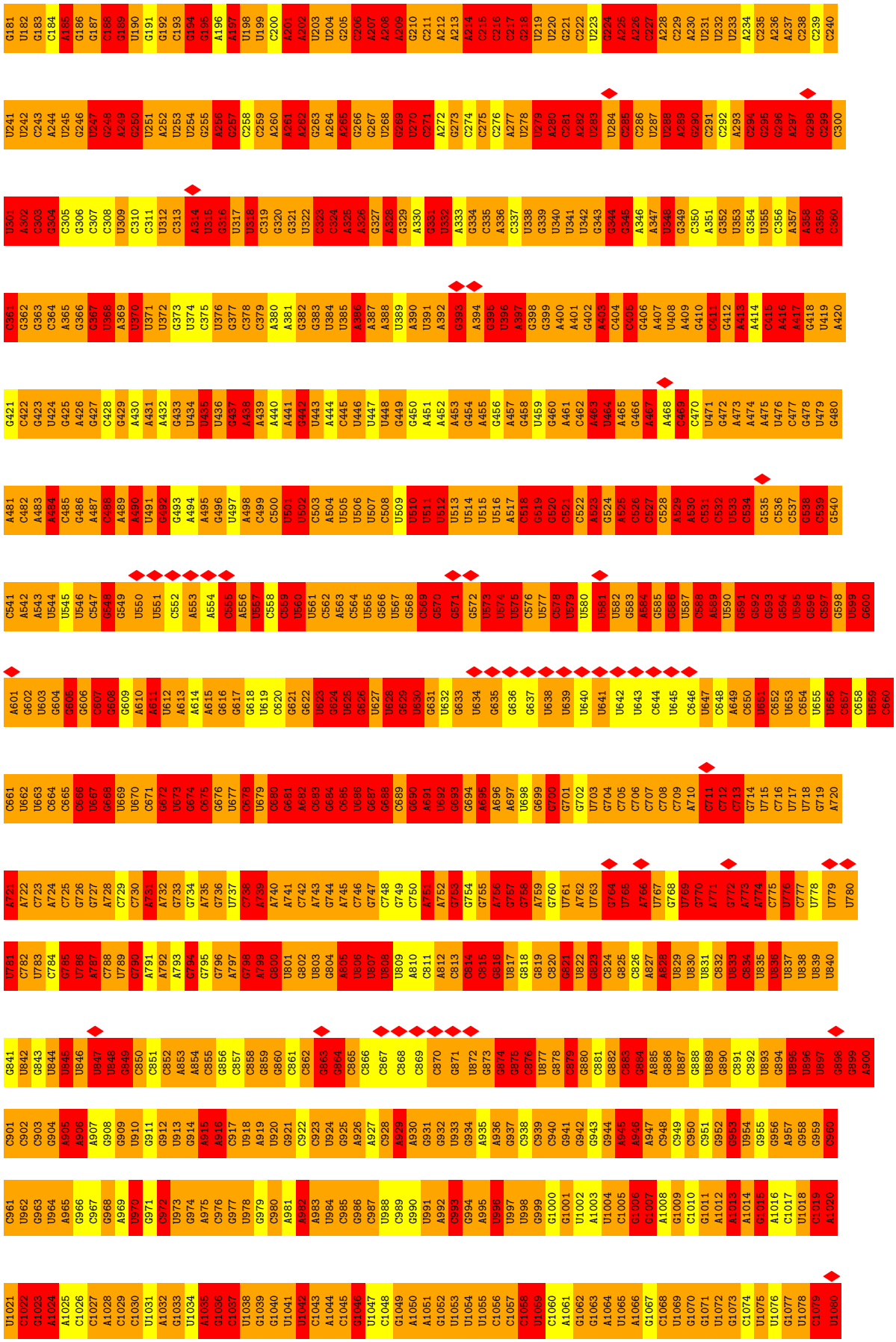
Chain AZ:

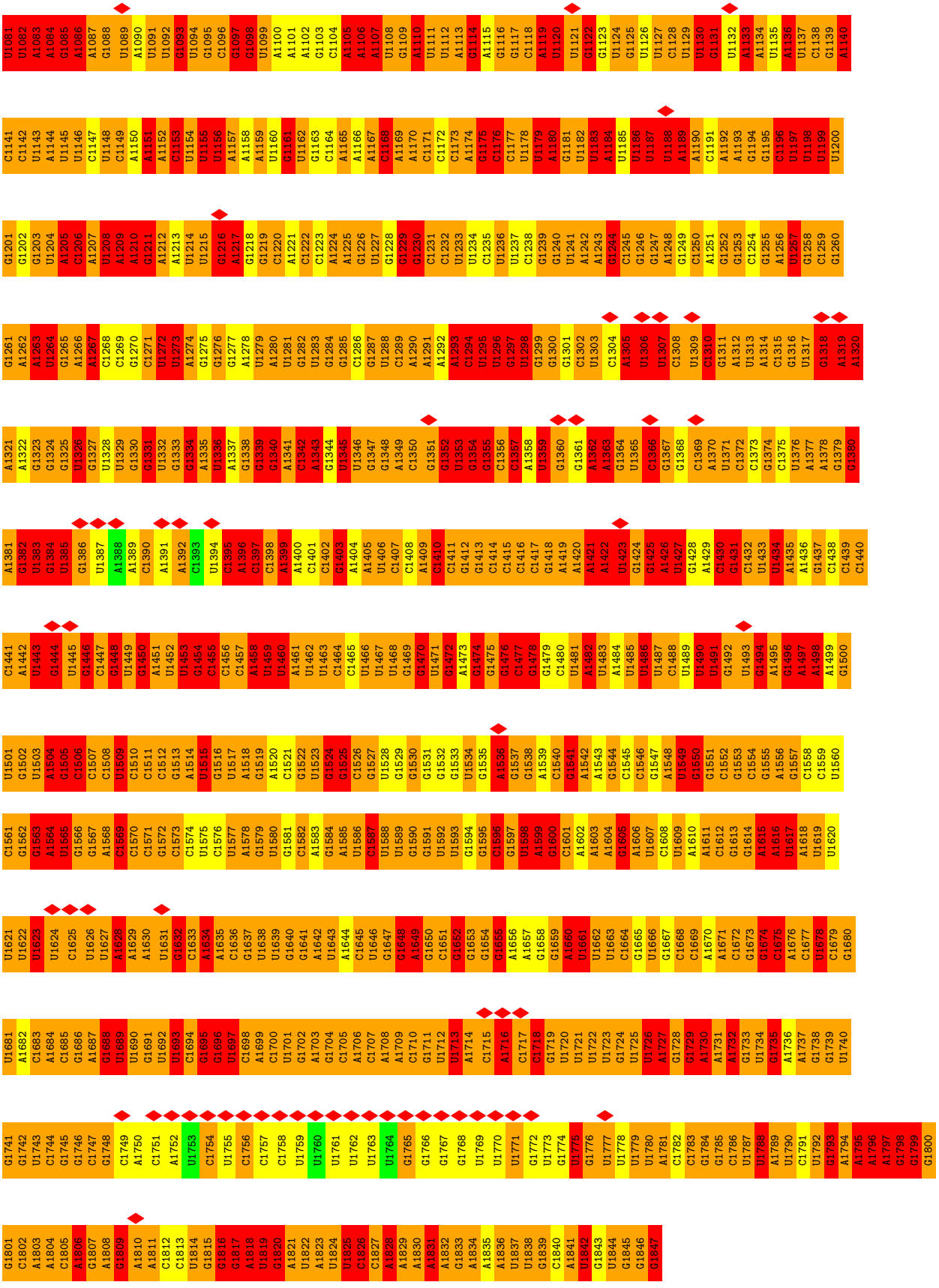


• Molecule 34: ALPHA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT 28S RRNA

Chain BA:

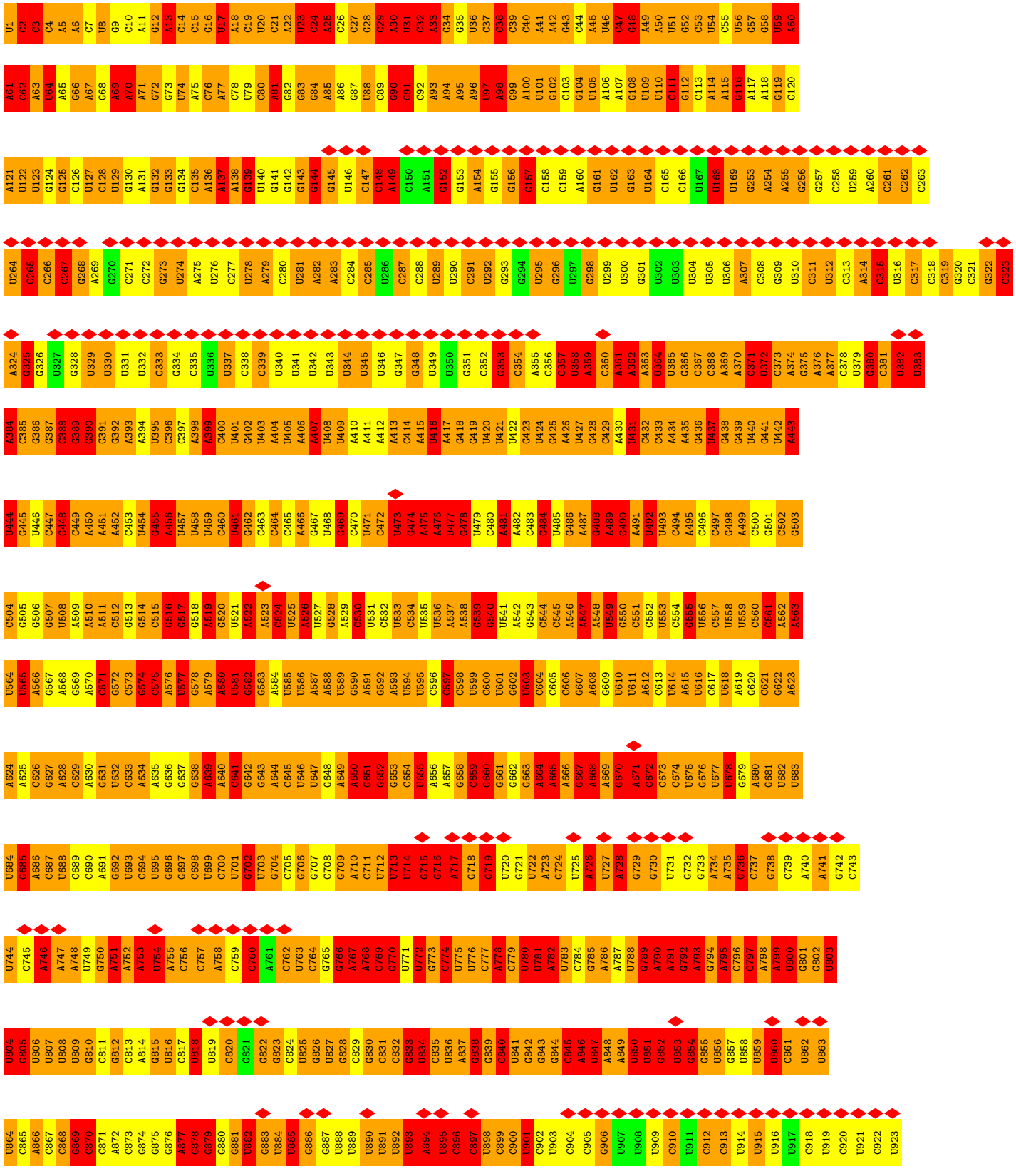


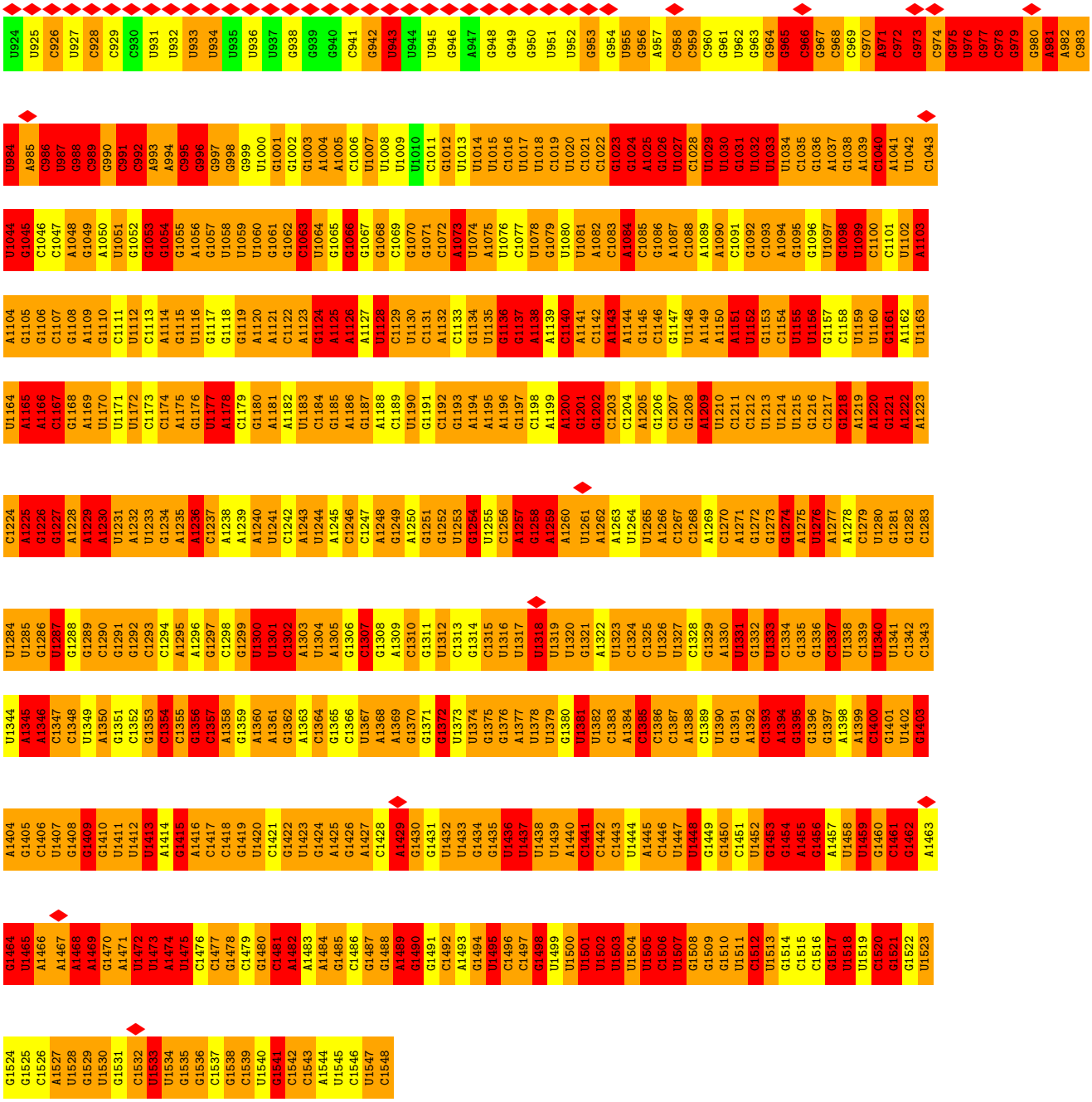




• Molecule 35: BETA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT 28S RRNA

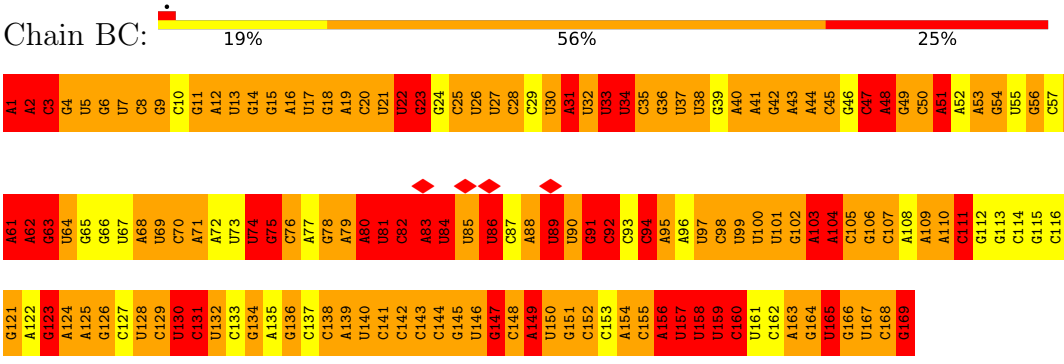
Chain BB:





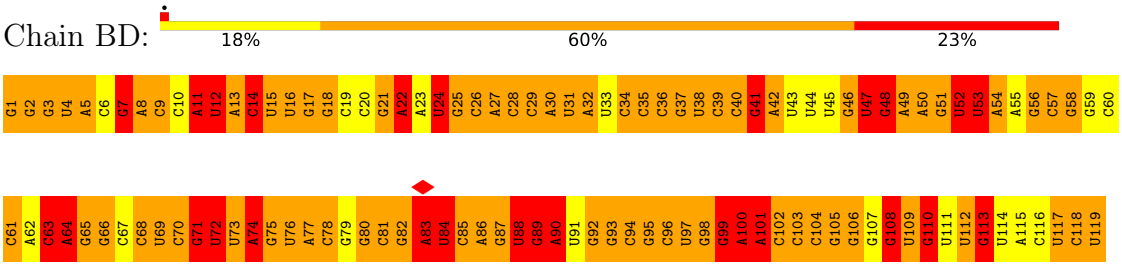
• Molecule 36: 5.8S RRNA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT

Chain BC:



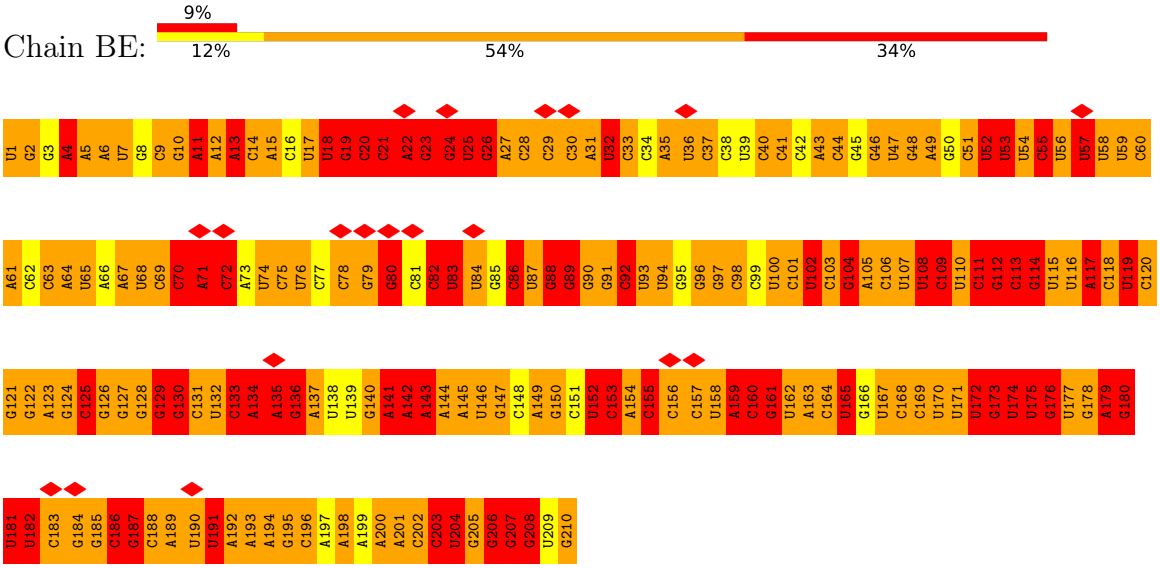
• Molecule 37: 5S RRNA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT

Chain BD:



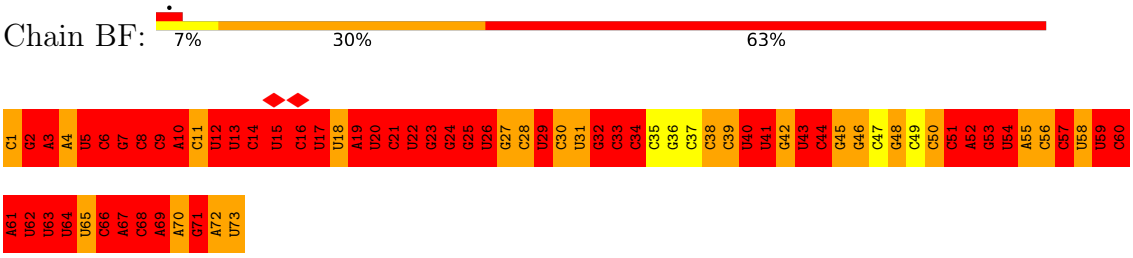
• Molecule 38: SHORT RRNA-I OF THE LARGE RIBOSOMAL SUBUNIT

Chain BE:



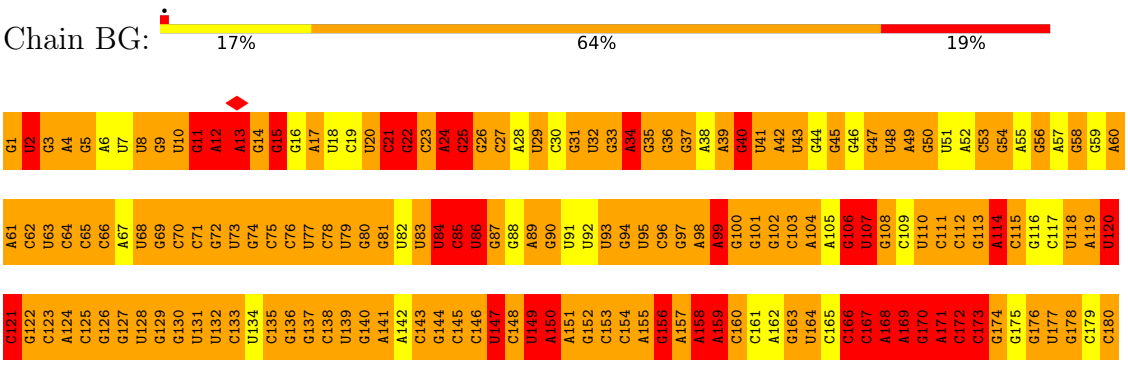
• Molecule 39: SHORT RRNA-II OF THE LARGE RIBOSOMAL SUBUNIT

Chain BF:



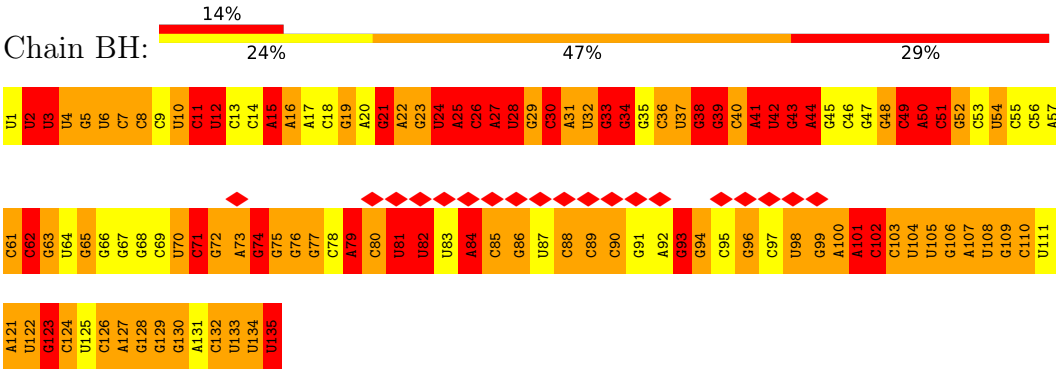
• Molecule 40: SHORT RRNA-III OF THE LARGE RIBOSOMAL SUBUNIT

Chain BG:



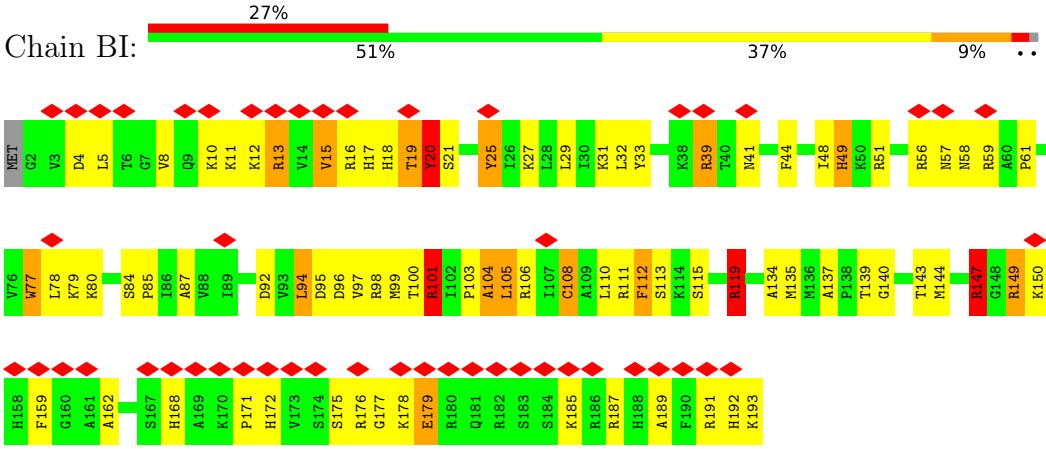
• Molecule 41: SHORT RRNA-IV OF THE LARGE RIBOSOMAL SUBUNIT

Chain BH:



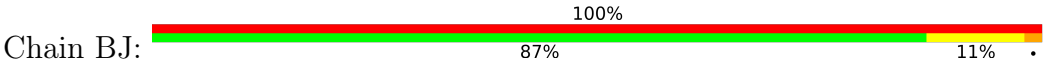
• Molecule 42: 60S RIBOSOMAL PROTEIN L18

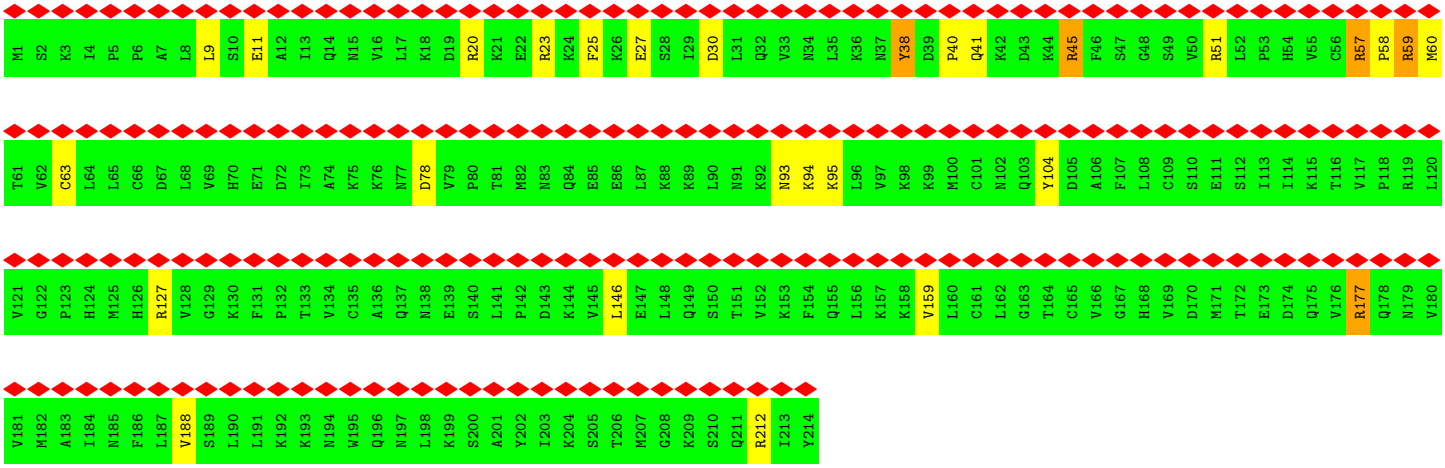
Chain BI:



• Molecule 43: RIBOSOMAL PROTEIN

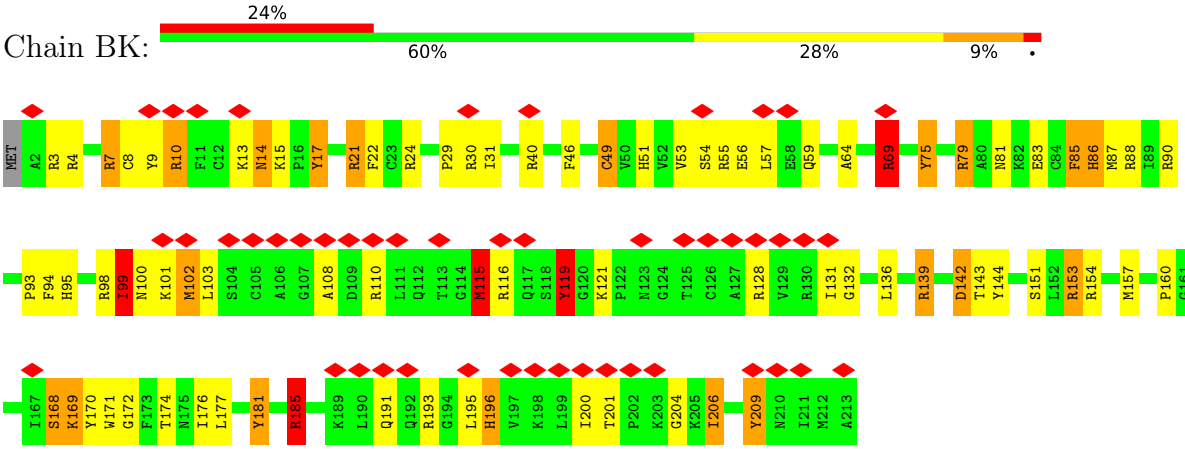
Chain BJ:





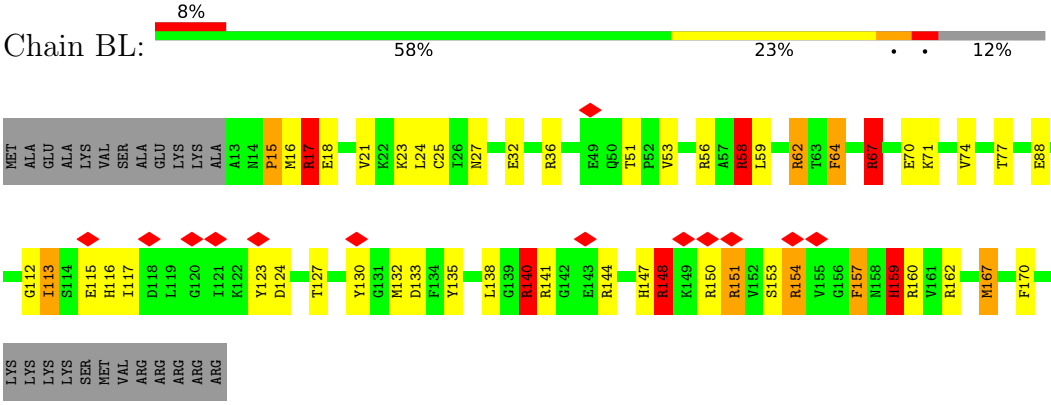
• Molecule 44: 60S RIBOSOMAL PROTEIN L10, PUTATIVE

Chain BK:



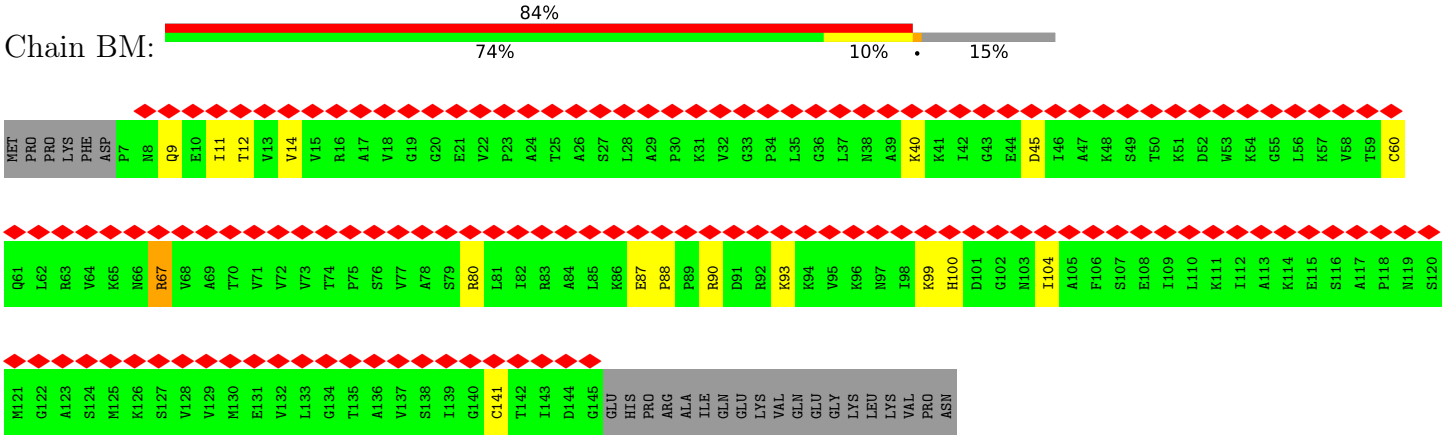
• Molecule 45: 60S RIBOSOMAL PROTEIN L11, PUTATIVE

Chain BL:



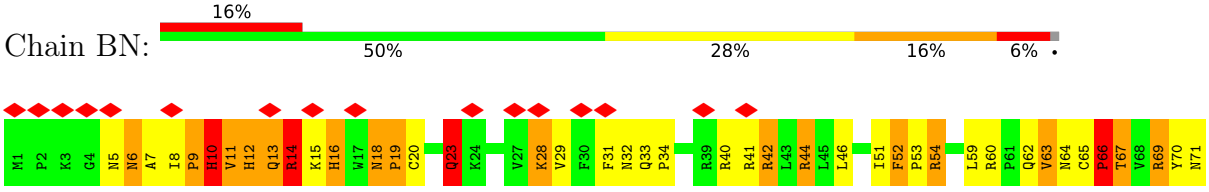
• Molecule 46: 60S RIBOSOMAL PROTEIN L12, PUTATIVE

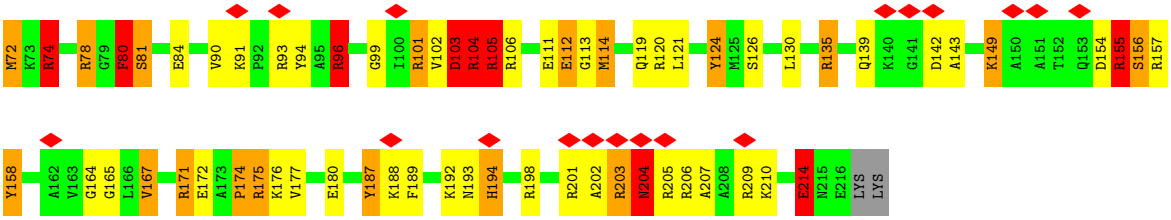
Chain BM:



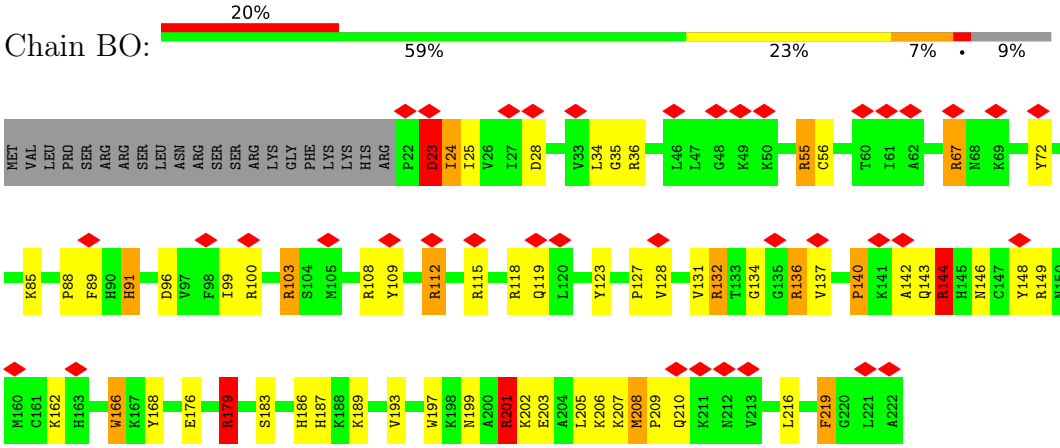
• Molecule 47: 60S RIBOSOMAL PROTEIN L13

Chain BN:

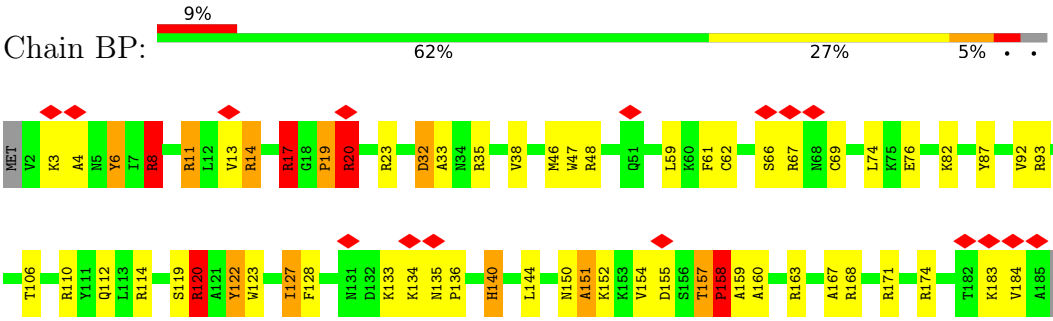




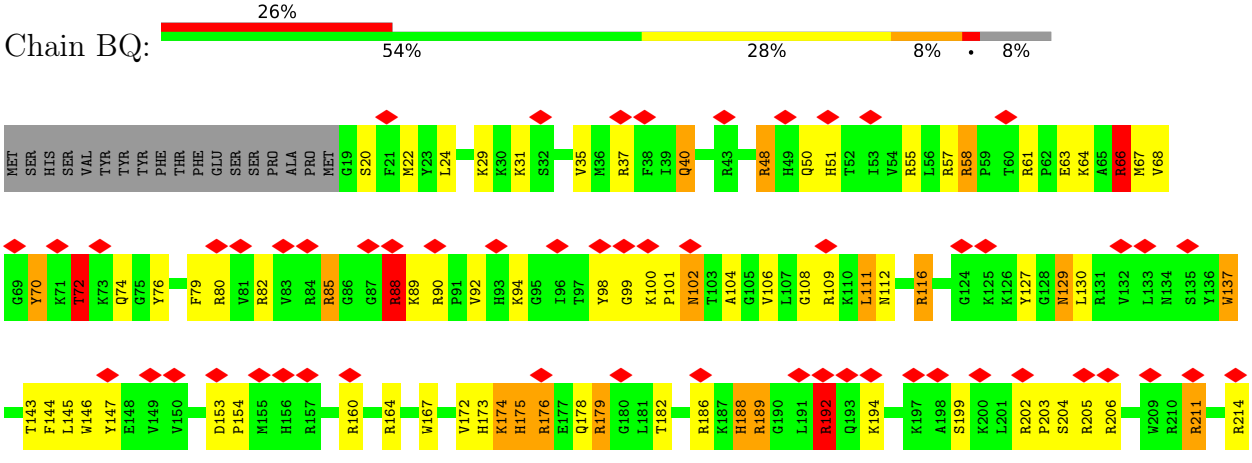
• Molecule 48: 60S RIBOSOMAL PROTEIN L13A, PUTATIVE

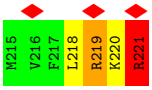


• Molecule 49: PROBABLE 60S RIBOSOMAL PROTEIN L14



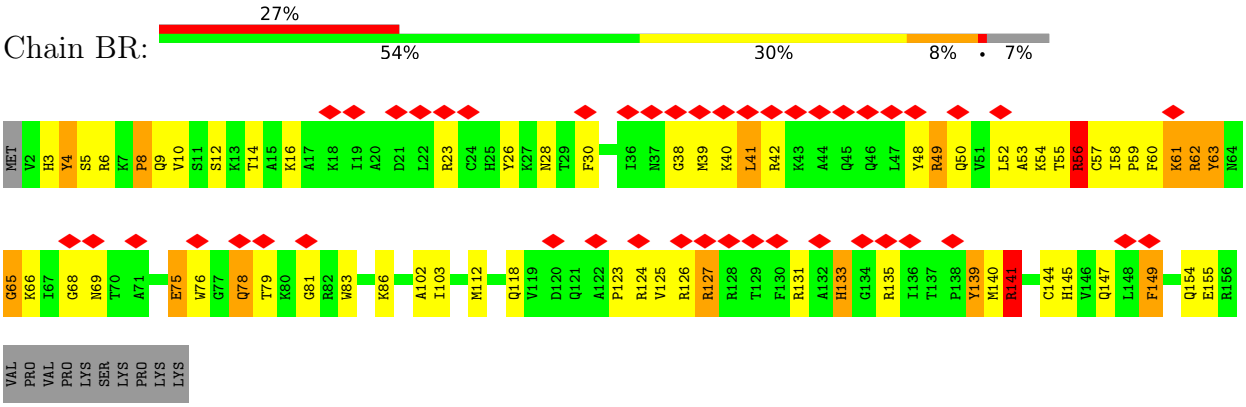
• Molecule 50: RIBOSOMAL PROTEIN L15





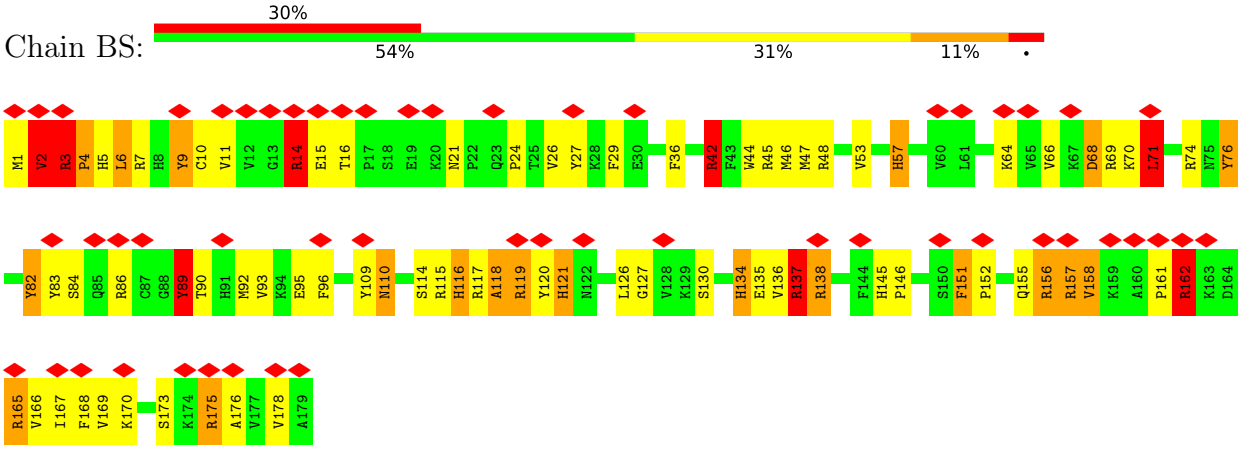
• Molecule 51: 60S RIBOSOMAL PROTEIN L17, PUTATIVE

Chain BR:



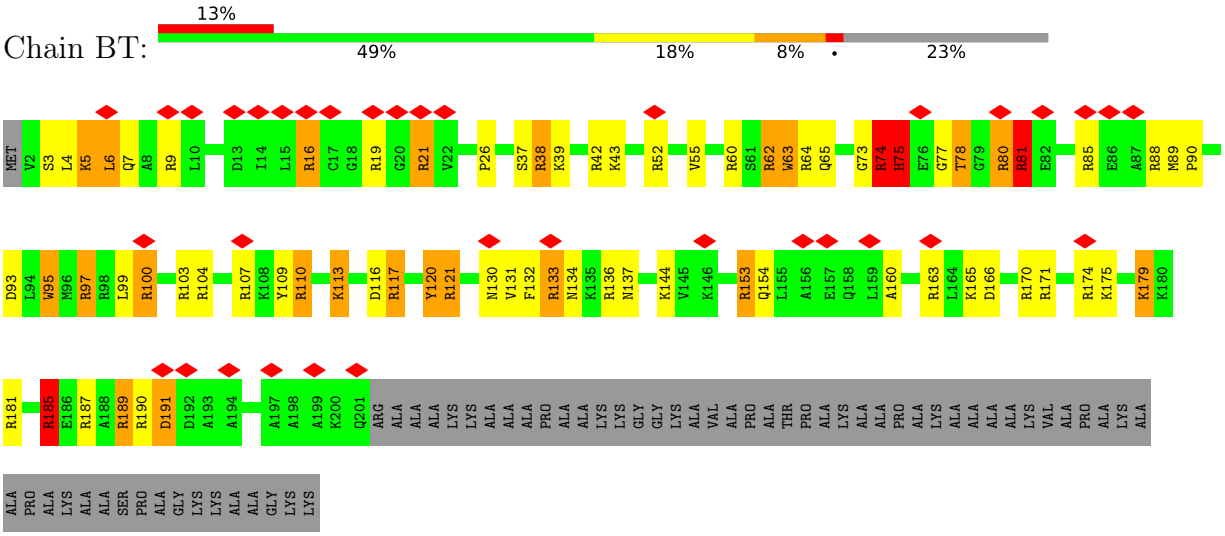
• Molecule 52: 60S RIBOSOMAL PROTEIN L18A

Chain BS:



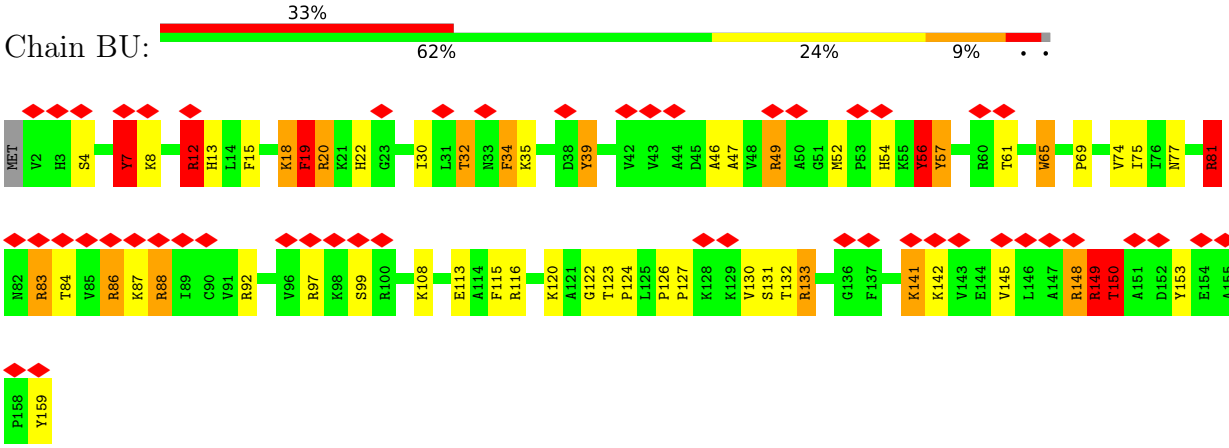
• Molecule 53: 60S RIBOSOMAL PROTEIN L19, PUTATIVE

Chain BT:



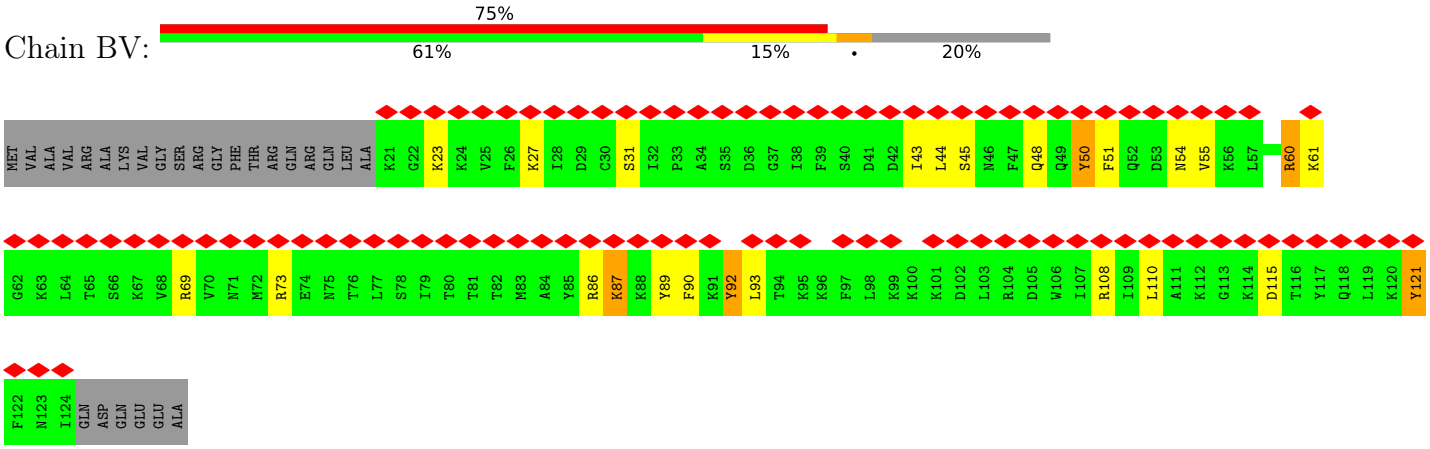
• Molecule 54: 60S RIBOSOMAL PROTEIN L21E, PUTATIVE

Chain BU:



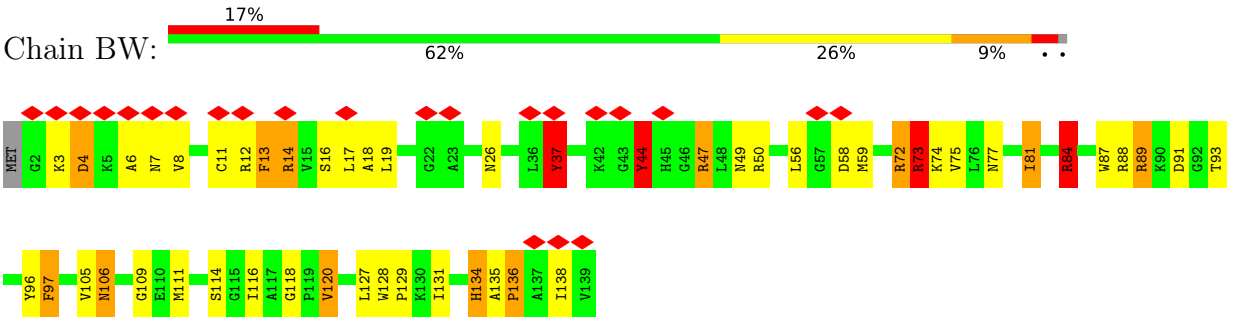
• Molecule 55: 60S RIBOSOMAL PROTEIN L22, PUTATIVE

Chain BV:



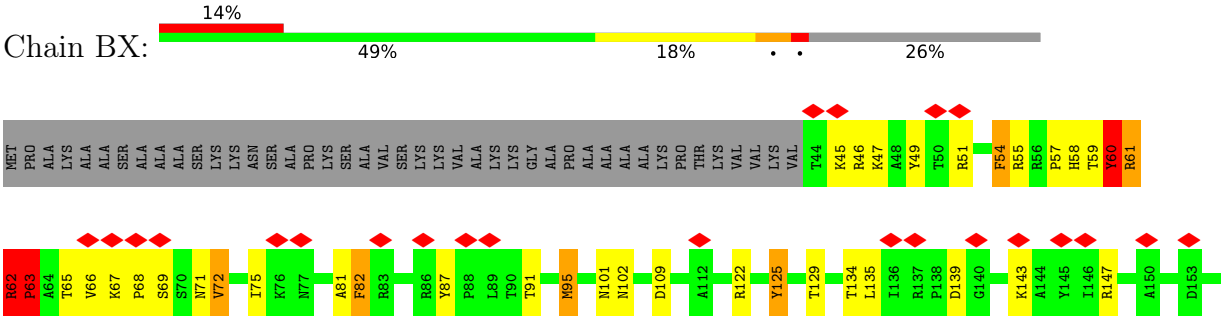
• Molecule 56: 60S RIBOSOMAL PROTEIN L23, PUTATIVE

Chain BW:



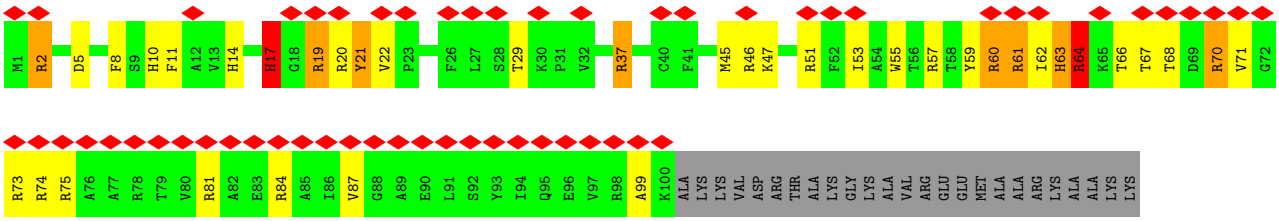
• Molecule 57: 60S RIBOSOMAL PROTEIN L23A

Chain BX:



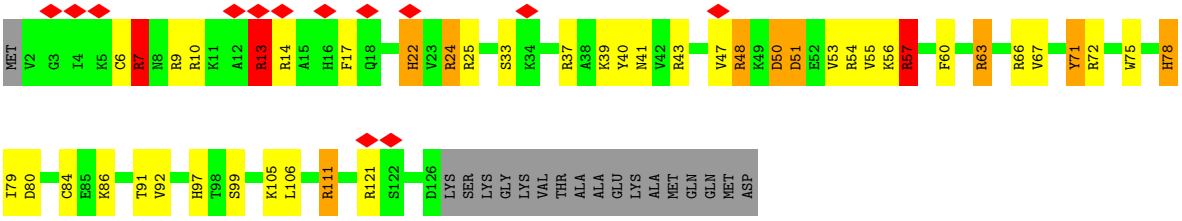
• Molecule 58: 60S RIBOSOMAL PROTEIN L24, PUTATIVE

Chain BY:



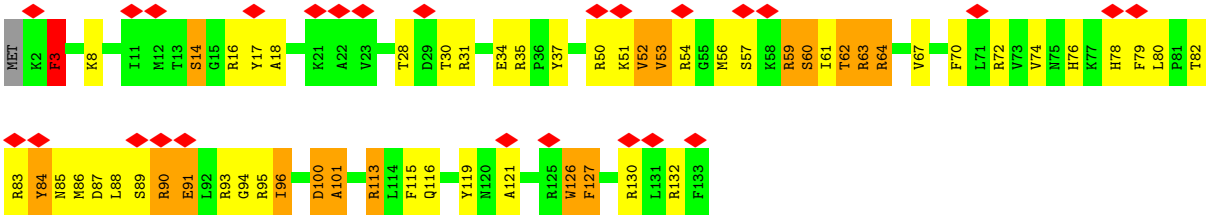
• Molecule 59: 60S RIBOSOMAL PROTEIN L26, PUTATIVE

Chain BZ:



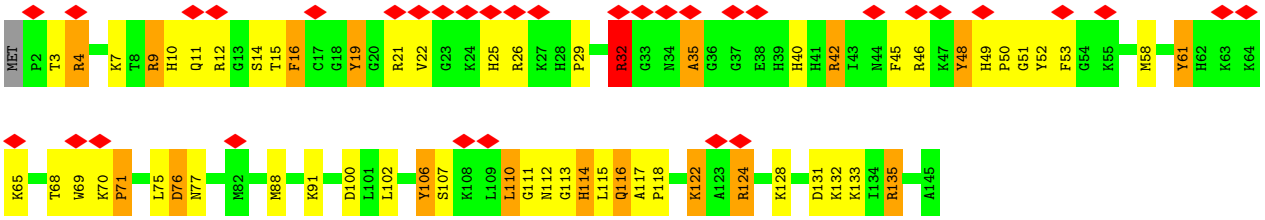
• Molecule 60: 60S RIBOSOMAL PROTEIN L27, PUTATIVE

Chain Ba:



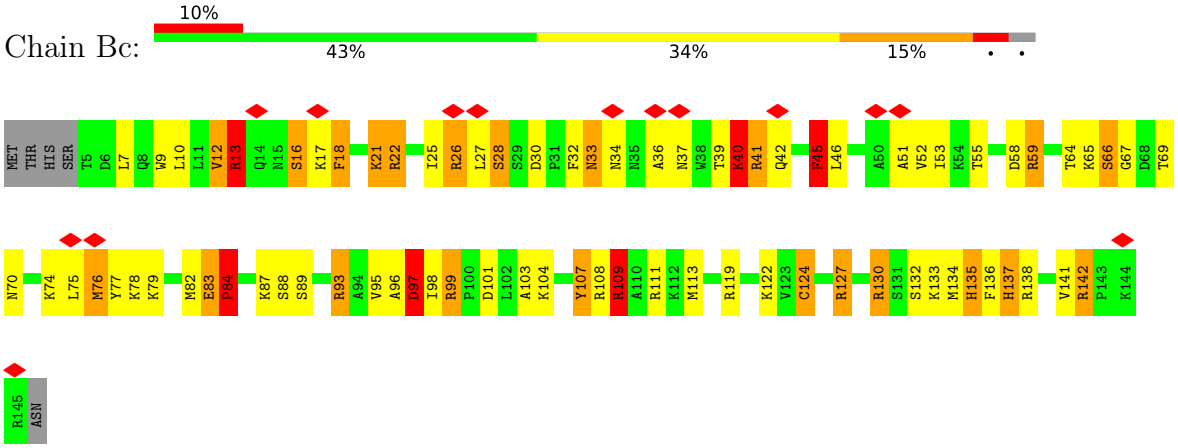
• Molecule 61: 60S RIBOSOMAL PROTEIN L27A

Chain Bb:



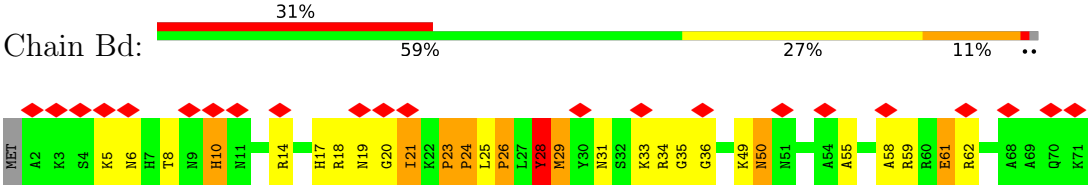
• Molecule 62: 60S RIBOSOMAL PROTEIN L28, PUTATIVE

Chain Bc:



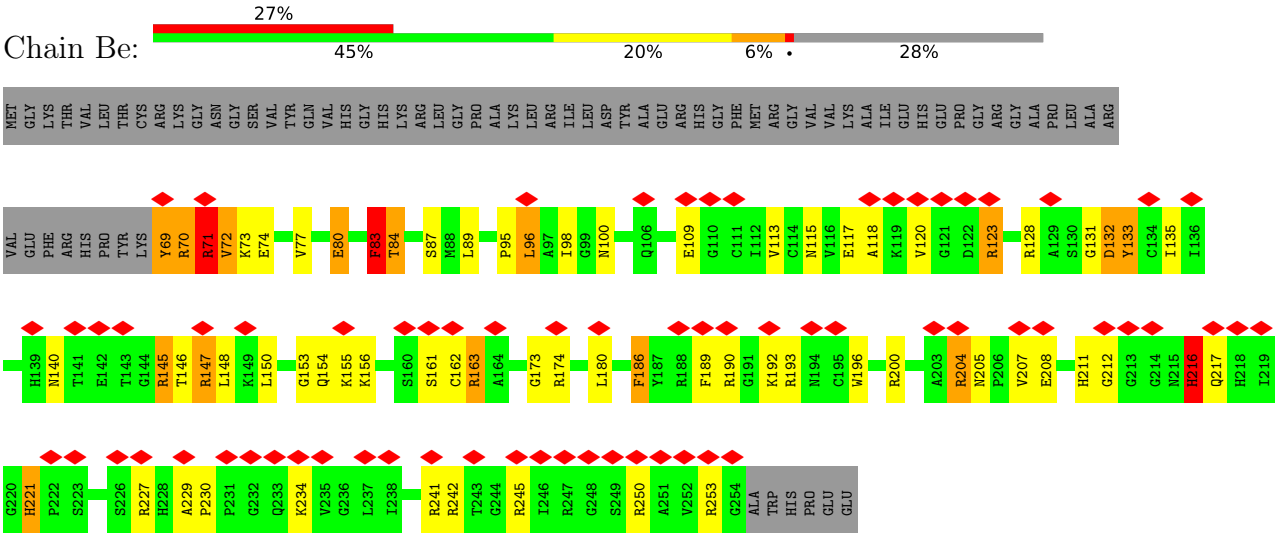
• Molecule 63: 60S RIBOSOMAL PROTEIN L29, PUTATIVE

Chain Bd:



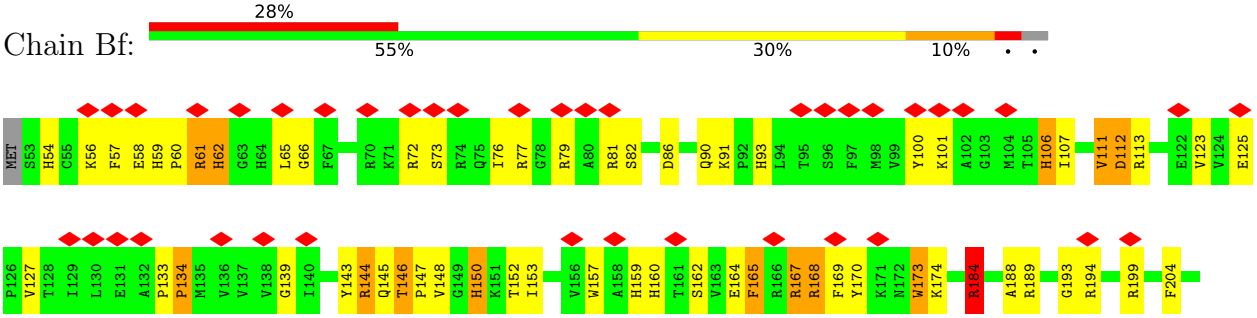
• Molecule 64: 60S RIBOSOMAL PROTEIN L2, PUTATIVE

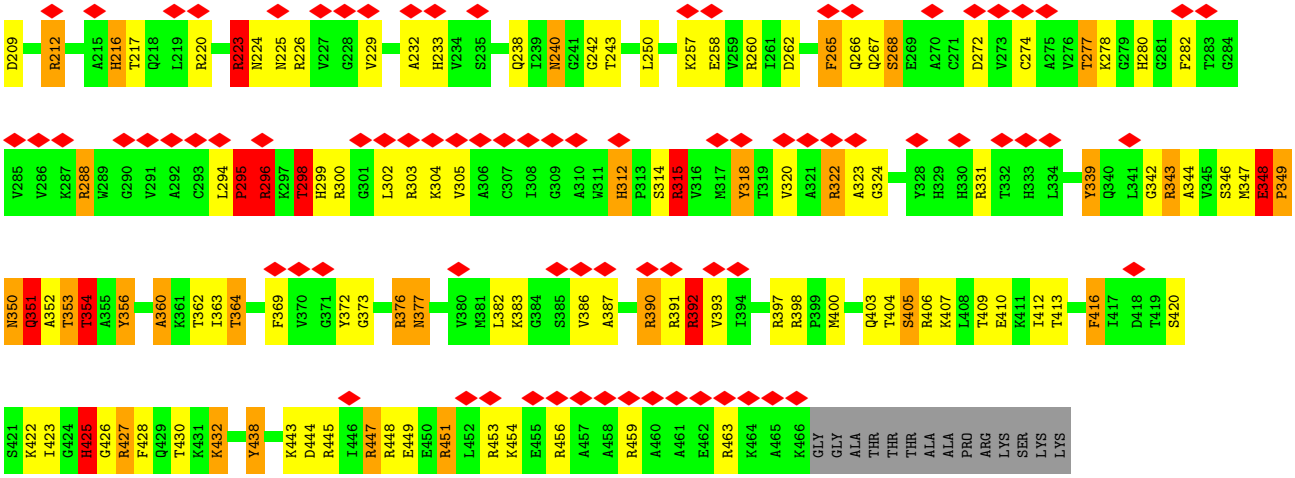
Chain Be:



• Molecule 65: RIBOSOMAL PROTEIN L3, MITOCHONDRIAL, PUTATIVE

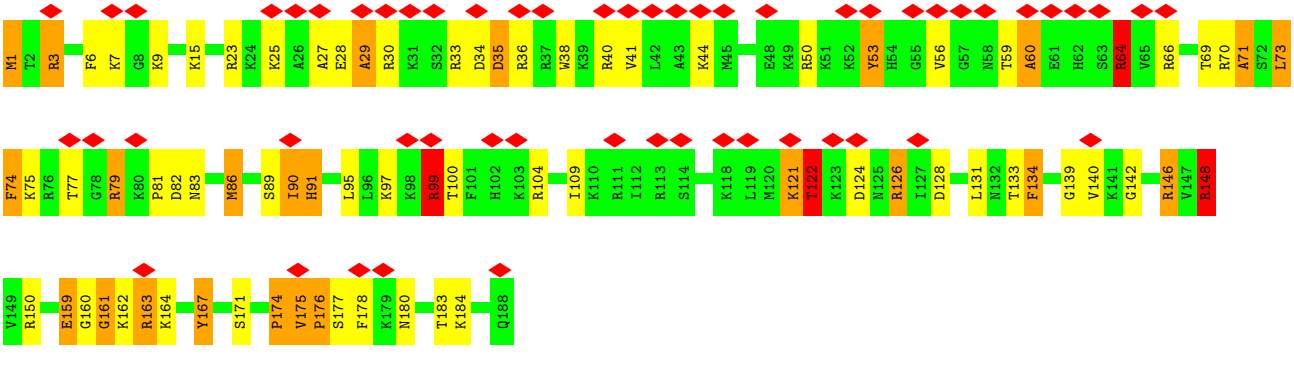
Chain Bf:



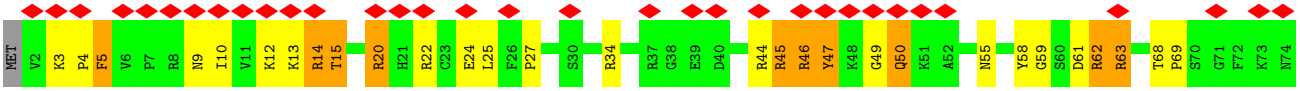


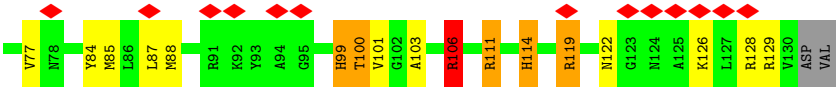
• Molecule 66: 60S RIBOSOMAL PROTEIN L30

• Molecule 67: 60S RIBOSOMAL SUBUNIT PROTEIN L31, PUTATIVE

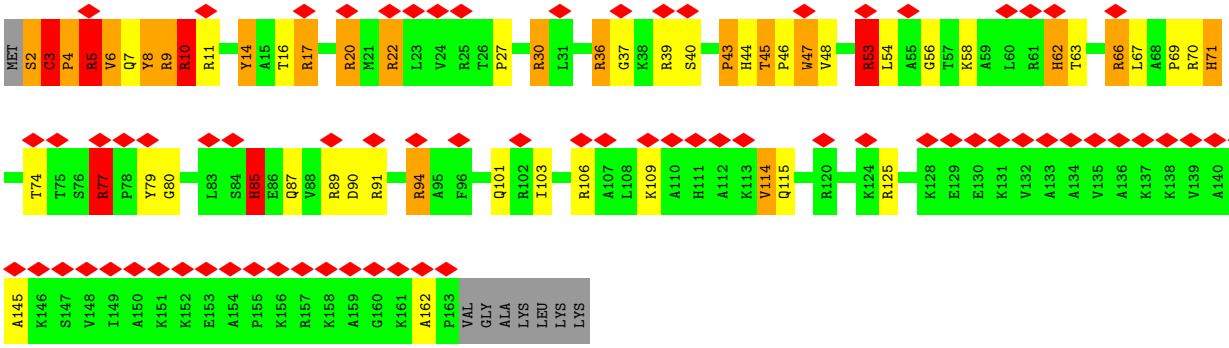


• Molecule 68: 60S RIBOSOMAL PROTEIN L32, PUTATIVE

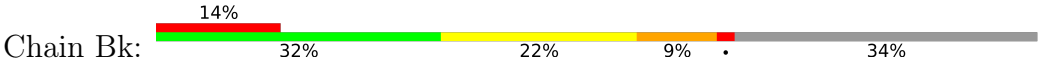


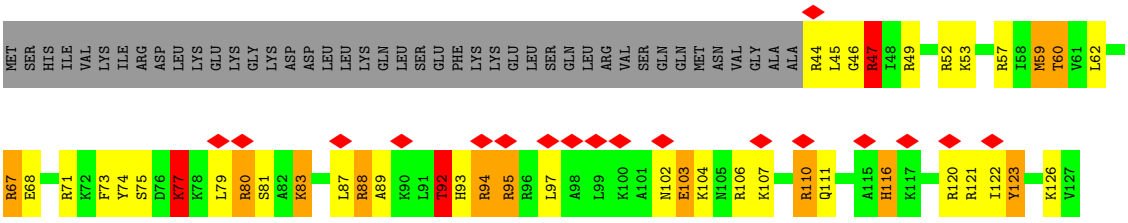


• Molecule 69: 60S RIBOSOMAL PROTEIN L34, PUTATIVE

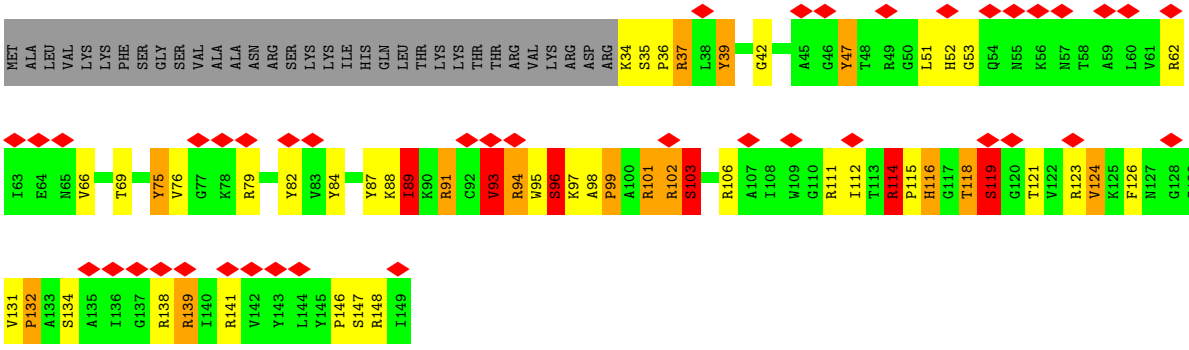


• Molecule 70: 60S RIBOSOMAL PROTEIN L35, PUTATIVE

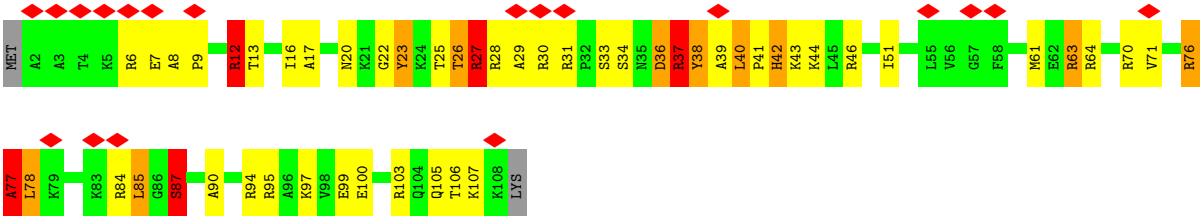




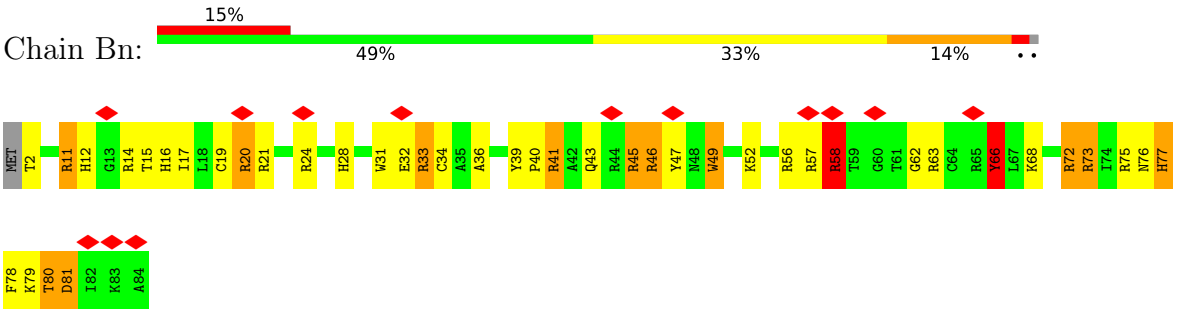
• Molecule 71: 60S RIBOSOMAL PROTEIN L35A, PUTATIVE



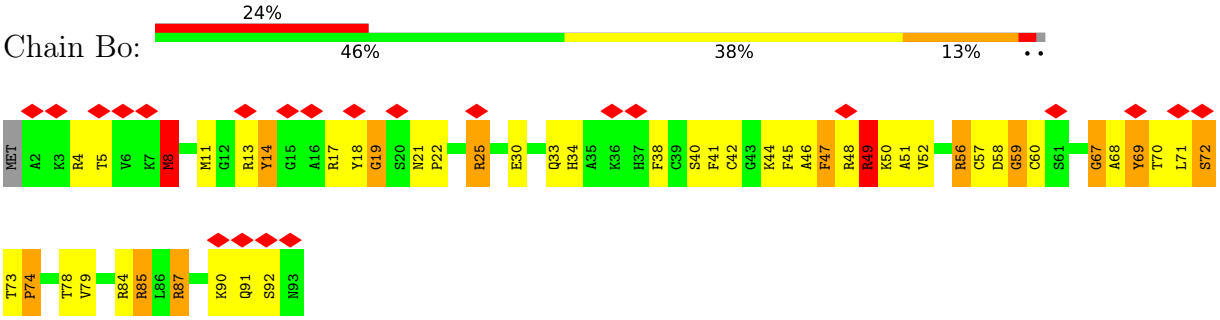
• Molecule 72: RIBOSOMAL PROTEIN L36, PUTATIVE



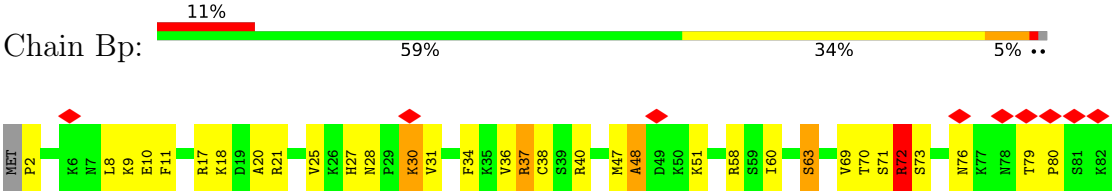
• Molecule 73: RIBOSOMAL PROTEIN L37



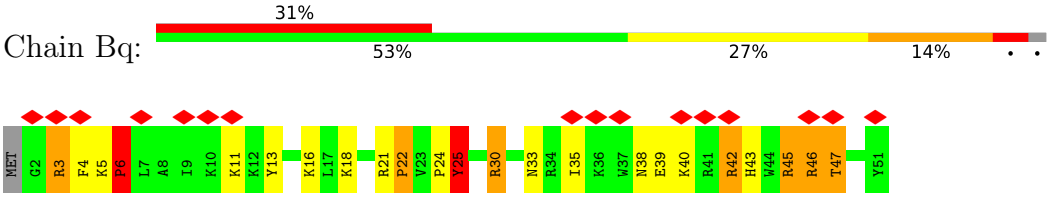
• Molecule 74: 60S RIBOSOMAL PROTEIN L37A, PUTATIVE



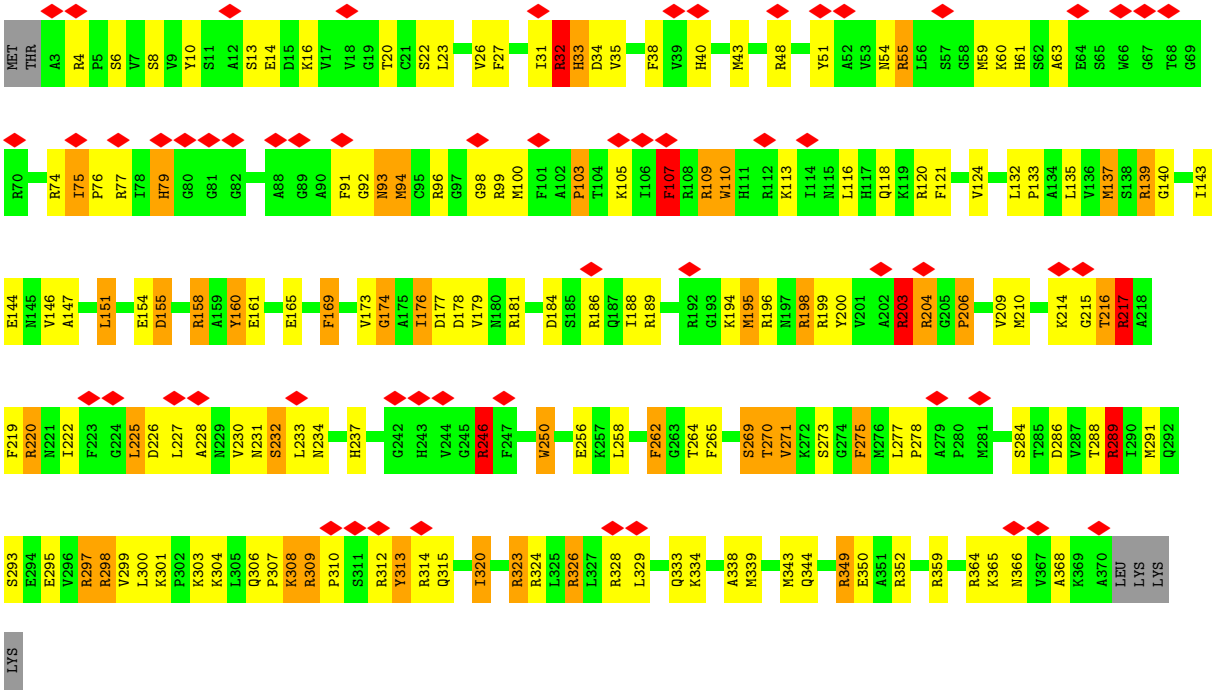
• Molecule 75: 60S RIBOSOMAL PROTEIN L38, PUTATIVE



• Molecule 76: 60S RIBOSOMAL PROTEIN L39, PUTATIVE

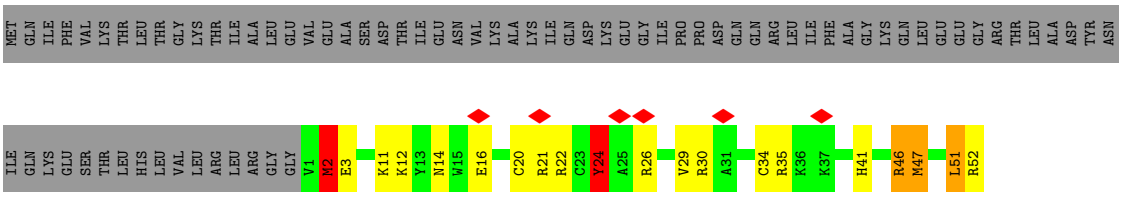


• Molecule 77: 60S RIBOSOMAL PROTEIN L4



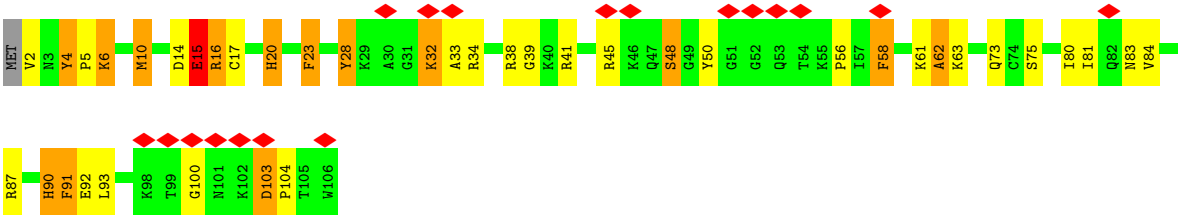
• Molecule 78: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

Chain Bs:



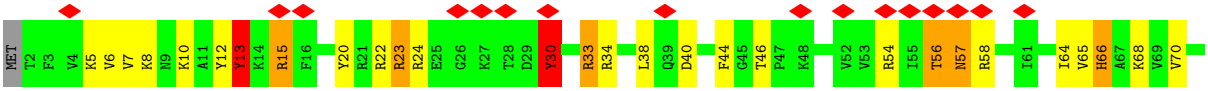
• Molecule 79: 60S RIBOSOMAL PROTEIN L44

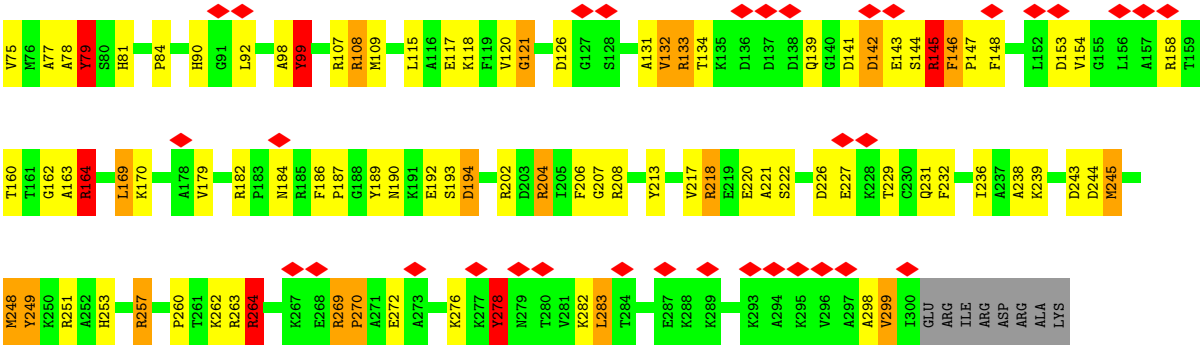
Chain Bt:



• Molecule 80: 60S RIBOSOMAL PROTEIN L5, PUTATIVE

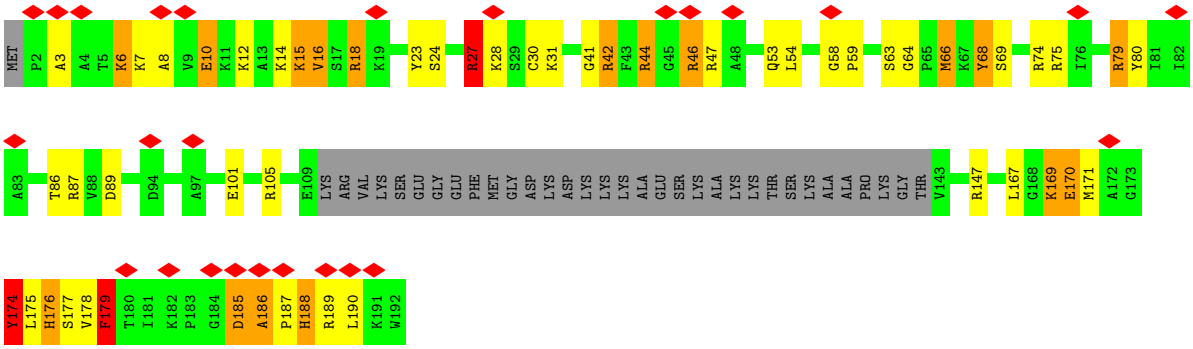
Chain Bu:





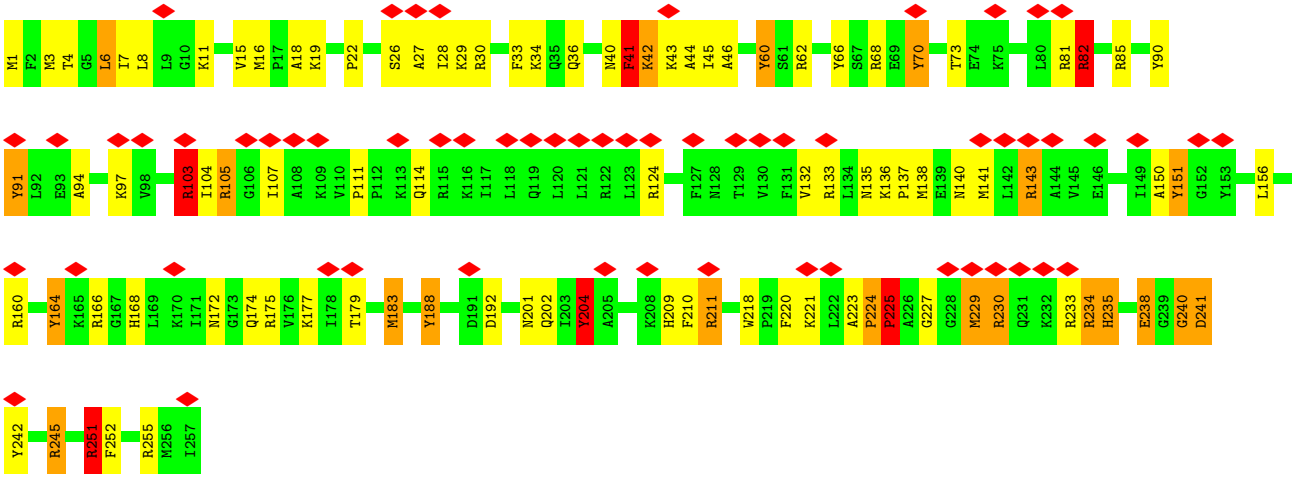
• Molecule 81: 60S RIBOSOMAL PROTEIN L6, PUTATIVE

Chain Bv:



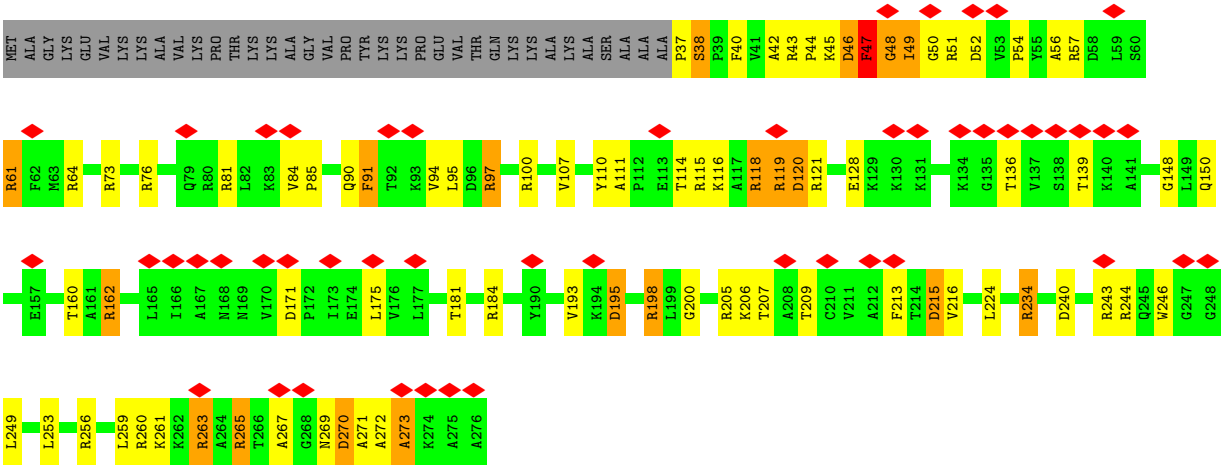
• Molecule 82: 60S RIBOSOMAL PROTEIN L7, PUTATIVE

Chain Bw:



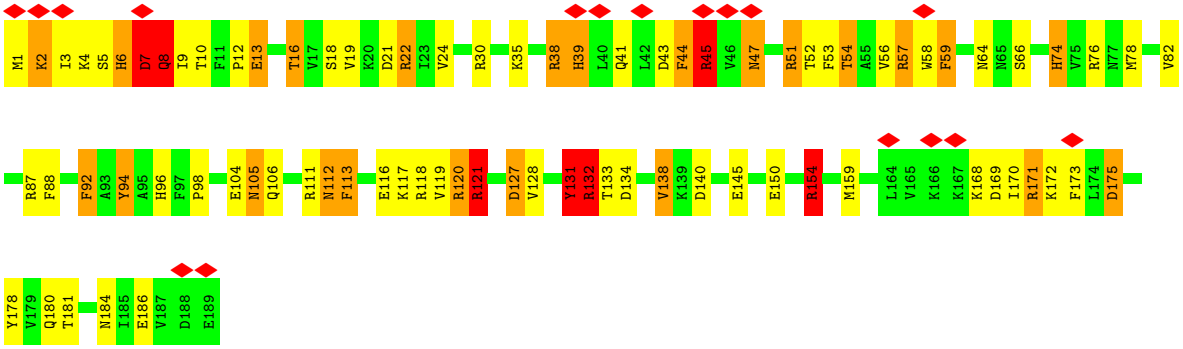
• Molecule 83: 60S RIBOSOMAL PROTEIN L7A, PUTATIVE

Chain Bx:



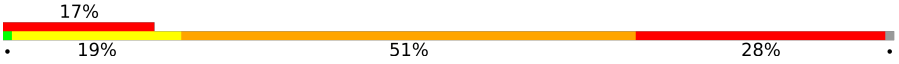
• Molecule 84: 60S RIBOSOMAL PROTEIN L9, PUTATIVE

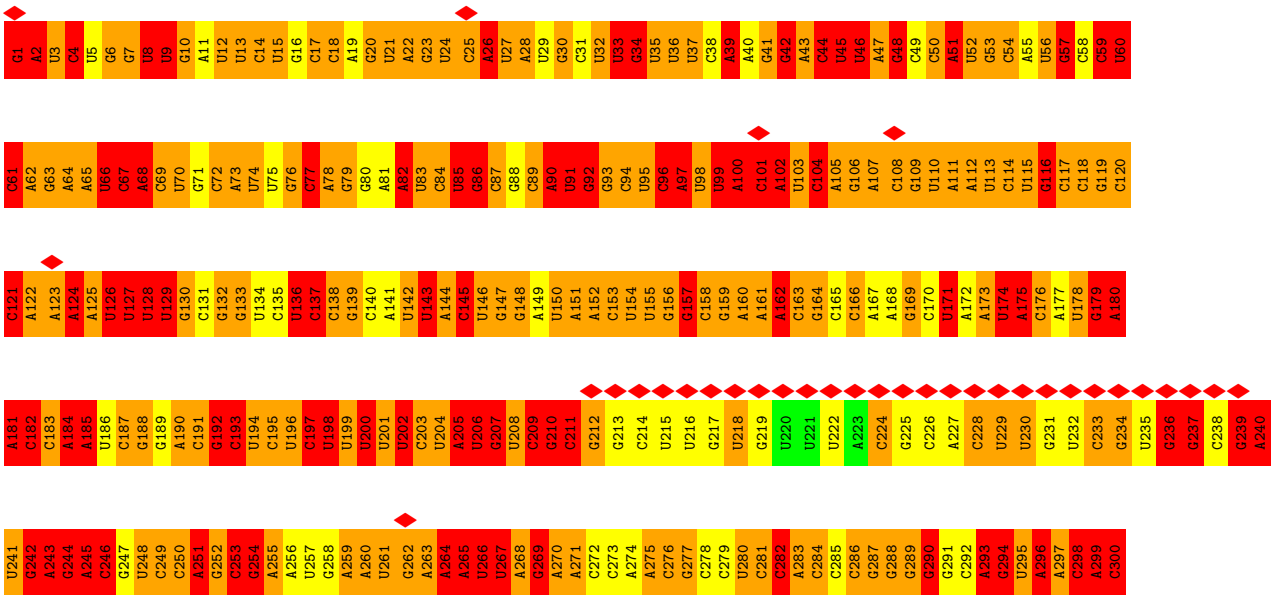
Chain By:

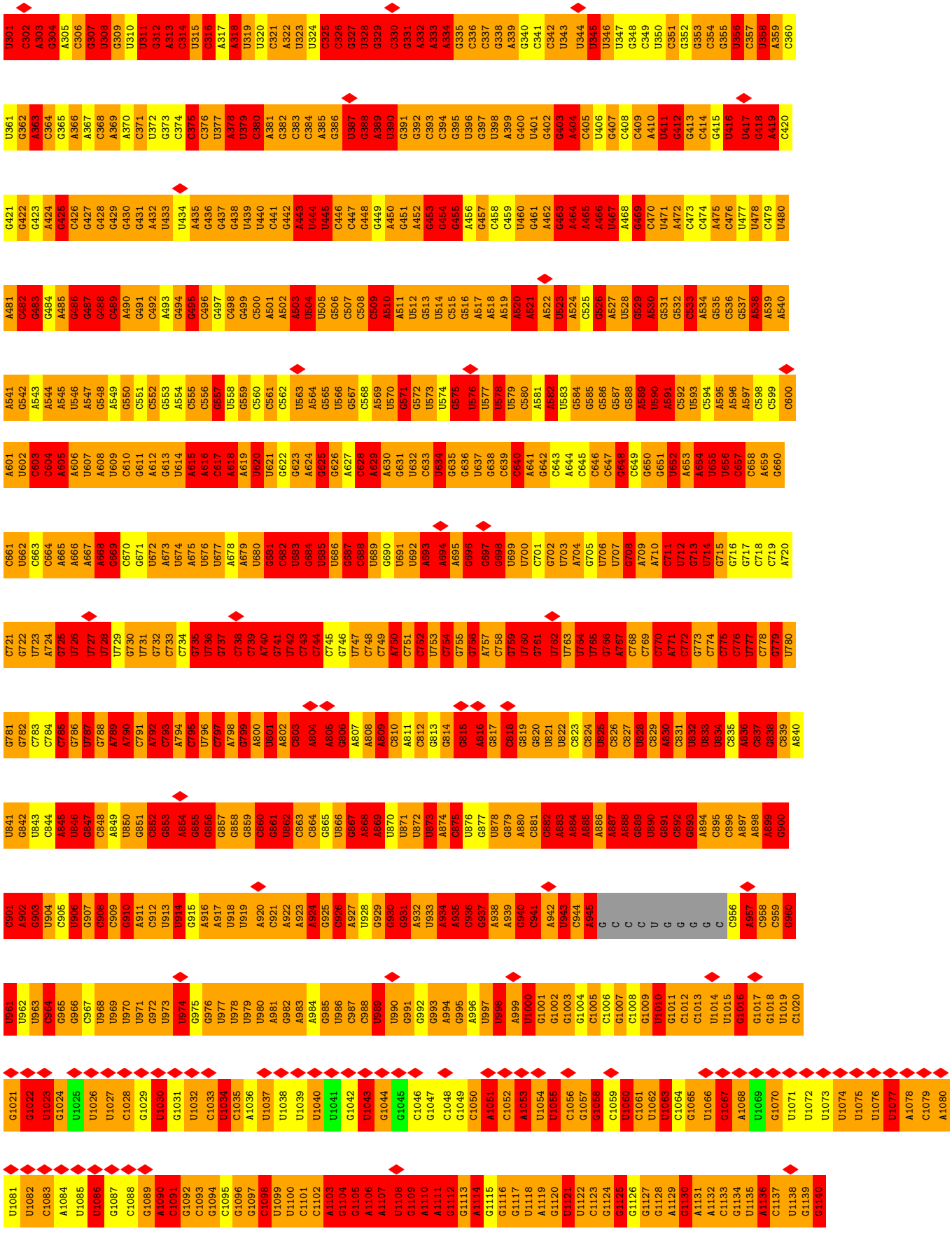


• Molecule 85: 18S RRNA OF THE SMALL RIBOSOMAL SUBUNIT

Chain AA:






U301 C302 A303 G304 A305 C306 G307 U308 G309 U310 U311 G312 A313 C314 U315 C316 A317 A318 U319 U320 C321 A322 U323 U324 C325 C326 G327 U328 G329 C330 G331 A332 A333 A334 G335 C336 C337 G338 A339 G340 C341 C342 U343 U344 U345 U346 U347 G348 C349 U350 C351 G352 G353 C354 G355 U356 C357 U358 A359 C360
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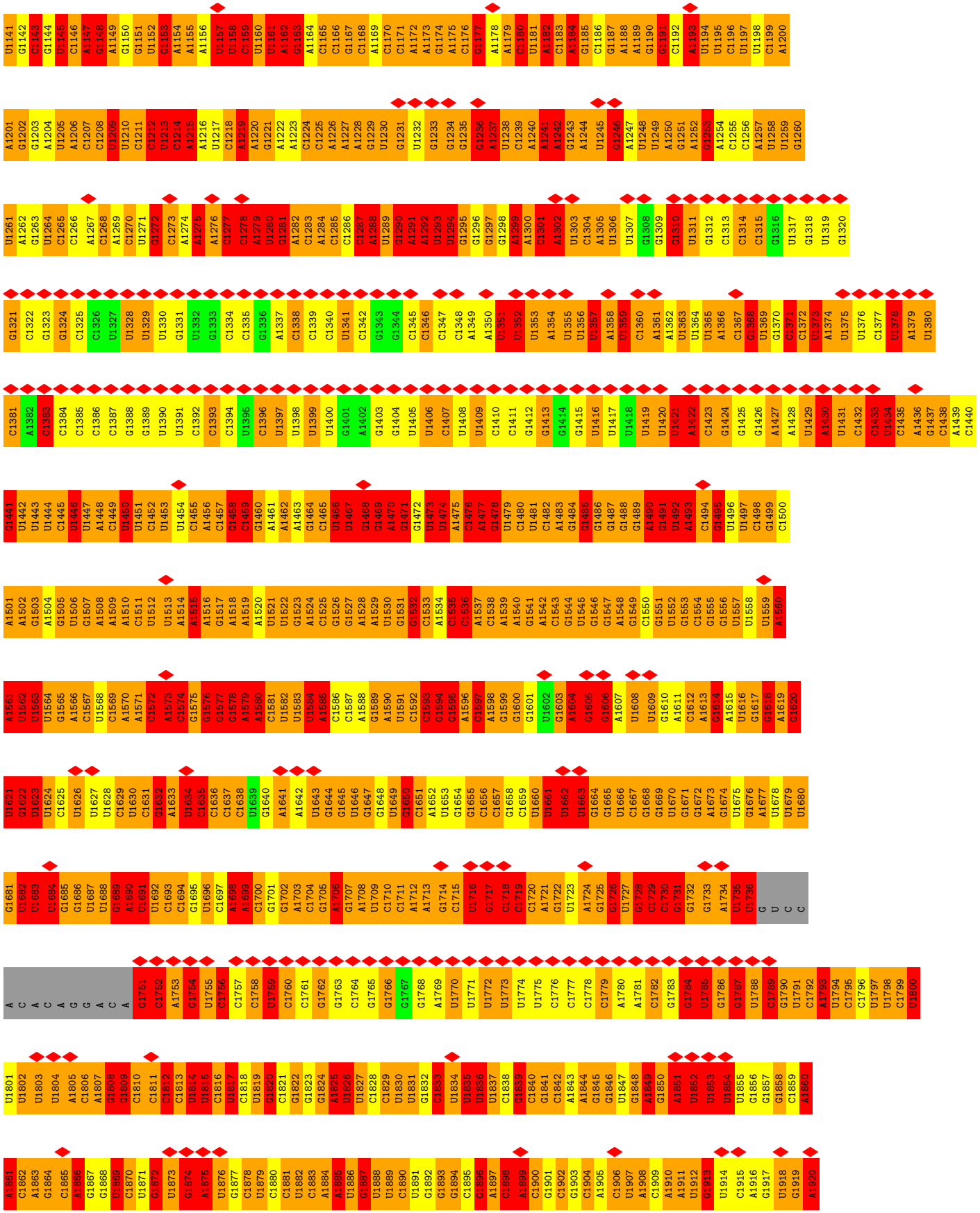
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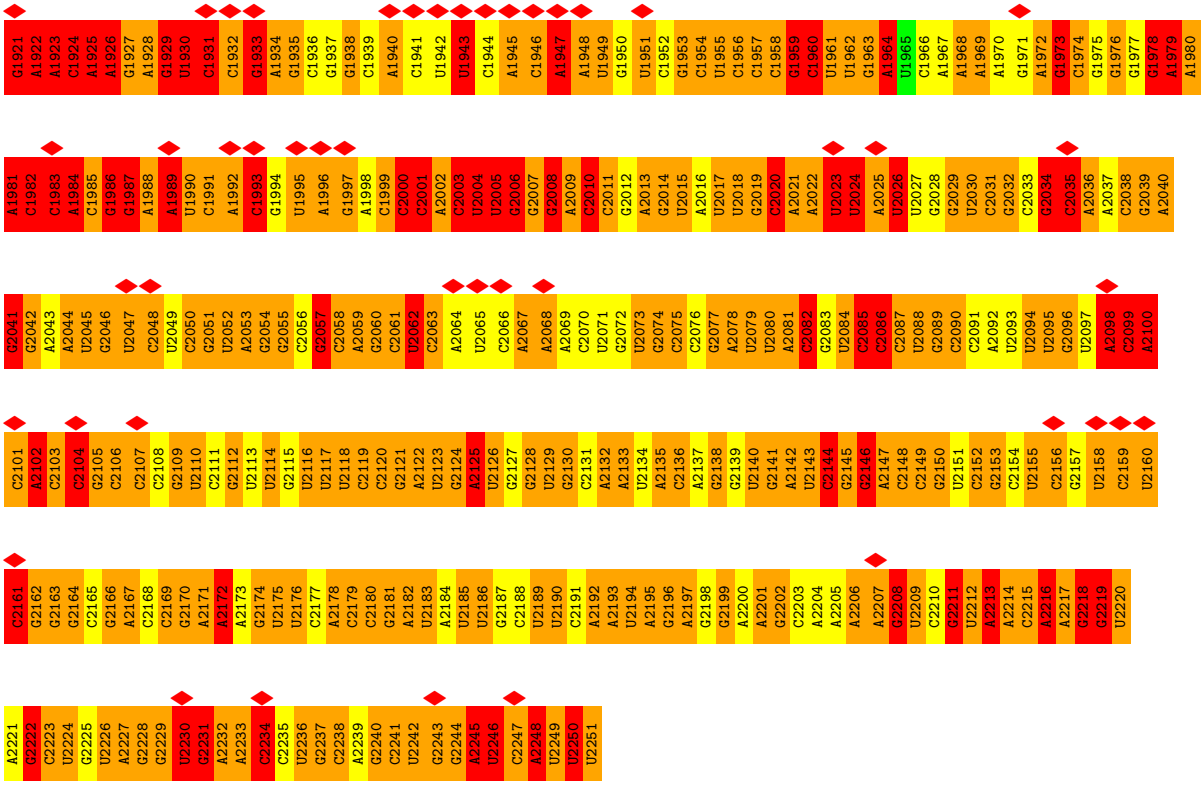
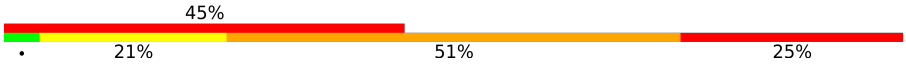
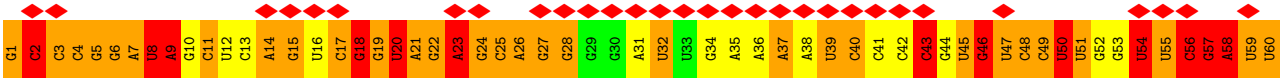
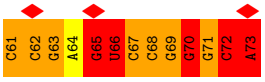


- Molecule 86: E-SITE TRNA

Chain AB:







4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	164000	Depositor
Resolution determination method	Not provided	
CTF correction method	PHASE-FLIPPING	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	59000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	483783.781	Depositor
Minimum map value	-202702.703	Depositor
Average map value	7679.429	Depositor
Map value standard deviation	33729.660	Depositor
Recommended contour level	108000	Depositor
Map size (Å)	391.31, 391.31, 391.31	wwPDB
Map dimensions	359, 359, 359	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A0	1.19	2/1808 (0.1%)	1.83	45/2432 (1.9%)
2	A1	1.37	5/1973 (0.3%)	1.90	53/2657 (2.0%)
3	A2	1.08	0/1507	1.76	36/2027 (1.8%)
4	A3	1.32	1/2026 (0.0%)	1.92	53/2699 (2.0%)
5	A4	1.33	2/1623 (0.1%)	2.04	60/2185 (2.7%)
6	A5	1.42	6/1574 (0.4%)	1.83	36/2100 (1.7%)
7	A6	1.38	3/1548 (0.2%)	1.95	44/2076 (2.1%)
8	A7	1.06	0/2471	1.64	33/3368 (1.0%)
9	A8	1.09	0/337	1.68	4/445 (0.9%)
10	A9	0.91	0/542	1.55	8/722 (1.1%)
11	AC	1.41	1/1655 (0.1%)	1.76	29/2240 (1.3%)
12	AD	1.02	0/877	1.60	13/1182 (1.1%)
13	AE	1.32	4/1324 (0.3%)	1.83	29/1771 (1.6%)
14	AF	0.76	0/946	1.36	11/1270 (0.9%)
15	AG	1.45	2/1170 (0.2%)	1.93	41/1567 (2.6%)
16	AH	1.24	0/937	1.77	21/1263 (1.7%)
17	AI	0.92	0/1098	1.64	15/1473 (1.0%)
18	AJ	1.29	0/1035	1.78	13/1386 (0.9%)
19	AK	1.06	0/1211	1.77	24/1625 (1.5%)
20	AL	1.24	1/1033 (0.1%)	1.91	27/1380 (2.0%)
21	AM	1.05	0/1247	1.76	29/1666 (1.7%)
22	AO	1.08	0/1206	1.81	23/1613 (1.4%)
23	AP	1.40	1/1766 (0.1%)	1.83	37/2383 (1.6%)
24	AQ	1.11	0/839	1.77	23/1139 (2.0%)
25	AR	1.52	3/612 (0.5%)	1.96	26/835 (3.1%)
26	AS	1.22	0/1137	1.73	27/1520 (1.8%)
27	AT	1.17	2/1065 (0.2%)	1.99	30/1411 (2.1%)
28	AU	1.00	0/681	1.54	6/907 (0.7%)
29	AV	1.17	0/825	1.95	19/1105 (1.7%)
30	AW	1.37	1/648 (0.2%)	1.84	14/868 (1.6%)
31	AX	1.11	2/1649 (0.1%)	1.71	35/2203 (1.6%)
32	AY	1.22	0/521	1.83	9/685 (1.3%)
33	AZ	1.20	1/527 (0.2%)	1.77	13/702 (1.9%)
34	BA	4.08	8852/44057 (20.1%)	3.34	8033/68678 (11.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	BB	3.66	5797/34826 (16.6%)	2.99	5090/54269 (9.4%)
36	BC	4.32	938/4004 (23.4%)	3.24	674/6235 (10.8%)
37	BD	4.09	601/2830 (21.2%)	3.33	521/4410 (11.8%)
38	BE	3.90	902/4956 (18.2%)	3.64	1067/7716 (13.8%)
39	BF	3.69	277/1691 (16.4%)	3.64	354/2627 (13.5%)
40	BG	4.34	1057/4358 (24.3%)	3.41	840/6797 (12.4%)
41	BH	3.79	548/3201 (17.1%)	3.52	652/4987 (13.1%)
42	BI	1.47	4/1553 (0.3%)	2.04	64/2070 (3.1%)
43	BJ	0.72	0/1743	1.28	12/2339 (0.5%)
44	BK	1.40	3/1760 (0.2%)	1.89	45/2359 (1.9%)
45	BL	1.33	1/1385 (0.1%)	1.80	33/1851 (1.8%)
46	BM	0.67	0/1033	1.21	1/1394 (0.1%)
47	BN	2.40	4/1793 (0.2%)	2.18	80/2392 (3.3%)
48	BO	1.46	2/1655 (0.1%)	1.84	44/2214 (2.0%)
49	BP	1.48	3/1506 (0.2%)	1.97	45/2014 (2.2%)
50	BQ	1.52	1/1755 (0.1%)	1.84	42/2346 (1.8%)
51	BR	1.39	1/1270 (0.1%)	1.99	39/1705 (2.3%)
52	BS	1.36	3/1508 (0.2%)	2.06	54/2028 (2.7%)
53	BT	1.45	1/1689 (0.1%)	1.97	65/2232 (2.9%)
54	BU	1.35	1/1290 (0.1%)	1.89	39/1734 (2.2%)
55	BV	0.96	0/878	1.57	13/1169 (1.1%)
56	BW	1.44	5/1059 (0.5%)	2.00	32/1424 (2.2%)
57	BX	1.56	4/1007 (0.4%)	1.97	35/1353 (2.6%)
58	BY	1.28	1/857 (0.1%)	1.82	26/1150 (2.3%)
59	BZ	1.44	3/1021 (0.3%)	2.07	43/1362 (3.2%)
60	Ba	1.40	0/1111	1.95	31/1479 (2.1%)
61	Bb	1.35	4/1165 (0.3%)	1.92	34/1554 (2.2%)
62	Bc	2.50	3/1145 (0.3%)	2.20	62/1528 (4.1%)
63	Bd	1.21	2/582 (0.3%)	1.98	22/777 (2.8%)
64	Be	1.50	7/1416 (0.5%)	1.91	38/1905 (2.0%)
65	Bf	1.43	8/3387 (0.2%)	1.99	129/4548 (2.8%)
66	Bg	1.75	3/745 (0.4%)	2.09	23/1005 (2.3%)
67	Bh	1.27	4/1551 (0.3%)	2.00	56/2059 (2.7%)
68	Bi	1.39	2/1076 (0.2%)	1.91	30/1439 (2.1%)
69	Bj	1.24	3/1312 (0.2%)	1.85	34/1743 (2.0%)
70	Bk	1.46	0/726	2.06	31/957 (3.2%)
71	Bl	1.44	4/958 (0.4%)	2.05	35/1290 (2.7%)
72	Bm	1.54	1/859 (0.1%)	1.97	29/1141 (2.5%)
73	Bn	1.60	1/713 (0.1%)	2.01	28/949 (3.0%)
74	Bo	1.70	8/727 (1.1%)	1.88	26/968 (2.7%)
75	Bp	1.50	1/666 (0.2%)	1.87	15/885 (1.7%)
76	Bq	1.31	1/471 (0.2%)	1.71	9/626 (1.4%)
77	Br	1.46	5/2937 (0.2%)	1.98	106/3943 (2.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
78	Bs	1.40	1/433 (0.2%)	1.86	12/572 (2.1%)
79	Bt	1.36	1/883 (0.1%)	1.87	24/1170 (2.1%)
80	Bu	1.30	1/2397 (0.0%)	1.88	65/3219 (2.0%)
81	Bv	1.30	1/1242 (0.1%)	1.84	29/1667 (1.7%)
82	Bw	1.44	2/2105 (0.1%)	1.91	49/2823 (1.7%)
83	Bx	1.48	5/1936 (0.3%)	1.85	38/2603 (1.5%)
84	By	1.32	1/1561 (0.1%)	1.95	62/2098 (3.0%)
85	AA	3.42	7237/52940 (13.7%)	3.10	8226/82489 (10.0%)
86	AB	2.36	80/1740 (4.6%)	2.66	188/2712 (6.9%)
All	All	3.06	26432/250887 (10.5%)	2.80	28260/369909 (7.6%)

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	A0	0	19
2	A1	0	18
3	A2	0	11
4	A3	0	23
5	A4	0	27
6	A5	0	23
7	A6	0	26
8	A7	0	17
9	A8	0	4
10	A9	0	4
11	AC	0	21
12	AD	0	10
13	AE	0	25
14	AF	0	6
15	AG	0	17
16	AH	0	8
17	AI	0	10
18	AJ	0	11
19	AK	0	20
20	AL	0	6
21	AM	0	18
22	AO	0	17
23	AP	0	14
24	AQ	0	7
25	AR	0	12

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Mol	Chain	#Chirality outliers	#Planarity outliers
26	AS	0	7
27	AT	0	27
28	AU	0	7
29	AV	0	13
30	AW	0	13
31	AX	0	10
32	AY	0	13
33	AZ	0	3
34	BA	0	1404
35	BB	0	967
36	BC	0	128
37	BD	0	89
38	BE	0	169
39	BF	0	61
40	BG	0	144
41	BH	0	87
42	BI	0	19
43	BJ	0	7
44	BK	0	26
45	BL	0	15
47	BN	1	31
48	BO	0	21
49	BP	0	24
50	BQ	0	28
51	BR	0	21
52	BS	0	21
53	BT	0	24
54	BU	0	21
55	BV	0	6
56	BW	0	10
57	BX	0	7
58	BY	0	15
59	BZ	0	12
60	Ba	0	20
61	Bb	0	15
62	Bc	0	27
63	Bd	0	10
64	Be	0	21
65	Bf	0	48
66	Bg	0	8
67	Bh	0	23
68	Bi	0	13

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Mol	Chain	#Chirality outliers	#Planarity outliers
69	Bj	1	23
70	Bk	0	12
71	Bl	0	23
72	Bm	0	16
73	Bn	0	14
74	Bo	0	12
75	Bp	0	6
76	Bq	0	9
77	Br	0	46
78	Bs	0	5
79	Bt	0	13
80	Bu	0	34
81	Bv	0	22
82	Bw	0	32
83	Bx	0	19
84	By	1	27
85	AA	0	1567
86	AB	0	45
All	All	3	5934

The worst 5 of 26432 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	AA	469	G	C5-C4	80.15	1.94	1.38
47	BN	7	ALA	CA-C	79.39	3.59	1.52
34	BA	743	A	N9-C4	74.20	1.82	1.37
62	Bc	78	LYS	CD-CE	69.91	3.26	1.51
34	BA	214	A	C6-N1	57.25	1.75	1.35

The worst 5 of 28260 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
85	AA	469	G	N9-C4-C5	-49.23	85.71	105.40
39	BF	32	G	P-O3'-C3'	41.15	169.07	119.70
35	BB	1212	C	C6-N1-C2	-40.14	104.24	120.30
85	AA	769	C	C6-N1-C2	-39.18	104.63	120.30
34	BA	692	U	P-O3'-C3'	38.13	165.46	119.70

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
47	BN	66	PRO	CA

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Mol	Chain	Res	Type	Atom
69	Bj	5	ARG	CA
84	By	7	ASP	CA

5 of 5934 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A0	103	HIS	Sidechain
1	A0	41	ARG	Sidechain
1	A0	43	PHE	Sidechain
1	A0	64	ARG	Sidechain
1	A0	83	TYR	Sidechain

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	A0	217/256 (85%)	180 (83%)	22 (10%)	15 (7%)	1 11
2	A1	246/273 (90%)	189 (77%)	38 (15%)	19 (8%)	1 9
3	A2	185/190 (97%)	159 (86%)	17 (9%)	9 (5%)	2 16
4	A3	248/250 (99%)	204 (82%)	24 (10%)	20 (8%)	1 9
5	A4	190/202 (94%)	148 (78%)	24 (13%)	18 (10%)	0 8
6	A5	191/220 (87%)	158 (83%)	18 (9%)	15 (8%)	1 9
7	A6	185/190 (97%)	135 (73%)	30 (16%)	20 (11%)	0 6
8	A7	313/318 (98%)	256 (82%)	39 (12%)	18 (6%)	1 13
9	A8	40/57 (70%)	34 (85%)	3 (8%)	3 (8%)	1 10
10	A9	64/153 (42%)	50 (78%)	9 (14%)	5 (8%)	1 9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
11	AC	202/277 (73%)	162 (80%)	25 (12%)	15 (7%)	1 10
12	AD	102/172 (59%)	79 (78%)	9 (9%)	14 (14%)	0 4
13	AE	158/174 (91%)	126 (80%)	12 (8%)	20 (13%)	0 4
14	AF	119/144 (83%)	105 (88%)	11 (9%)	3 (2%)	4 26
15	AG	139/151 (92%)	120 (86%)	12 (9%)	7 (5%)	1 15
16	AH	124/144 (86%)	99 (80%)	14 (11%)	11 (9%)	0 8
17	AI	132/152 (87%)	100 (76%)	21 (16%)	11 (8%)	0 9
18	AJ	127/130 (98%)	114 (90%)	7 (6%)	6 (5%)	2 16
19	AK	146/149 (98%)	118 (81%)	18 (12%)	10 (7%)	1 11
20	AL	125/142 (88%)	94 (75%)	19 (15%)	12 (10%)	0 7
21	AM	151/153 (99%)	114 (76%)	16 (11%)	21 (14%)	0 4
22	AO	147/167 (88%)	128 (87%)	10 (7%)	9 (6%)	1 13
23	AP	222/266 (84%)	171 (77%)	29 (13%)	22 (10%)	0 7
24	AQ	103/117 (88%)	86 (84%)	10 (10%)	7 (7%)	1 11
25	AR	79/194 (41%)	59 (75%)	12 (15%)	8 (10%)	0 7
26	AS	140/143 (98%)	111 (79%)	18 (13%)	11 (8%)	1 9
27	AT	129/137 (94%)	100 (78%)	15 (12%)	14 (11%)	0 6
28	AU	84/113 (74%)	66 (79%)	12 (14%)	6 (7%)	1 10
29	AV	99/111 (89%)	64 (65%)	20 (20%)	15 (15%)	0 3
30	AW	81/86 (94%)	61 (75%)	11 (14%)	9 (11%)	0 6
31	AX	204/214 (95%)	176 (86%)	17 (8%)	11 (5%)	1 14
32	AY	63/66 (96%)	46 (73%)	8 (13%)	9 (14%)	0 3
33	AZ	66/103 (64%)	56 (85%)	7 (11%)	3 (4%)	2 17
42	BI	190/193 (98%)	126 (66%)	37 (20%)	27 (14%)	0 3
43	BJ	212/214 (99%)	186 (88%)	20 (9%)	6 (3%)	4 24
44	BK	210/213 (99%)	161 (77%)	26 (12%)	23 (11%)	0 6
45	BL	168/194 (87%)	134 (80%)	21 (12%)	13 (8%)	1 9
46	BM	137/164 (84%)	103 (75%)	25 (18%)	9 (7%)	1 12
47	BN	214/218 (98%)	158 (74%)	20 (9%)	36 (17%)	0 3
48	BO	199/222 (90%)	164 (82%)	21 (11%)	14 (7%)	1 11
49	BP	182/189 (96%)	149 (82%)	19 (10%)	14 (8%)	1 9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
50	BQ	201/221 (91%)	160 (80%)	21 (10%)	20 (10%)	0 7
51	BR	153/166 (92%)	121 (79%)	21 (14%)	11 (7%)	1 10
52	BS	177/179 (99%)	133 (75%)	15 (8%)	29 (16%)	0 3
53	BT	198/260 (76%)	168 (85%)	20 (10%)	10 (5%)	1 15
54	BU	156/159 (98%)	118 (76%)	19 (12%)	19 (12%)	0 4
55	BV	102/130 (78%)	84 (82%)	13 (13%)	5 (5%)	2 16
56	BW	136/139 (98%)	103 (76%)	18 (13%)	15 (11%)	0 6
57	BX	119/164 (73%)	97 (82%)	9 (8%)	13 (11%)	0 6
58	BY	98/125 (78%)	81 (83%)	9 (9%)	8 (8%)	1 9
59	BZ	123/143 (86%)	104 (85%)	12 (10%)	7 (6%)	1 14
60	Ba	130/133 (98%)	93 (72%)	21 (16%)	16 (12%)	0 4
61	Bb	142/145 (98%)	108 (76%)	19 (13%)	15 (11%)	0 6
62	Bc	139/146 (95%)	103 (74%)	18 (13%)	18 (13%)	0 4
63	Bd	68/71 (96%)	50 (74%)	8 (12%)	10 (15%)	0 3
64	Be	184/260 (71%)	135 (73%)	32 (17%)	17 (9%)	0 8
65	Bf	412/429 (96%)	296 (72%)	66 (16%)	50 (12%)	0 4
66	Bg	94/105 (90%)	88 (94%)	5 (5%)	1 (1%)	12 46
67	Bh	186/188 (99%)	155 (83%)	13 (7%)	18 (10%)	0 7
68	Bi	127/132 (96%)	98 (77%)	18 (14%)	11 (9%)	0 9
69	Bj	160/170 (94%)	123 (77%)	22 (14%)	15 (9%)	0 8
70	Bk	82/127 (65%)	56 (68%)	14 (17%)	12 (15%)	0 3
71	Bl	114/149 (76%)	84 (74%)	10 (9%)	20 (18%)	0 2
72	Bm	105/109 (96%)	79 (75%)	8 (8%)	18 (17%)	0 2
73	Bn	81/84 (96%)	56 (69%)	15 (18%)	10 (12%)	0 4
74	Bo	90/93 (97%)	71 (79%)	6 (7%)	13 (14%)	0 3
75	Bp	79/82 (96%)	59 (75%)	10 (13%)	10 (13%)	0 4
76	Bq	48/51 (94%)	34 (71%)	6 (12%)	8 (17%)	0 3
77	Br	366/374 (98%)	274 (75%)	56 (15%)	36 (10%)	0 7
78	Bs	50/128 (39%)	44 (88%)	4 (8%)	2 (4%)	2 18
79	Bt	103/106 (97%)	75 (73%)	16 (16%)	12 (12%)	0 4
80	Bu	297/308 (96%)	216 (73%)	46 (16%)	35 (12%)	0 4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
81	Bv	154/192 (80%)	114 (74%)	25 (16%)	15 (10%)	0 7
82	Bw	255/257 (99%)	200 (78%)	33 (13%)	22 (9%)	0 9
83	Bx	238/276 (86%)	188 (79%)	26 (11%)	24 (10%)	0 7
84	By	187/189 (99%)	155 (83%)	15 (8%)	17 (9%)	0 8
All	All	11687/13211 (88%)	9172 (78%)	1415 (12%)	1100 (9%)	1 8

5 of 1100 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A0	37	ASN
1	A0	119	TRP
1	A0	145	THR
1	A0	212	LEU
1	A0	225	PHE

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A0	189/218 (87%)	159 (84%)	30 (16%)	2 10
2	A1	209/231 (90%)	172 (82%)	37 (18%)	1 8
3	A2	158/160 (99%)	132 (84%)	26 (16%)	2 10
4	A3	207/207 (100%)	174 (84%)	33 (16%)	2 10
5	A4	176/187 (94%)	144 (82%)	32 (18%)	1 8
6	A5	158/180 (88%)	140 (89%)	18 (11%)	4 17
7	A6	162/166 (98%)	137 (85%)	25 (15%)	2 11
8	A7	264/267 (99%)	232 (88%)	32 (12%)	4 16
9	A8	36/49 (74%)	32 (89%)	4 (11%)	5 18
10	A9	57/126 (45%)	52 (91%)	5 (9%)	8 25
11	AC	179/243 (74%)	143 (80%)	36 (20%)	1 6
12	AD	92/131 (70%)	81 (88%)	11 (12%)	4 16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
13	AE	143/156 (92%)	126 (88%)	17 (12%)	4 16
14	AF	102/120 (85%)	99 (97%)	3 (3%)	37 56
15	AG	124/131 (95%)	110 (89%)	14 (11%)	4 17
16	AH	95/112 (85%)	83 (87%)	12 (13%)	3 15
17	AI	110/128 (86%)	102 (93%)	8 (7%)	11 31
18	AJ	108/109 (99%)	90 (83%)	18 (17%)	2 9
19	AK	123/124 (99%)	105 (85%)	18 (15%)	2 12
20	AL	111/122 (91%)	101 (91%)	10 (9%)	8 24
21	AM	133/133 (100%)	121 (91%)	12 (9%)	8 24
22	AO	123/137 (90%)	107 (87%)	16 (13%)	3 14
23	AP	185/204 (91%)	154 (83%)	31 (17%)	1 9
24	AQ	94/104 (90%)	84 (89%)	10 (11%)	5 19
25	AR	66/150 (44%)	55 (83%)	11 (17%)	2 9
26	AS	117/118 (99%)	105 (90%)	12 (10%)	6 20
27	AT	110/116 (95%)	82 (74%)	28 (26%)	0 3
28	AU	73/94 (78%)	67 (92%)	6 (8%)	9 28
29	AV	87/97 (90%)	74 (85%)	13 (15%)	2 12
30	AW	71/75 (95%)	58 (82%)	13 (18%)	1 8
31	AX	173/180 (96%)	155 (90%)	18 (10%)	5 19
32	AY	52/53 (98%)	41 (79%)	11 (21%)	1 5
33	AZ	57/84 (68%)	52 (91%)	5 (9%)	8 25
42	BI	164/165 (99%)	140 (85%)	24 (15%)	2 12
43	BJ	201/201 (100%)	189 (94%)	12 (6%)	16 37
44	BK	184/185 (100%)	154 (84%)	30 (16%)	2 10
45	BL	146/167 (87%)	120 (82%)	26 (18%)	1 8
46	BM	114/137 (83%)	106 (93%)	8 (7%)	12 32
47	BN	185/188 (98%)	142 (77%)	43 (23%)	0 4
48	BO	175/195 (90%)	150 (86%)	25 (14%)	2 12
49	BP	156/160 (98%)	139 (89%)	17 (11%)	5 18
50	BQ	176/193 (91%)	147 (84%)	29 (16%)	2 10
51	BR	132/144 (92%)	106 (80%)	26 (20%)	1 7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
52	BS	160/160 (100%)	130 (81%)	30 (19%)	1 7
53	BT	170/198 (86%)	144 (85%)	26 (15%)	2 11
54	BU	133/134 (99%)	115 (86%)	18 (14%)	3 13
55	BV	95/116 (82%)	85 (90%)	10 (10%)	5 19
56	BW	107/108 (99%)	86 (80%)	21 (20%)	1 7
57	BX	108/136 (79%)	97 (90%)	11 (10%)	6 20
58	BY	85/102 (83%)	78 (92%)	7 (8%)	9 28
59	BZ	110/125 (88%)	98 (89%)	12 (11%)	5 18
60	Ba	116/117 (99%)	100 (86%)	16 (14%)	3 13
61	Bb	115/116 (99%)	95 (83%)	20 (17%)	1 9
62	Bc	124/130 (95%)	95 (77%)	29 (23%)	0 4
63	Bd	58/59 (98%)	54 (93%)	4 (7%)	13 33
64	Be	145/204 (71%)	122 (84%)	23 (16%)	2 10
65	Bf	349/360 (97%)	305 (87%)	44 (13%)	3 15
66	Bg	84/92 (91%)	72 (86%)	12 (14%)	2 12
67	Bh	162/162 (100%)	136 (84%)	26 (16%)	2 10
68	Bi	113/117 (97%)	96 (85%)	17 (15%)	2 11
69	Bj	130/137 (95%)	105 (81%)	25 (19%)	1 7
70	Bk	75/114 (66%)	60 (80%)	15 (20%)	1 6
71	Bl	97/126 (77%)	81 (84%)	16 (16%)	2 10
72	Bm	87/90 (97%)	72 (83%)	15 (17%)	1 9
73	Bn	70/71 (99%)	55 (79%)	15 (21%)	1 5
74	Bo	74/76 (97%)	59 (80%)	15 (20%)	1 6
75	Bp	76/77 (99%)	68 (90%)	8 (10%)	5 19
76	Bq	46/47 (98%)	35 (76%)	11 (24%)	0 4
77	Br	304/310 (98%)	251 (83%)	53 (17%)	1 9
78	Bs	46/111 (41%)	38 (83%)	8 (17%)	1 9
79	Bt	94/95 (99%)	83 (88%)	11 (12%)	4 16
80	Bu	238/247 (96%)	199 (84%)	39 (16%)	2 10
81	Bv	132/160 (82%)	112 (85%)	20 (15%)	2 11
82	Bw	213/213 (100%)	176 (83%)	37 (17%)	1 9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
83	Bx	203/229 (89%)	173 (85%)	30 (15%)	2 12
84	By	172/172 (100%)	138 (80%)	34 (20%)	1 7
All	All	10068/11158 (90%)	8575 (85%)	1493 (15%)	5 12

5 of 1493 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	BX	134	THR
69	Bj	27	PRO
60	Ba	31	ARG
57	BX	109	ASP
64	Be	241	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 164 such sidechains are listed below:

Mol	Chain	Res	Type
64	Be	216	HIS
77	Br	145	ASN
65	Bf	160	HIS
69	Bj	62	HIS
80	Bu	39	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	BA	1846/1847 (99%)	616 (33%)	225 (12%)
35	BB	1464/1465 (99%)	460 (31%)	143 (9%)
36	BC	169/169 (100%)	46 (27%)	20 (11%)
37	BD	118/119 (99%)	31 (26%)	9 (7%)
38	BE	209/210 (99%)	78 (37%)	27 (12%)
39	BF	73/73 (100%)	48 (65%)	23 (31%)
40	BG	181/182 (99%)	40 (22%)	8 (4%)
41	BH	134/135 (99%)	49 (36%)	16 (11%)
85	AA	2226/2251 (98%)	767 (34%)	312 (14%)
86	AB	72/73 (98%)	30 (41%)	7 (9%)
All	All	6492/6524 (99%)	2165 (33%)	790 (12%)

5 of 2165 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	BA	11	U
34	BA	13	U
34	BA	22	C
34	BA	23	A
34	BA	37	A

5 of 790 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
41	BH	62	C
85	AA	687	G
85	AA	33	U
41	BH	42	U
85	AA	326	C

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

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
34	BA	3
40	BG	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BA	546:U	O3'	547:C	P	2.11
1	BA	557:U	O3'	558:C	P	1.87
1	BA	547:C	O3'	548:G	P	1.78
1	BG	24:A	O3'	25:G	P	1.39
1	BG	9:G	O3'	10:U	P	1.37

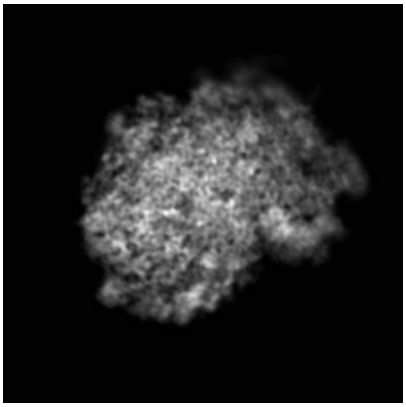
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-2239. These allow visual inspection of the internal detail of the map and identification of artifacts.

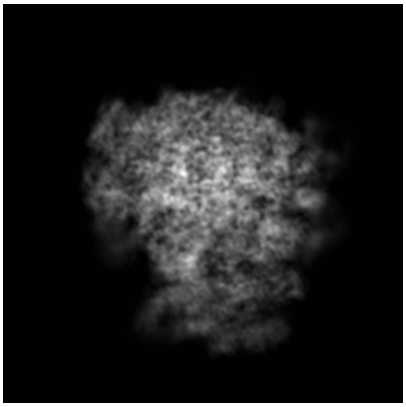
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

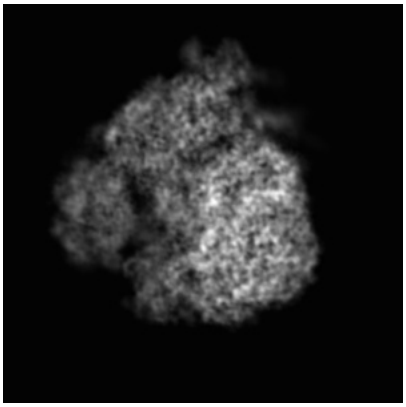
6.1.1 Primary map



X



Y

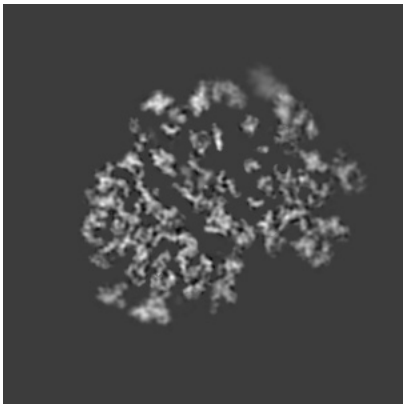


Z

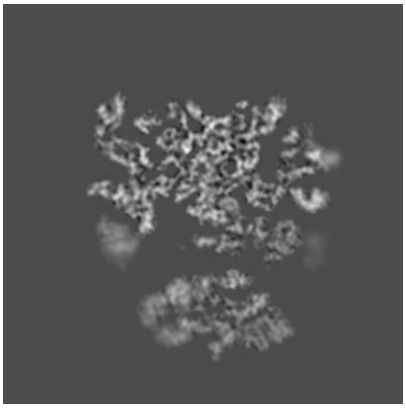
The images above show the map projected in three orthogonal directions.

6.2 Central slices

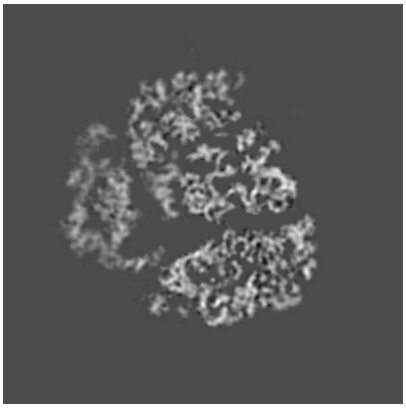
6.2.1 Primary map



X Index: 179



Y Index: 179

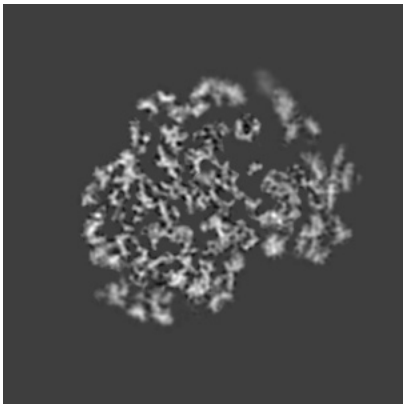


Z Index: 179

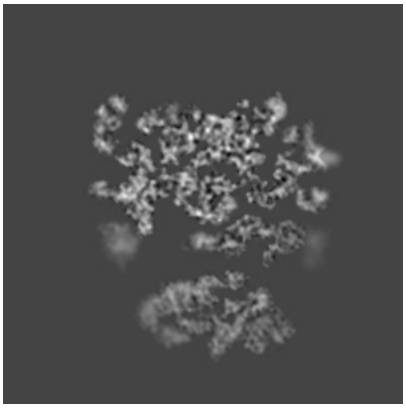
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

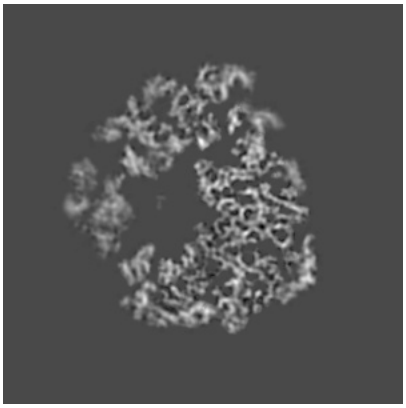
6.3.1 Primary map



X Index: 184



Y Index: 182

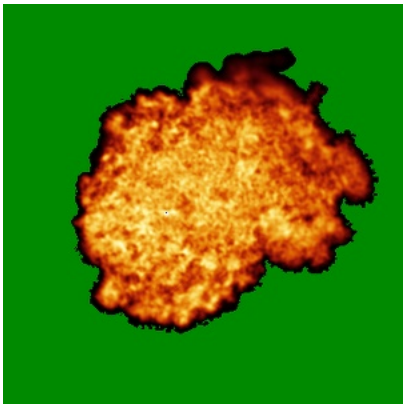


Z Index: 161

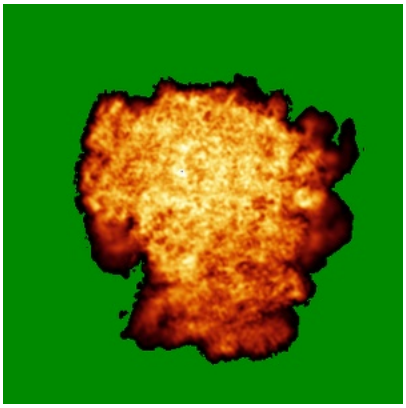
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

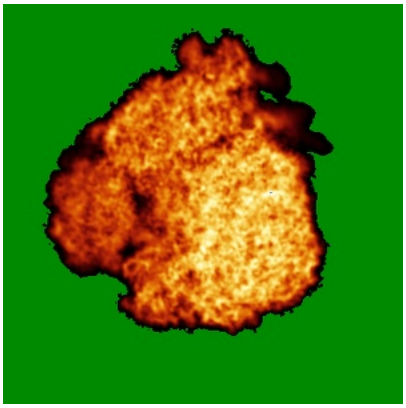
6.4.1 Primary map



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

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 108000.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

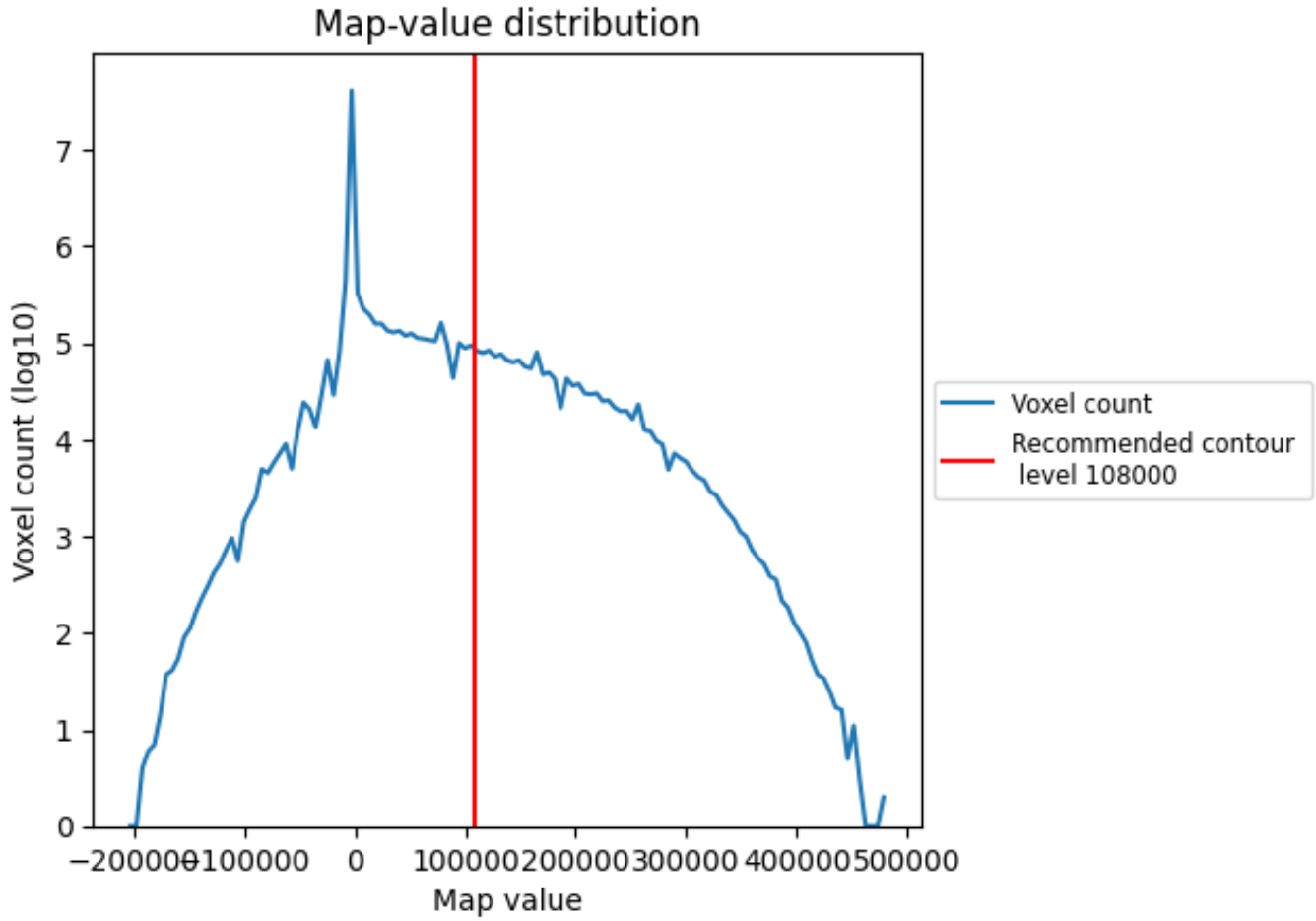
6.6 Mask visualisation (i)

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

7 Map analysis

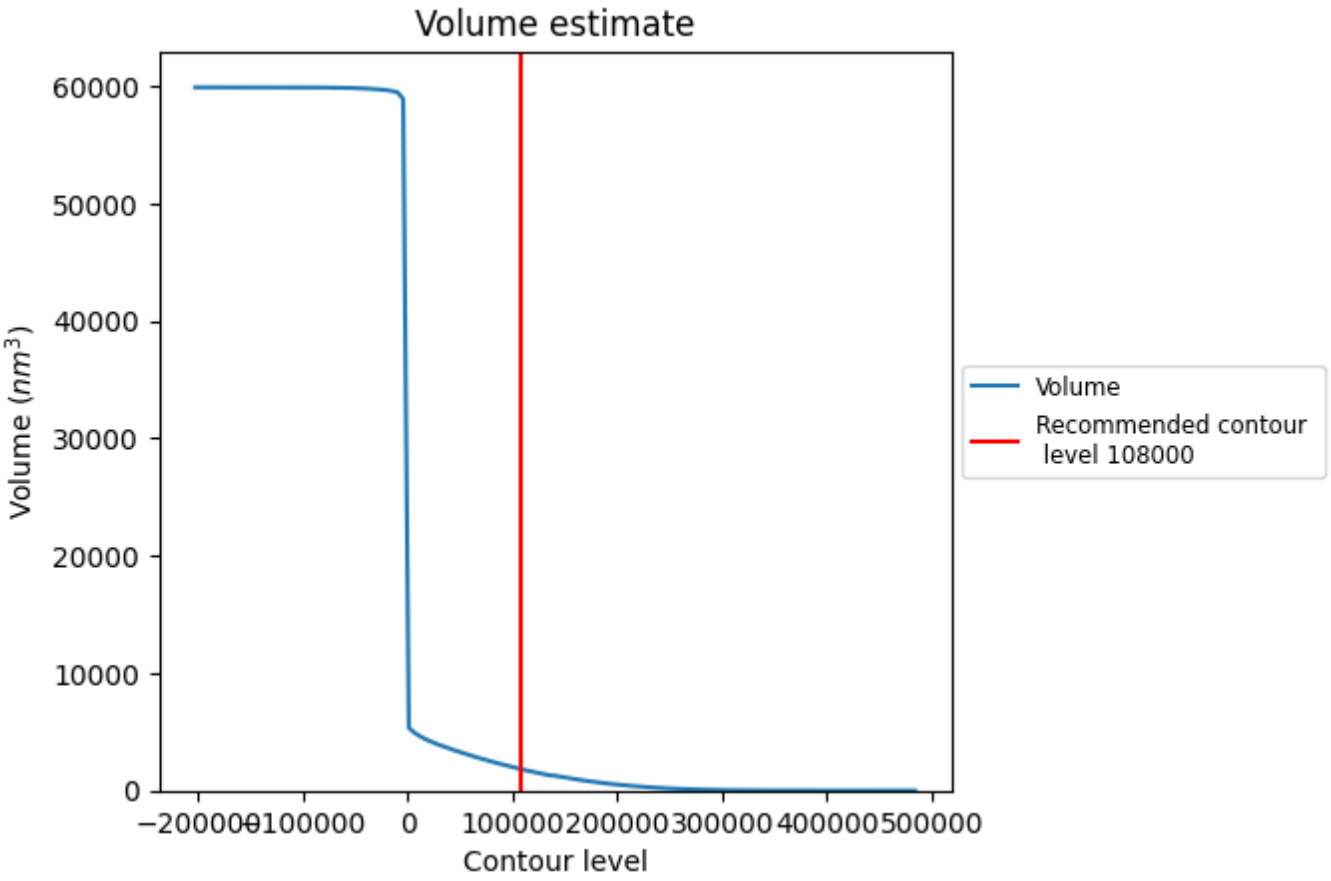
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

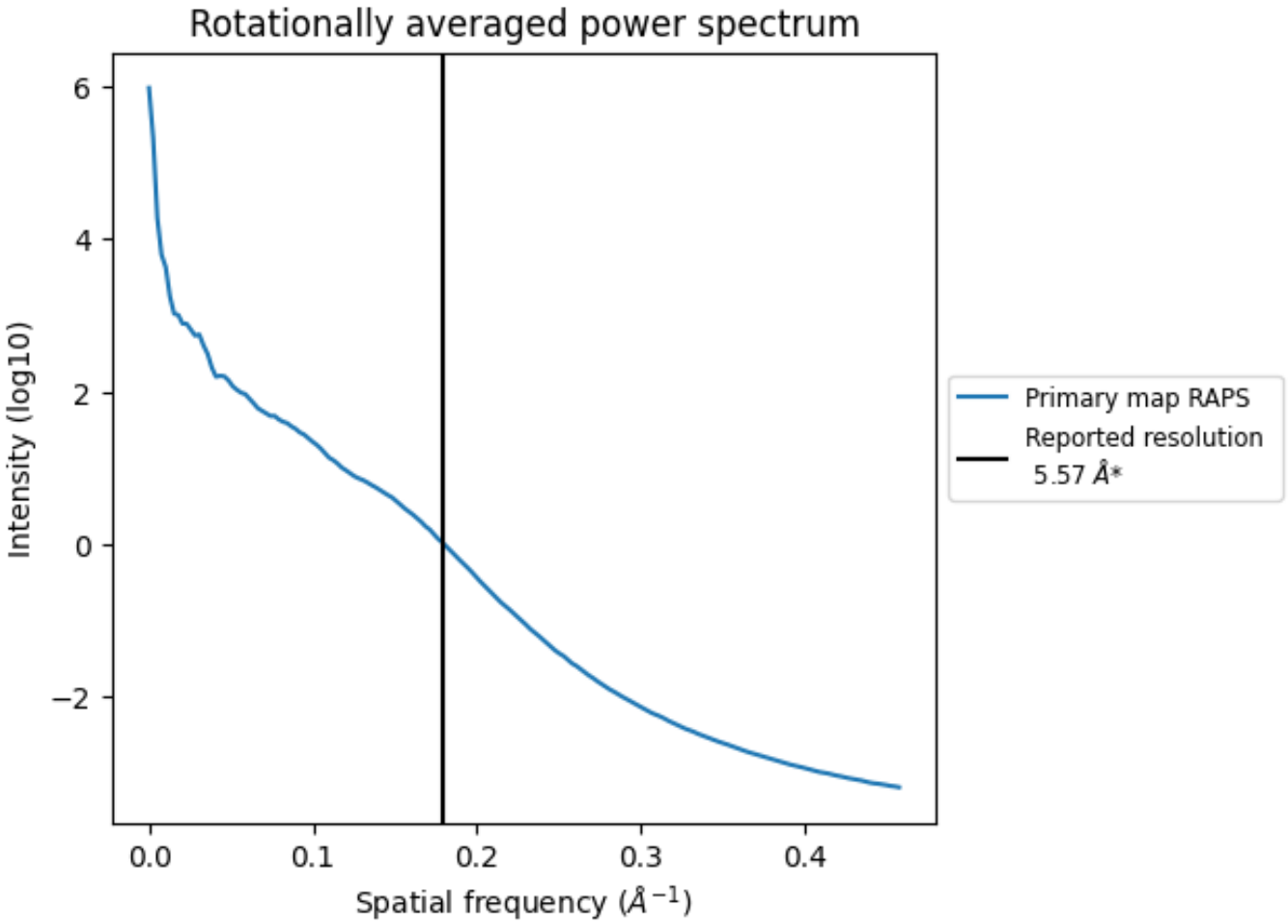
7.2 Volume estimate



The volume at the recommended contour level is 1820 nm^3; this corresponds to an approximate mass of 1644 kDa.

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

7.3 Rotationally averaged power spectrum (i)

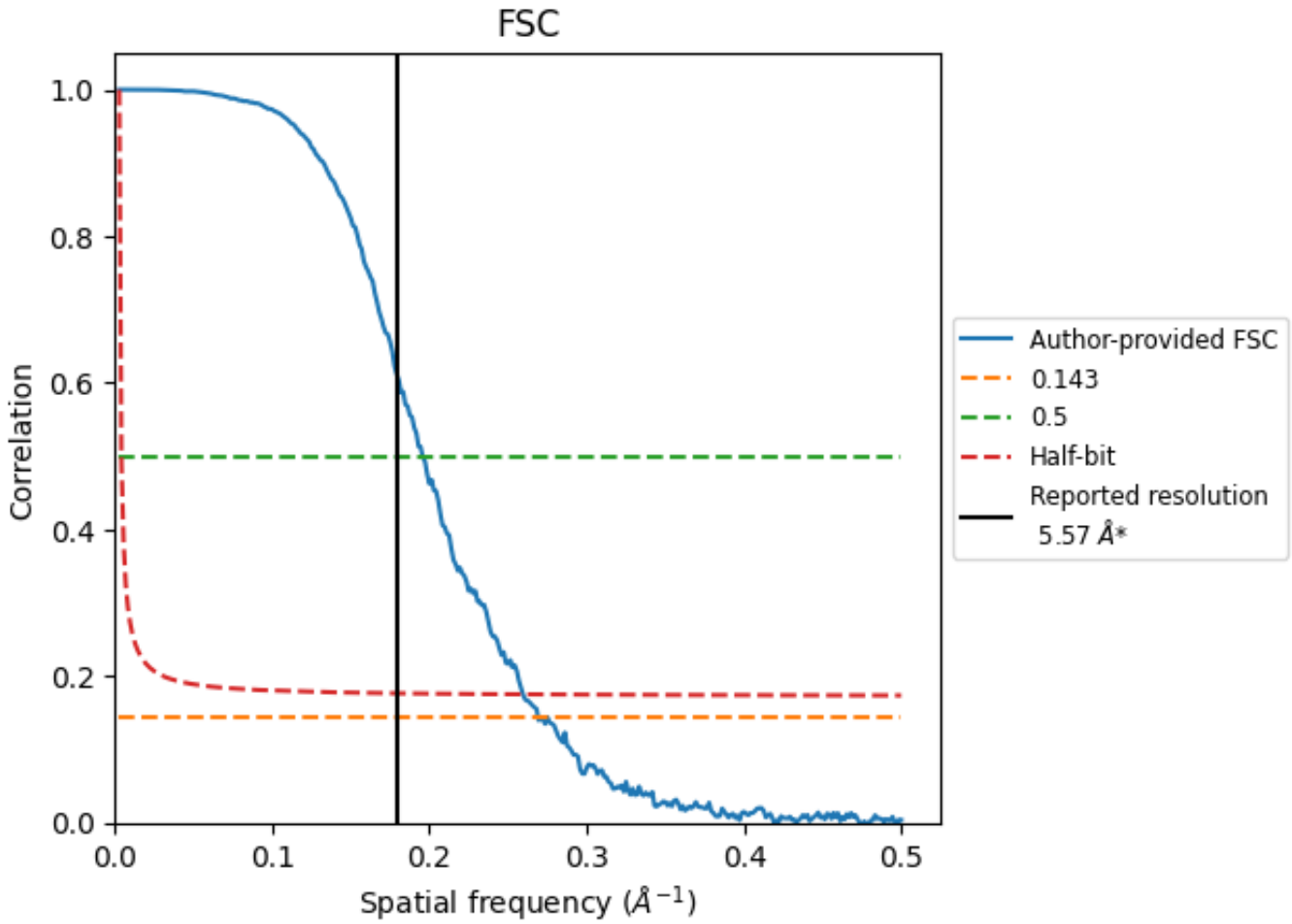


*Reported resolution corresponds to spatial frequency of 0.180 Å^{-1}

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.180 Å^{-1}

8.2 Resolution estimates (i)

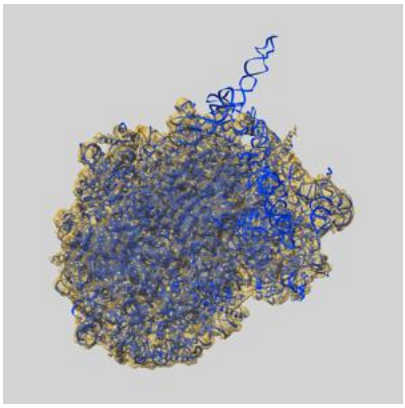
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	3.72	5.11	3.85
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

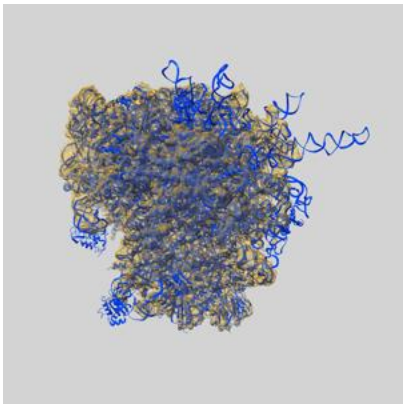
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-2239 and PDB model 4V8M. Per-residue inclusion information can be found in section 3 on page 21.

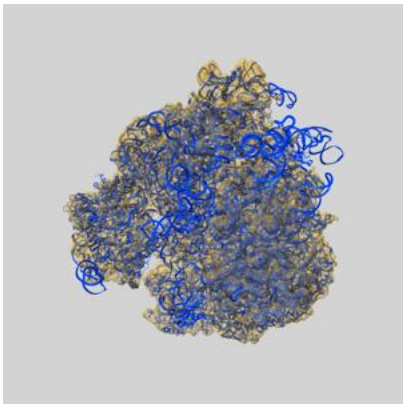
9.1 Map-model overlay



X



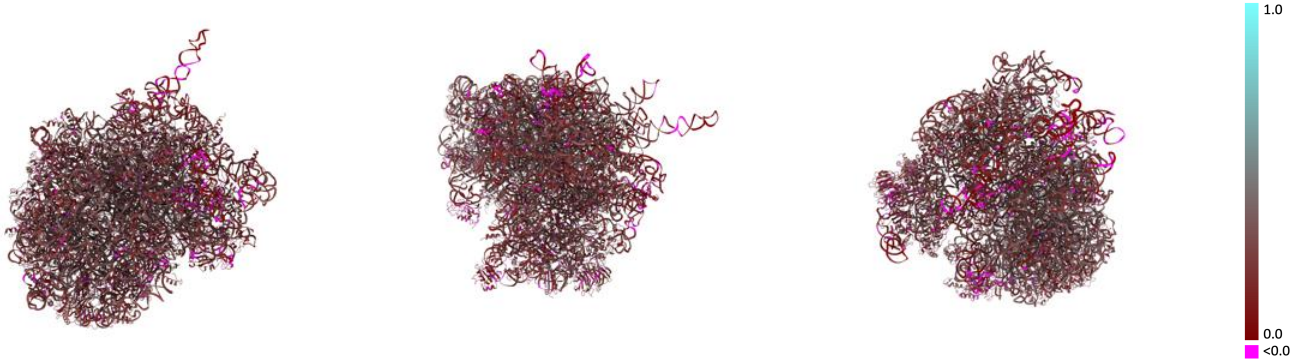
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 108000.0 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.

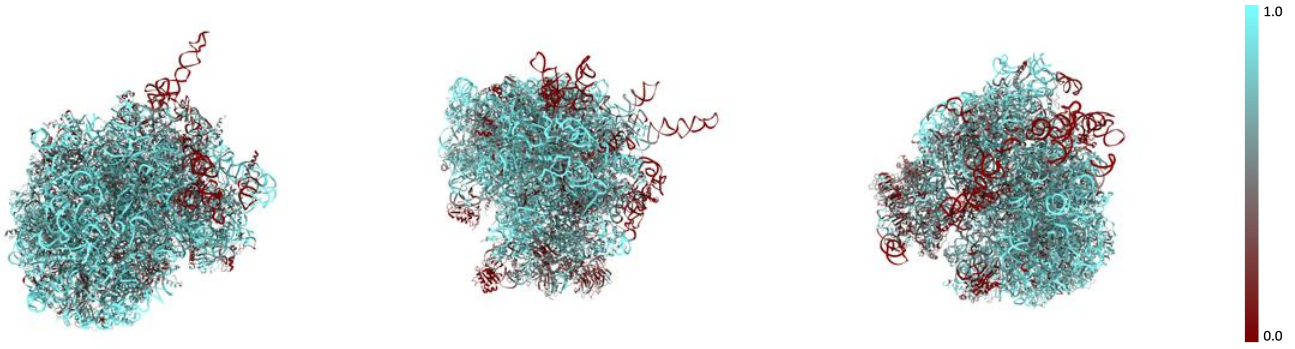
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

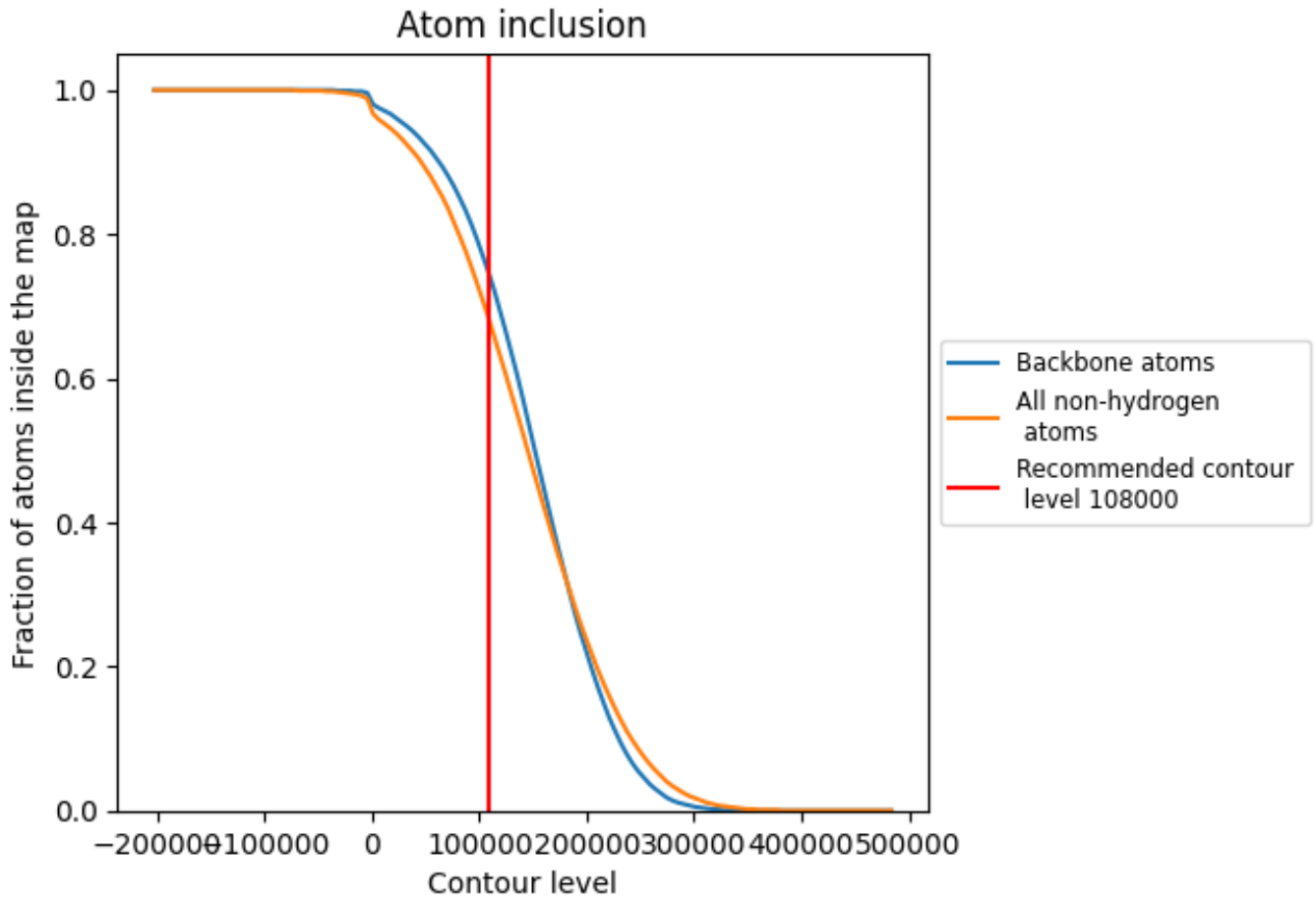
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (108000).

9.4 Atom inclusion (i)



At the recommended contour level, 75% of all backbone atoms, 69% 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 (108000) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6860	0.2390
A0	0.5170	0.2360
A1	0.5980	0.2390
A2	0.3430	0.1910
A3	0.6080	0.2070
A4	0.6130	0.2320
A5	0.4740	0.2180
A6	0.6720	0.2270
A7	0.3000	0.1870
A8	0.1980	0.1170
A9	0.1860	0.1310
AA	0.7340	0.2390
AB	0.4690	0.1630
AC	0.6380	0.2440
AD	0.3260	0.1670
AE	0.3730	0.2080
AF	0.0100	0.1110
AG	0.5170	0.2330
AH	0.3730	0.1990
AI	0.2750	0.1480
AJ	0.4700	0.2300
AK	0.3240	0.2000
AL	0.5290	0.2220
AM	0.2880	0.1420
AO	0.4990	0.1980
AP	0.6320	0.2360
AQ	0.3770	0.1720
AR	0.6530	0.2550
AS	0.4020	0.1980
AT	0.6470	0.2000
AU	0.3200	0.1280
AV	0.2260	0.2090
AW	0.6460	0.2790
AX	0.3660	0.1860
AY	0.5460	0.1940

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Chain	Atom inclusion	Q-score
AZ	0.4490	0.2050
BA	0.8610	0.2760
BB	0.7680	0.2580
BC	0.9190	0.3090
BD	0.9510	0.2740
BE	0.8330	0.2680
BF	0.8680	0.2620
BG	0.9360	0.2990
BH	0.7890	0.2190
BI	0.5580	0.2150
BJ	0.0020	0.0520
BK	0.6170	0.2440
BL	0.7250	0.2310
BM	0.0060	0.0470
BN	0.6690	0.2310
BO	0.5960	0.2140
BP	0.7160	0.2300
BQ	0.5560	0.2370
BR	0.5830	0.2270
BS	0.5430	0.2280
BT	0.6370	0.2260
BU	0.5080	0.2240
BV	0.0750	0.0940
BW	0.6440	0.2610
BX	0.6060	0.2500
BY	0.3600	0.1320
BZ	0.6920	0.2300
Ba	0.5800	0.2450
Bb	0.5890	0.2360
Bc	0.7570	0.2500
Bd	0.5270	0.1590
Be	0.4990	0.2320
Bf	0.5470	0.2240
Bg	0.7180	0.2600
Bh	0.5850	0.2040
Bi	0.4600	0.2010
Bj	0.4200	0.1440
Bk	0.6270	0.2390
Bl	0.5120	0.2040
Bm	0.6440	0.2360
Bn	0.6380	0.2130
Bo	0.5410	0.2050

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Chain	Atom inclusion	Q-score
Bp	0.7110	0.2480
Bq	0.5520	0.2320
Br	0.6450	0.2410
Bs	0.6410	0.2440
Bt	0.6610	0.2570
Bu	0.6820	0.2240
Bv	0.6580	0.2470
Bw	0.5990	0.2310
Bx	0.6090	0.2340
By	0.7460	0.2370