



wwPDB EM Validation Summary Report ⓘ

Apr 5, 2026 – 11:54 PM UTC

PDB ID : 9B0Q / pdb_00009b0q
EMDB ID : EMD-44050
Title : In situ human top-back di-ribosome structure (Composite map)
Authors : Wei, Z.; Yong, Z.
Deposited on : 2024-03-12
Resolution : 3.20 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

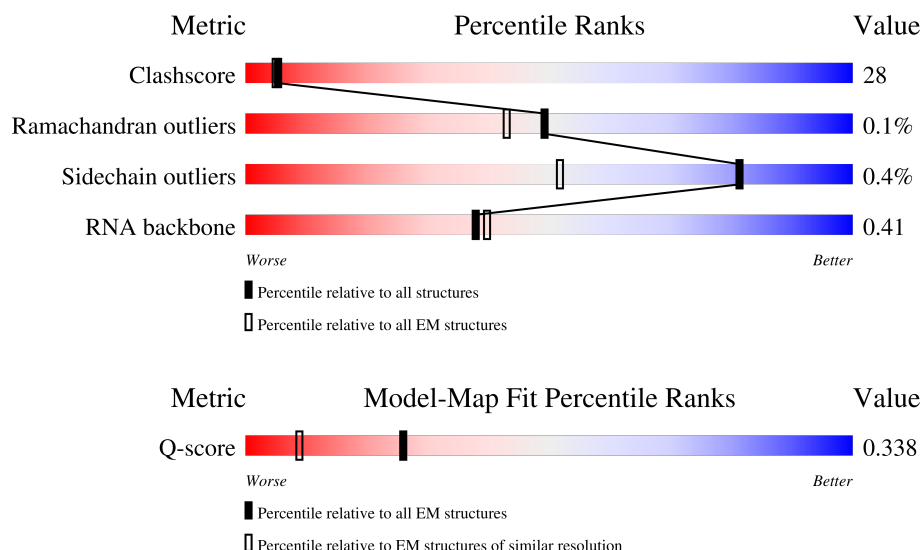
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 Å.

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



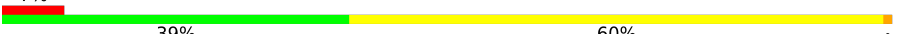
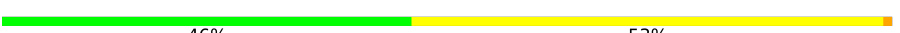
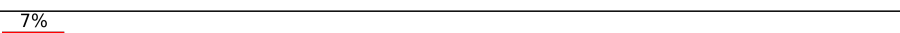
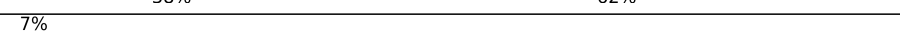
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	CH	125	
1	cH	125	
2	SE	262	

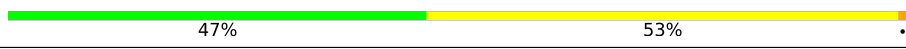
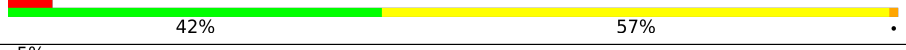
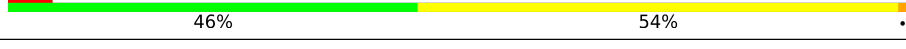
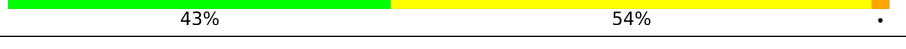
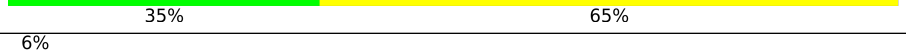
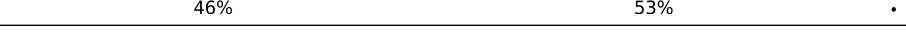
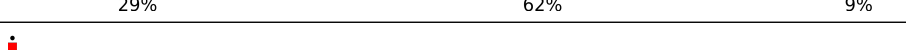
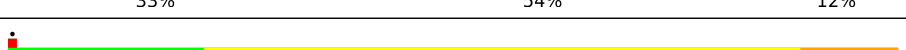
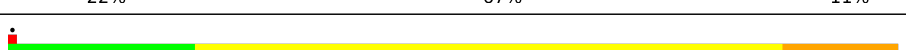
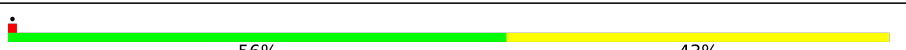
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Mol	Chain	Length	Quality of chain
2	sE	262	 49%50%
3	SI	206	 50%50%
3	sI	206	 48%52%
4	SL	153	 5%47%52%
4	sL	153	 7%39%60%
5	SX	141	 46%53%
5	sX	141	 52%48%
6	SG	237	 5%43%56%
6	sG	237	 5%38%61%
7	SJ	185	 42%58%
7	sJ	185	 42%58%
8	SY	131	 40%60%
8	sY	131	 45%54%
9	se	58	 16%43%57%
10	SA	221	 7%38%62%
10	sA	221	 7%33%66%
11	SB	214	 35%64%
11	sB	214	 38%61%
12	SH	189	 8%36%62%
12	sH	189	 9%42%56%
13	SV	83	 47%53%
13	sV	83	 23%76%
14	Sa	102	 45%53%
14	sa	102	 43%54%
15	SC	222	 43%57%

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Mol	Chain	Length	Quality of chain
15	sC	222	
16	SN	150	
16	sN	150	
17	SO	140	
17	sO	140	
18	SW	129	
18	sW	129	
19	Sb	83	
19	sb	83	
20	L7	120	
20	l7	120	
21	L8	156	
21	l8	156	
22	LA	248	
22	lA	248	
23	LB	402	
23	lB	402	
24	LC	368	
24	lC	368	
25	LD	293	
25	lD	293	
26	LE	247	
26	lE	247	
27	LF	225	
27	lF	225	

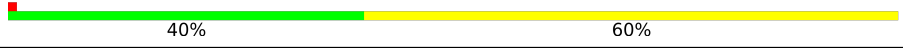
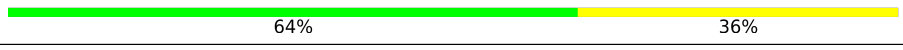
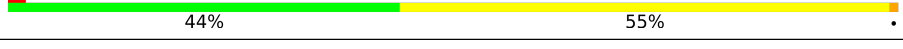
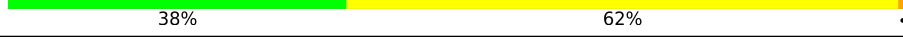
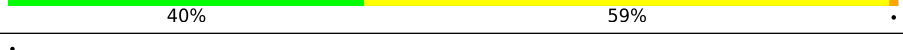
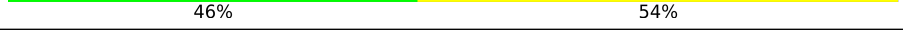
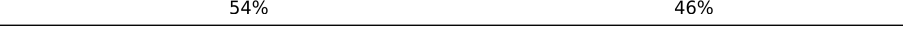
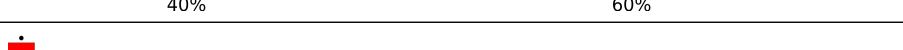
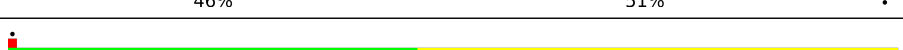
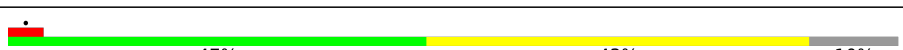
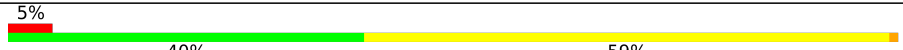
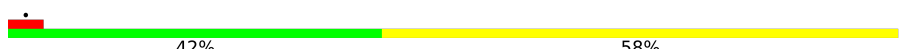
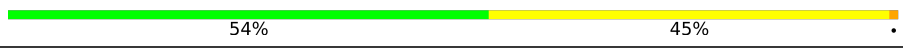
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Mol	Chain	Length	Quality of chain
28	LG	241	5% 53% 47%
28	IG	241	5% 59% 41%
29	LH	190	48% 52%
29	IH	190	46% 53% .
30	LI	213	51% 44% 5%
30	II	213	53% 41% 5%
31	LJ	176	5% 46% 53% .
31	IJ	176	7% 49% 51%
32	LL	210	5% 55% 45%
32	IL	210	. 50% 49%
33	LM	139	39% 60% .
33	IM	139	. 39% 58% .
34	LN	203	49% 50% .
34	IN	203	49% 50%
35	LO	201	52% 47% .
35	IO	201	48% 52%
36	LP	153	50% 50%
36	IP	153	54% 45% .
37	LQ	187	49% 51%
37	IQ	187	51% 49%
38	LR	187	5% 48% 52%
38	IR	187	6% 52% 48%
39	LS	175	54% 46%
39	IS	175	56% 43% .
40	LT	159	. 47% 53% .

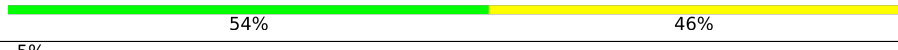
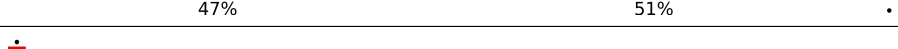
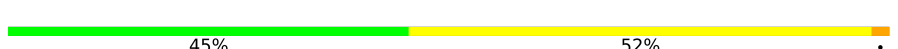
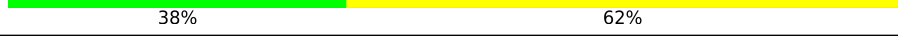
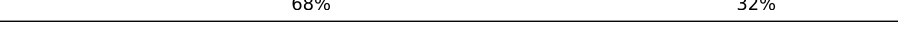
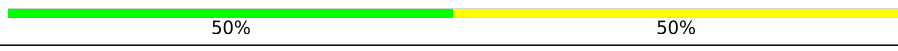
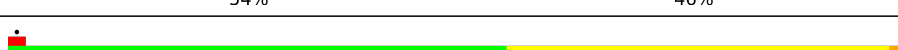
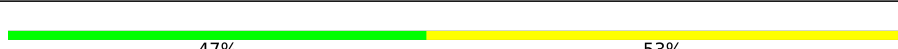
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Mol	Chain	Length	Quality of chain
40	IT	159	
41	LU	101	
41	IU	101	
42	LV	131	
42	IV	131	
43	LX	120	
43	IX	120	
44	LY	134	
44	IY	134	
45	LZ	135	
45	IZ	135	
46	La	147	
46	la	147	
47	Lb	121	
47	lb	121	
48	Lc	98	
48	lc	98	
49	Ld	107	
49	ld	107	
50	Le	128	
50	le	128	
51	Lf	109	
51	lf	109	
52	Lg	114	
52	lg	114	

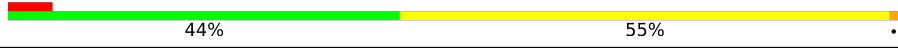
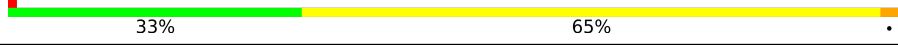
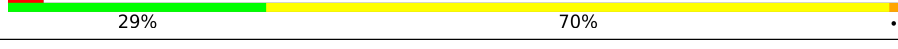
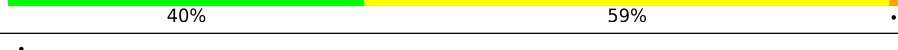
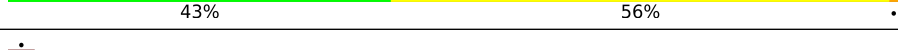
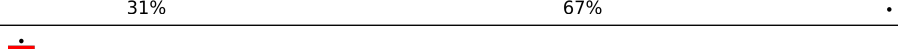
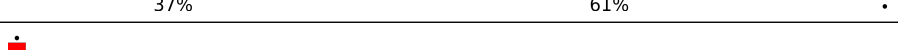
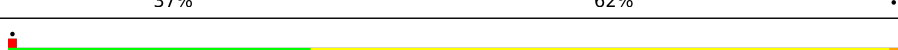
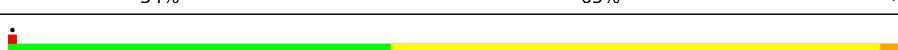
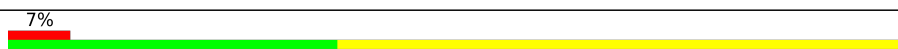
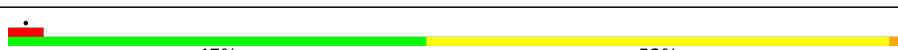
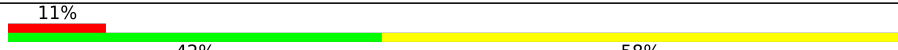
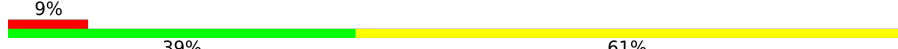
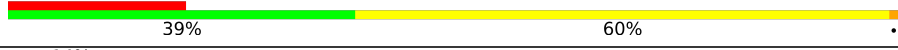
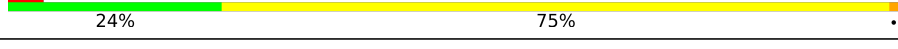
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Mol	Chain	Length	Quality of chain
53	Lh	122	
53	lh	122	
54	Li	102	
54	li	102	
55	Lj	86	
55	lj	86	
56	Lk	69	
56	lk	69	
57	Ll	50	
57	ll	50	
58	Lm	52	
58	lm	52	
59	Ln	24	
59	ln	24	
60	Lo	105	
60	lo	105	
61	Lp	91	
61	lp	91	
62	Lr	125	
62	lr	125	
63	Lz	217	
63	lz	217	
64	SR	135	
64	sR	135	
65	SD	227	

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Mol	Chain	Length	Quality of chain
65	sD	227	
66	SF	189	
66	sF	189	
67	SK	98	
67	sK	98	
68	SP	121	
68	sP	121	
69	SQ	144	
69	sQ	144	
70	SS	145	
70	sS	145	
71	ST	143	
71	sT	143	
72	SU	104	
72	sU	104	
73	Sc	64	
73	sc	64	
74	Sd	55	
74	sd	55	
75	Sg	313	
75	sg	313	
76	SM	122	
76	sM	122	
77	SZ	75	
77	sZ	75	

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Mol	Chain	Length	Quality of chain
78	Sf	67	
78	sf	67	
79	S2	1740	
79	s2	1740	
80	CB	856	
80	cB	856	
81	AP	73	
81	aP	73	
82	PE	76	
82	pE	76	
83	Ls	196	
83	ls	196	
84	Lt	141	
84	lt	141	
85	L5	3740	
85	l5	3740	
86	Se	47	
87	LW	124	
87	IW	124	

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 459641 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 Endothelial differentiation-related factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	CH	125	Total	C	N	O	0	0
			968	595	189	184		
1	cH	125	Total	C	N	O	0	0
			968	595	189	184		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CH	30	ARG	GLN	conflict	UNP O60869
CH	32	ALA	ARG	conflict	UNP O60869
CH	33	ALA	-	insertion	UNP O60869
CH	34	ALA	-	insertion	UNP O60869
cH	30	ARG	GLN	conflict	UNP O60869
cH	32	ALA	ARG	conflict	UNP O60869
cH	33	ALA	-	insertion	UNP O60869
cH	34	ALA	-	insertion	UNP O60869

- Molecule 2 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	sE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		
2	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 3 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	sI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		
3	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 4 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	sL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		
4	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 5 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	sX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		
5	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 6 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	sG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		
6	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 7 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	sJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		
7	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 8 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	sY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		
8	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 9 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 10 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	sA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		
10	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 11 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	sB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		
11	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 12 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	sH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		
12	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 13 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	sV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		
13	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 14 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		
14	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 15 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	sC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		
15	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 16 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	sN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		
16	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	sO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		
17	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 18 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	sW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		
18	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 19 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		
19	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 20 is a RNA chain called RNA (120-MER)5S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
20	17	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		
20	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 21 is a RNA chain called RNA (156-MER)5.8S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
21	18	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		
21	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 22 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		
22	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 23 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	1B	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		
23	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 24 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1C	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		
24	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 25 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1D	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
25	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 26 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	lE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		
26	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 27 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	lF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		
27	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 28 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	lG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		
28	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 29 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	lH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		
29	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 30 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	lI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		
30	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 31 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	IJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		
31	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 32 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	IL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		
32	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 33 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	IM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		
33	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 34 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	IN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		
34	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 35 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	IO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		
35	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 36 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	IP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		
36	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 37 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	lQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		
37	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 38 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	lR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		
38	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 39 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	lS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		
39	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 40 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	lT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		
40	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 41 is a protein called Heparin-binding protein HBp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	lU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
41	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 42 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	IV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		
42	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 43 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	IX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		
43	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 44 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	IY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		
44	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 45 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	IZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		
45	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 46 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	la	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		
46	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 47 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		
47	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 48 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		
48	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 49 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		
49	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 50 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		
50	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 51 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		
51	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 52 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		
52	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 53 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		
53	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 54 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		
54	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 55 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		
55	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 56 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		
56	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 57 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 58 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		
58	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 59 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		
59	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 60 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		
60	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 61 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		
61	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 62 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		
62	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 63 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		
63	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 64 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	sR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		
64	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 65 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	sD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		
65	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 66 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	sF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		
66	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 67 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	sK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		
67	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 68 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	sP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		
68	SP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

- Molecule 69 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	sQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		
69	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 70 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	sS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		
70	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 71 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	sT	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		
71	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 72 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	sU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		
72	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 73 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 74 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		
74	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 75 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		
75	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 76 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	sM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		
76	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 77 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	sZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		
77	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 78 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		
78	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 79 is a RNA chain called 18S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
79	s2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		
79	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		

- Molecule 80 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	cB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		
80	CB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		

- Molecule 81 is a RNA chain called A/P site tRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
81	aP	71	Total	C	N	O	P	0	0
			1514	677	275	492	70		
81	AP	71	Total	C	N	O	P	0	0
			1514	677	275	492	70		

- Molecule 82 is a RNA chain called P/E site tRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
82	pE	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		
82	PE	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 83 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		
83	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 84 is a protein called 60S ribosomal protein L12 [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
84	lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		
84	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 85 is a RNA chain called 28S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
85	l5	3708	Total	C	N	O	P	0	0
			79496	35401	14553	25835	3707		
85	L5	3708	Total	C	N	O	P	0	0
			79496	35401	14553	25835	3707		

- Molecule 86 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Se	47	Total	C	N	O	S	0	0
			378	234	84	59	1		

- Molecule 87 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	lW	118	Total	C	N	O	S	0	0
			965	604	199	158	4		
87	LW	118	Total	C	N	O	S	0	0
			965	604	199	158	4		

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
88	sa	1	Total	Zn	0
			1	1	
88	lg	1	Total	Zn	0
			1	1	
88	lj	1	Total	Zn	0
			1	1	
88	lm	1	Total	Zn	0
			1	1	
88	lo	1	Total	Zn	0
			1	1	
88	lp	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
88	Sa	1	Total 1	Zn 1	0
88	Lg	1	Total 1	Zn 1	0
88	Lj	1	Total 1	Zn 1	0
88	Lm	1	Total 1	Zn 1	0
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
89	l7	3	Total 3	Mg 3	0
89	l8	5	Total 5	Mg 5	0
89	lA	1	Total 1	Mg 1	0
89	lB	1	Total 1	Mg 1	0
89	le	2	Total 2	Mg 2	0
89	lg	1	Total 1	Mg 1	0
89	lj	1	Total 1	Mg 1	0
89	s2	29	Total 29	Mg 29	0
89	l5	212	Total 212	Mg 212	0
89	L5	213	Total 213	Mg 213	0
89	L7	3	Total 3	Mg 3	0
89	L8	5	Total 5	Mg 5	0
89	LA	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
89	LP	1	Total 1	Mg 1	0
89	LV	1	Total 1	Mg 1	0
89	Le	1	Total 1	Mg 1	0
89	Lj	1	Total 1	Mg 1	0
89	S2	29	Total 29	Mg 29	0

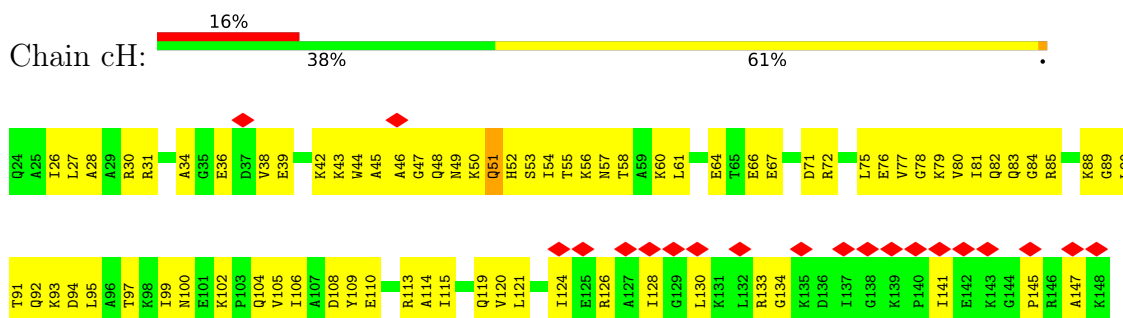
3 Residue-property plots

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

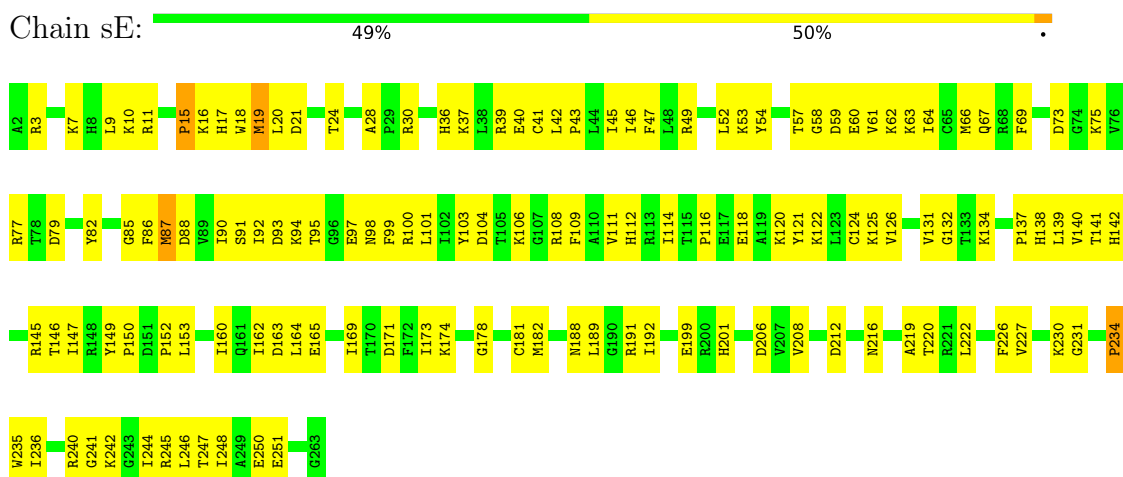
- Molecule 1: Endothelial differentiation-related factor 1



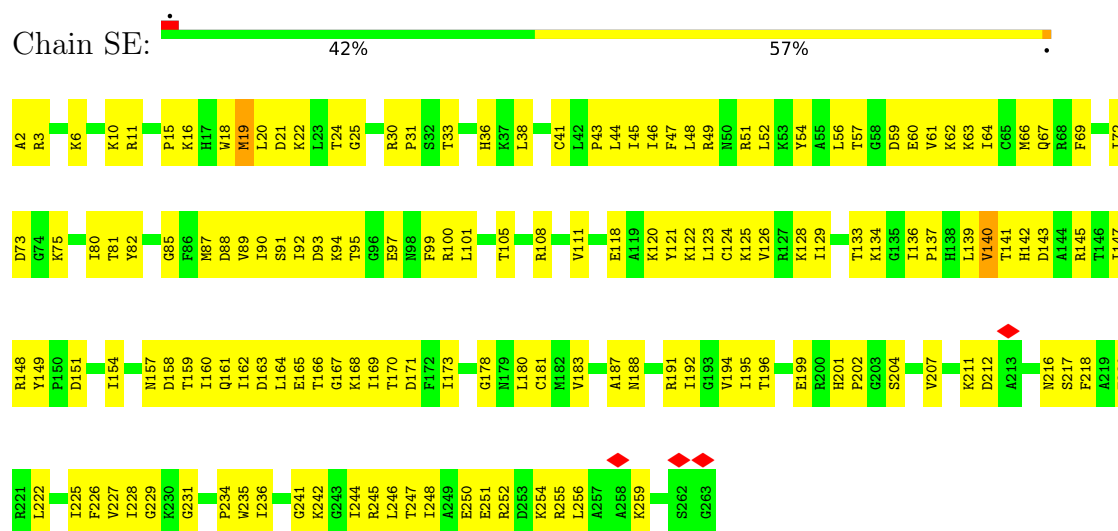
- Molecule 1: Endothelial differentiation-related factor 1



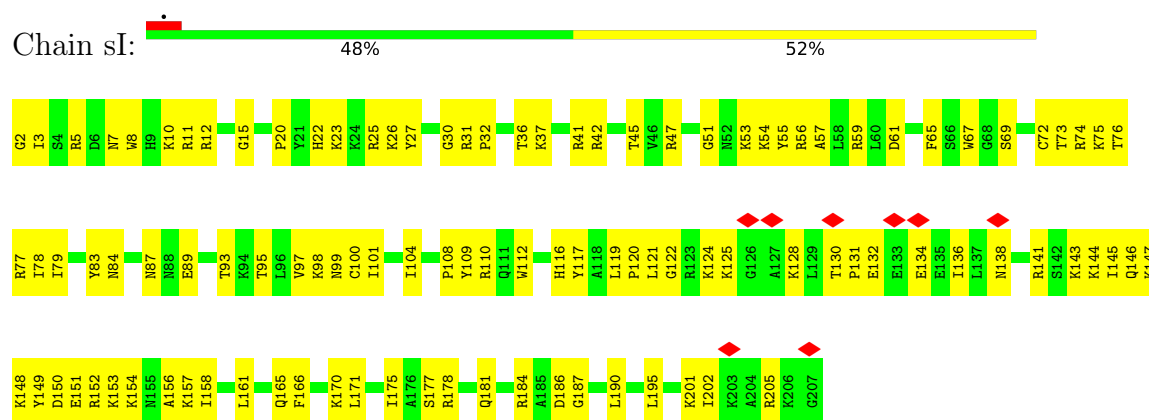
- Molecule 2: Small ribosomal subunit protein eS4, X isoform



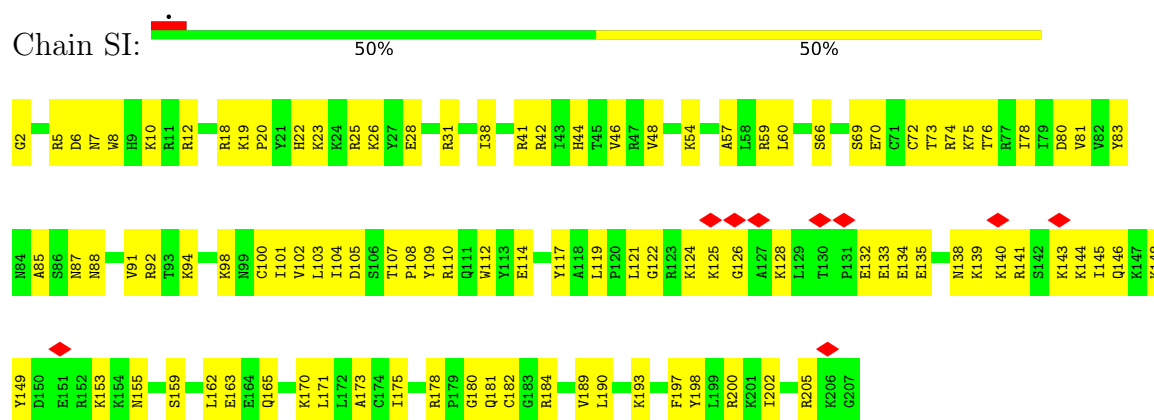
- Molecule 2: Small ribosomal subunit protein eS4, X isoform



- Molecule 3: 40S ribosomal protein S8

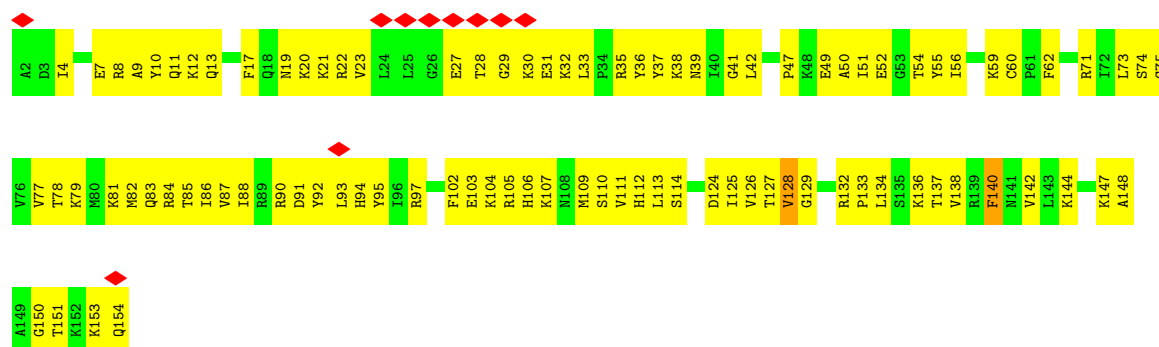


- Molecule 3: 40S ribosomal protein S8

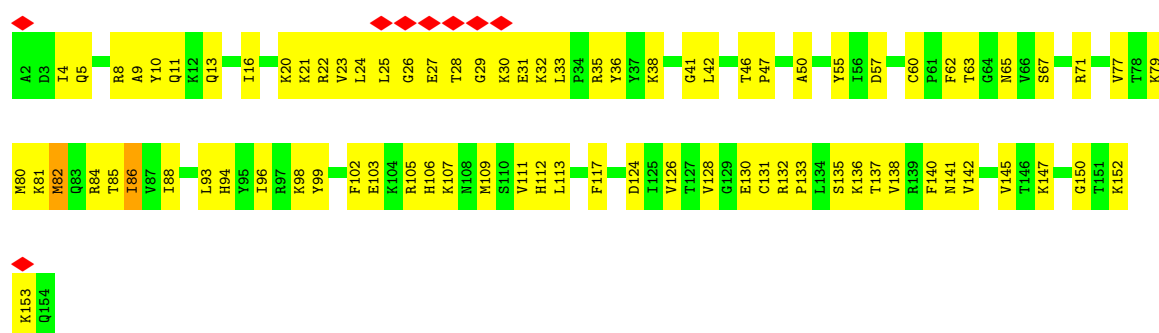


- Molecule 4: 40S ribosomal protein S11

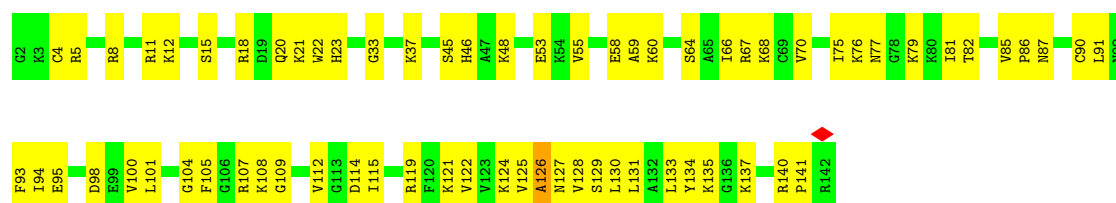




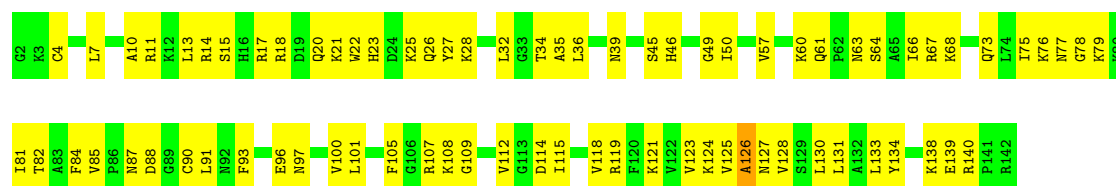
• Molecule 4: 40S ribosomal protein S11



• Molecule 5: 40S ribosomal protein S23

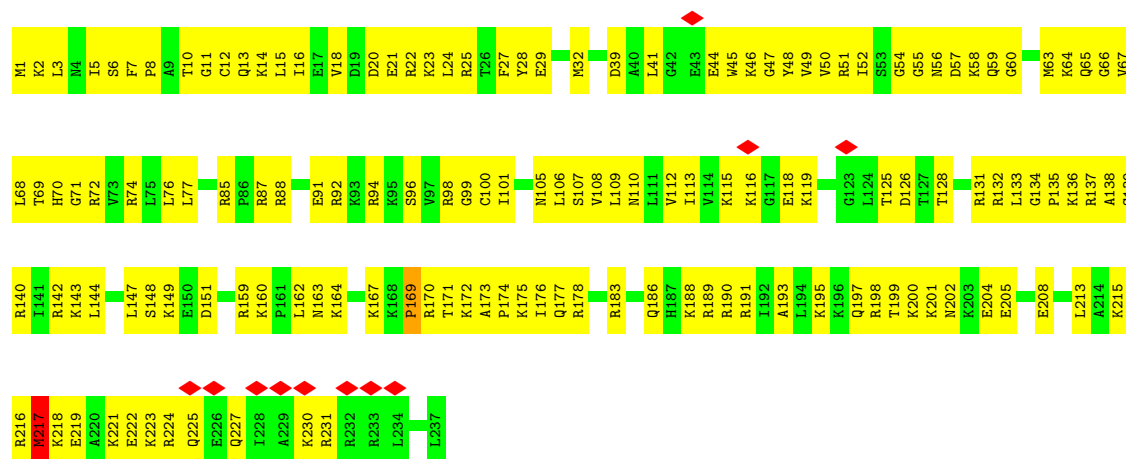


• Molecule 5: 40S ribosomal protein S23

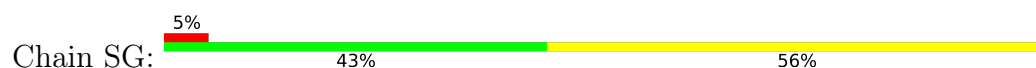


• Molecule 6: 40S ribosomal protein S6

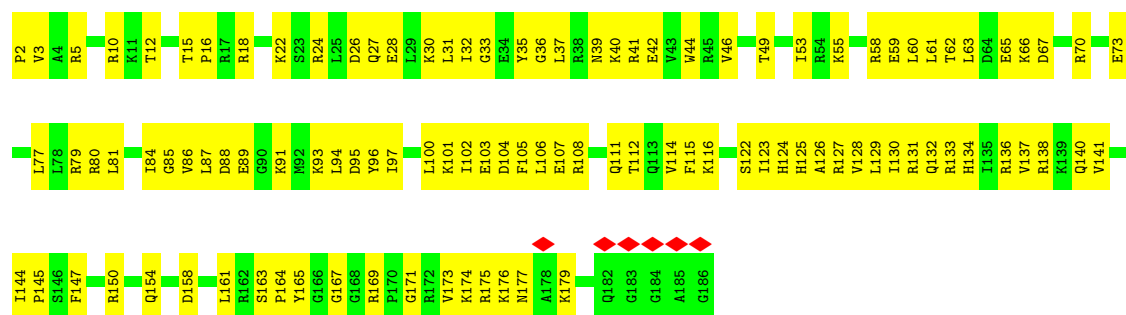




• Molecule 6: 40S ribosomal protein S6

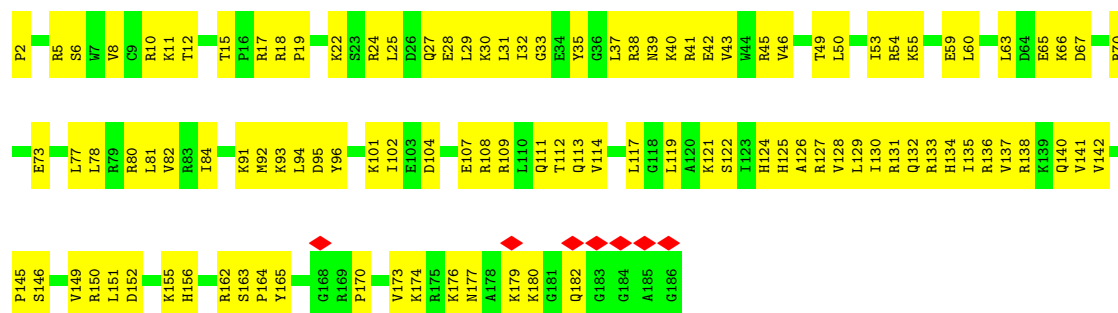


• Molecule 7: 40S ribosomal protein S9



• Molecule 7: 40S ribosomal protein S9

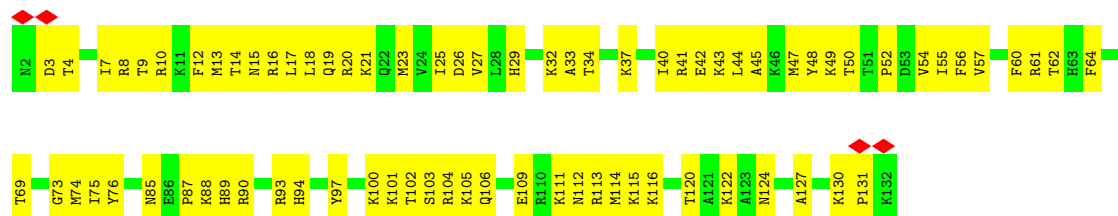




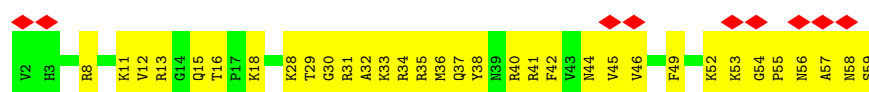
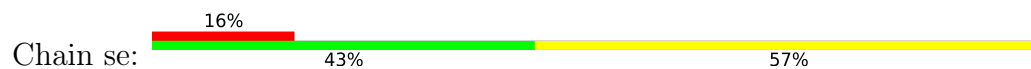
• Molecule 8: 40S ribosomal protein S24



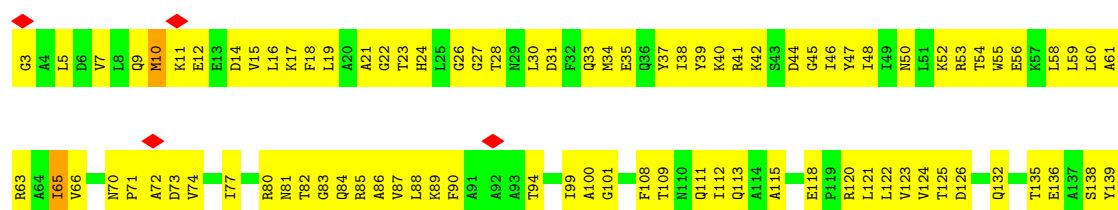
• Molecule 8: 40S ribosomal protein S24

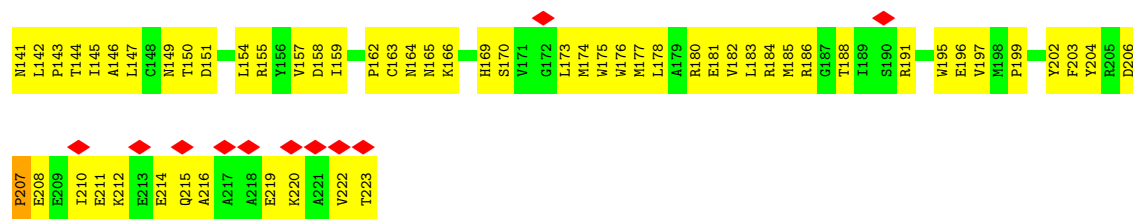


• Molecule 9: Small ribosomal subunit protein eS30

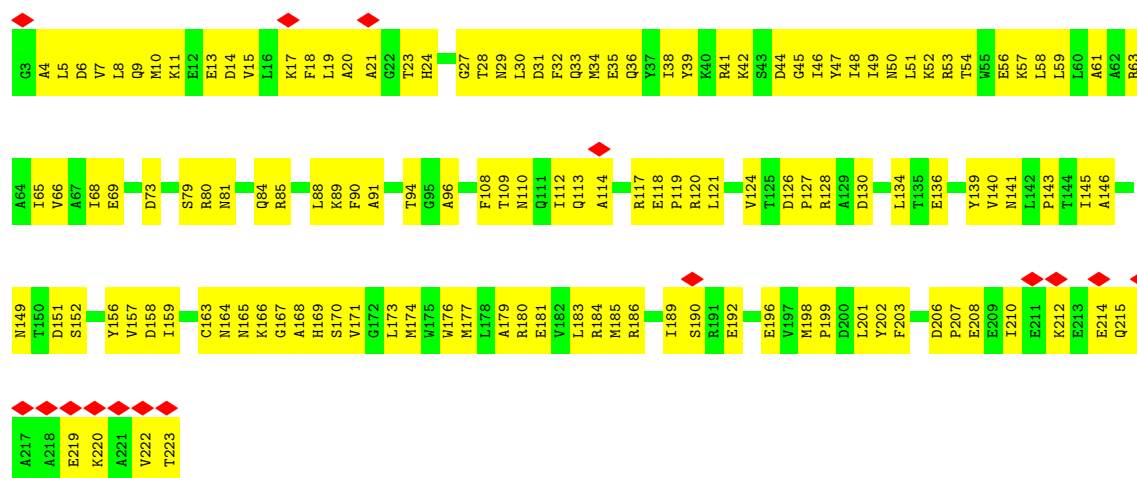


• Molecule 10: 40S ribosomal protein SA

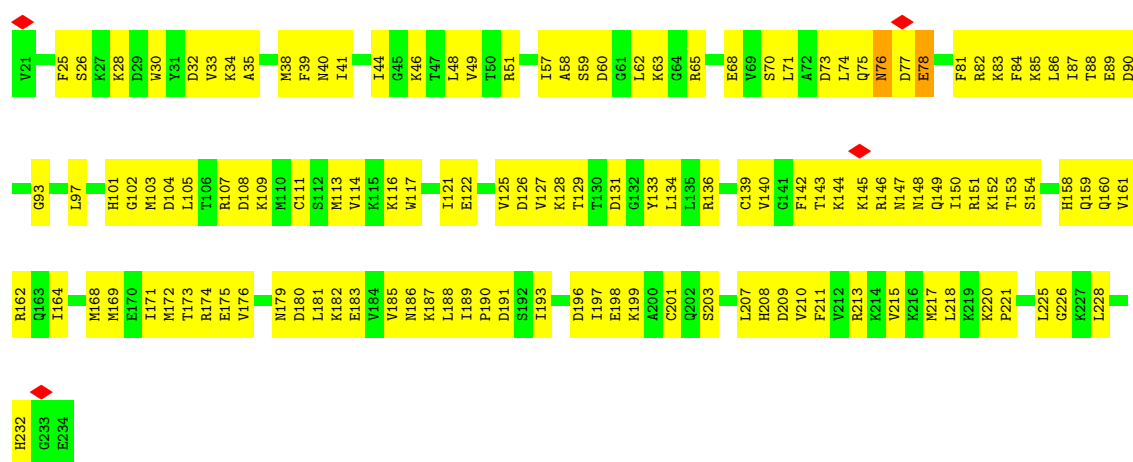




• Molecule 10: 40S ribosomal protein SA

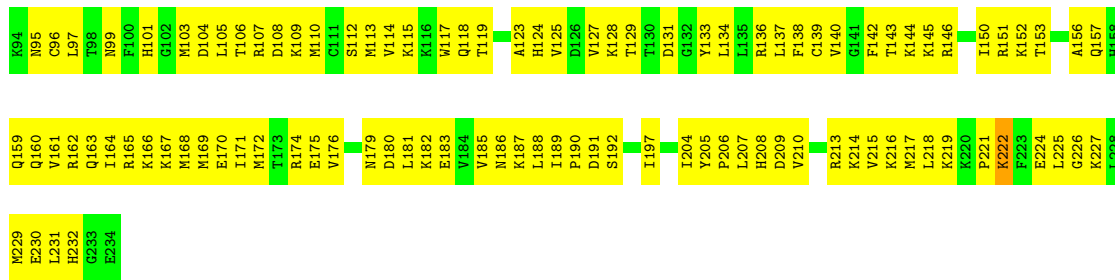


• Molecule 11: 40S ribosomal protein S3a

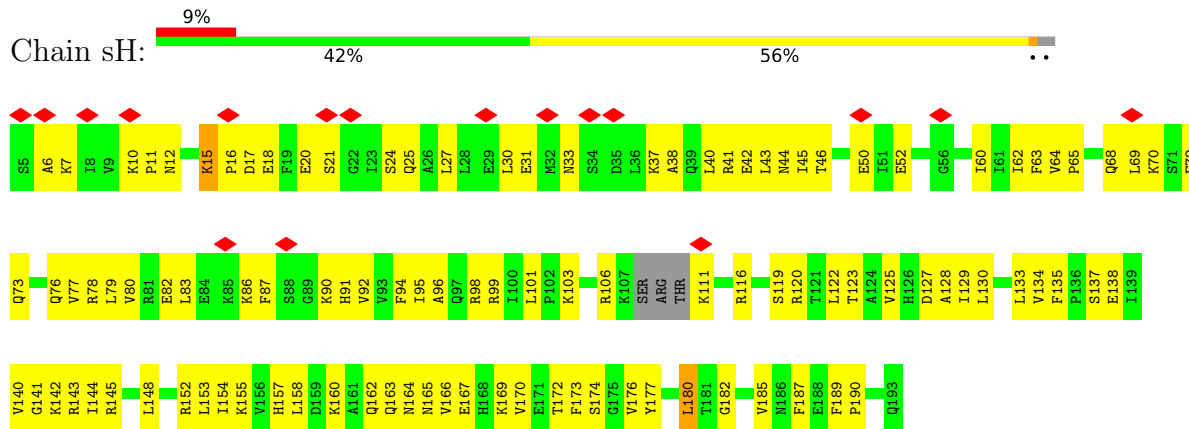


• Molecule 11: 40S ribosomal protein S3a

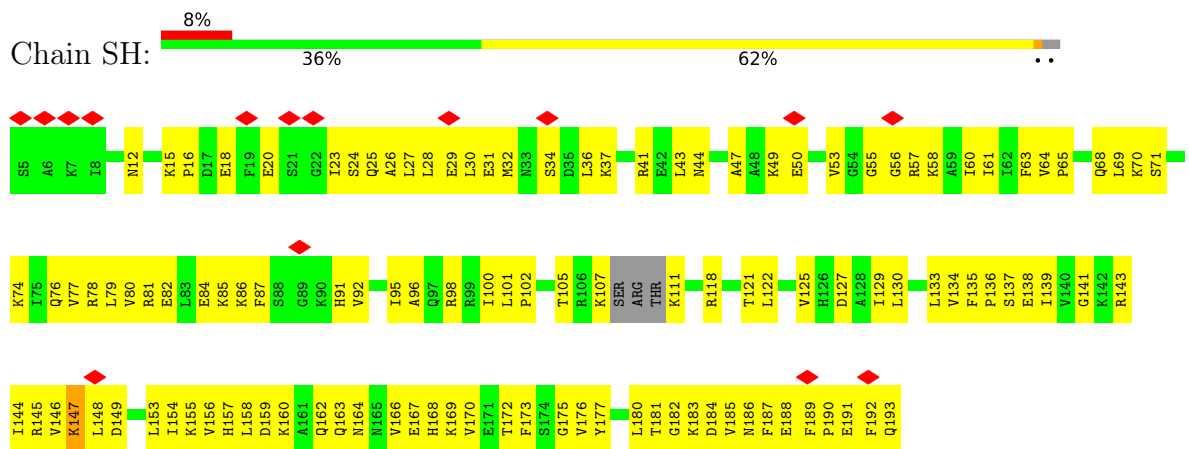




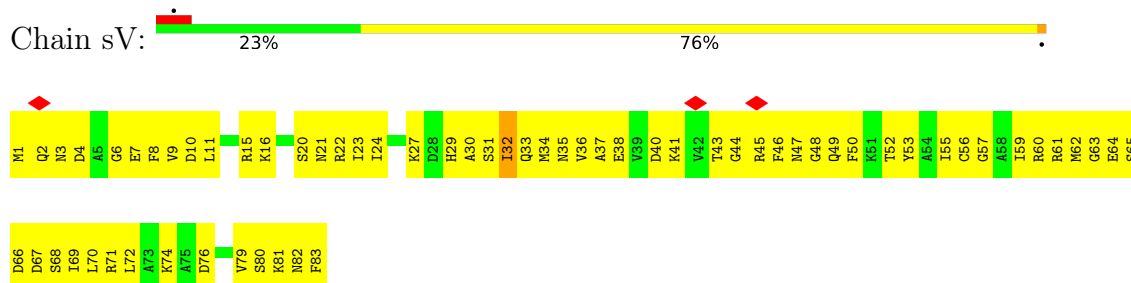
• Molecule 12: Small ribosomal subunit protein eS7



• Molecule 12: Small ribosomal subunit protein eS7

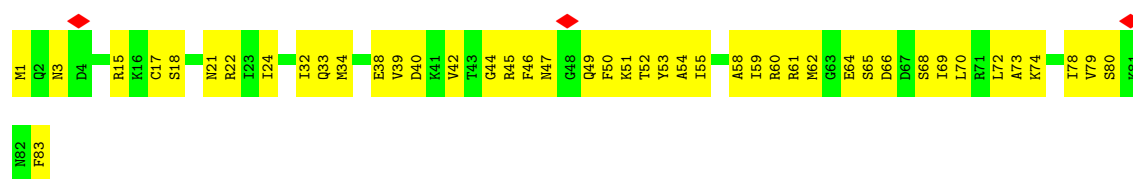


• Molecule 13: 40S ribosomal protein S21

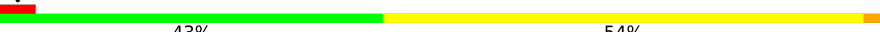


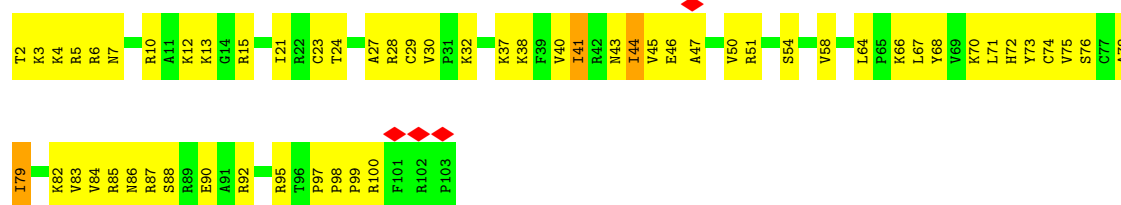
• Molecule 13: 40S ribosomal protein S21

Chain SV:  47% 53%

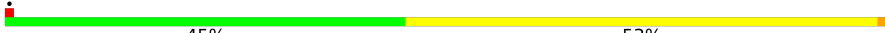


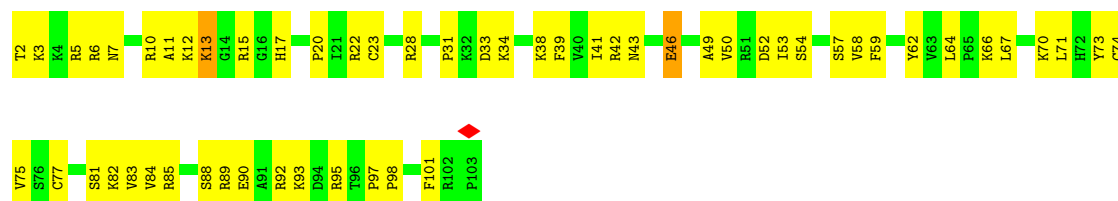
- Molecule 14: 40S ribosomal protein S26

Chain sa:  43% 54%

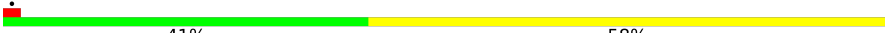


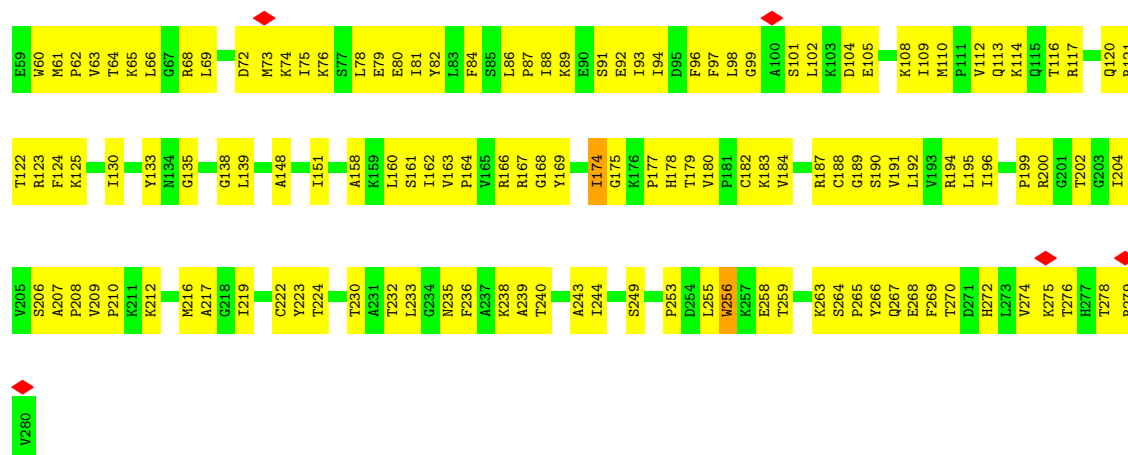
- Molecule 14: 40S ribosomal protein S26

Chain Sa:  45% 53%

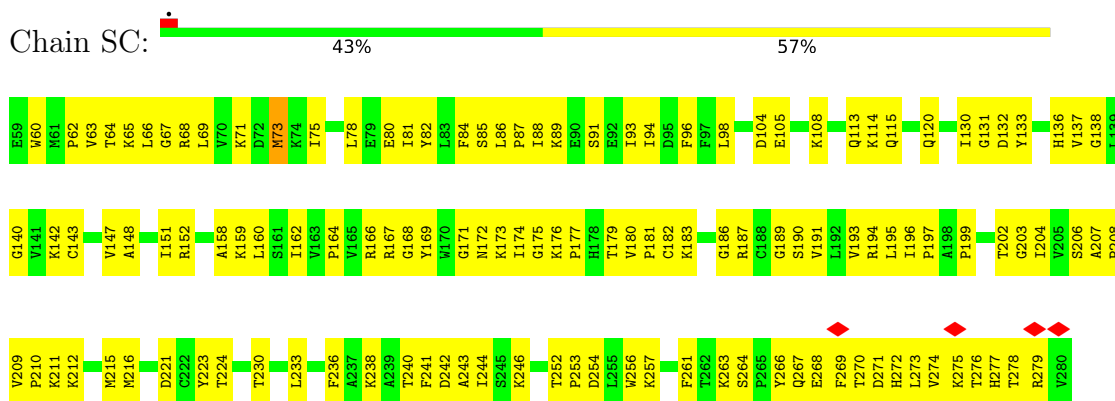


- Molecule 15: 40S ribosomal protein S2

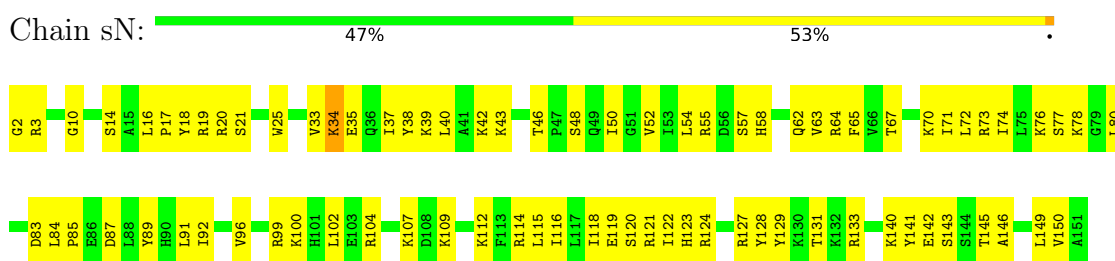
Chain sC:  41% 58%



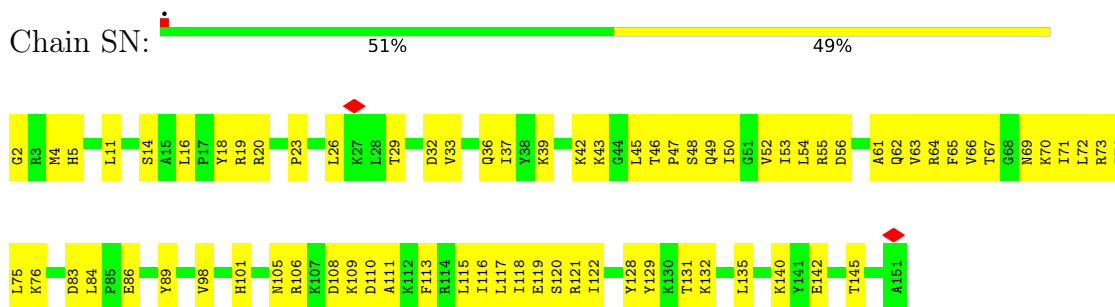
- Molecule 15: 40S ribosomal protein S2



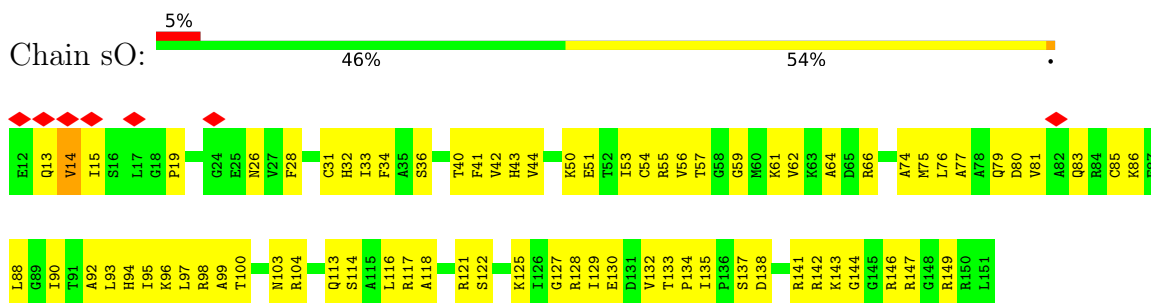
• Molecule 16: 40S ribosomal protein S13



• Molecule 16: 40S ribosomal protein S13

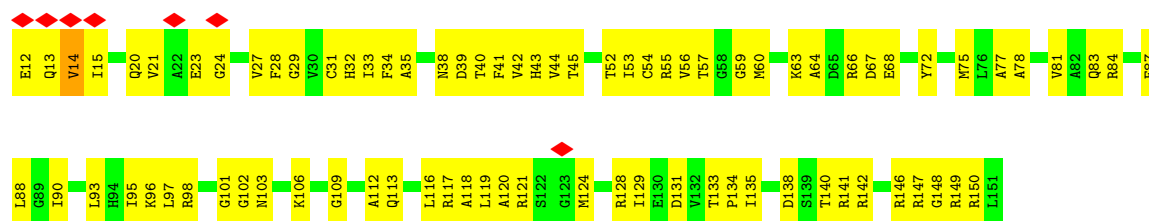


• Molecule 17: Small ribosomal subunit protein uS11



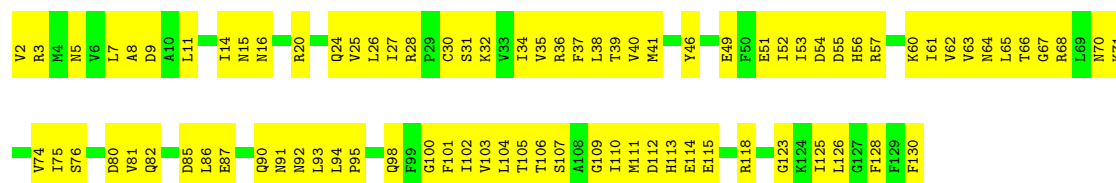
• Molecule 17: Small ribosomal subunit protein uS11





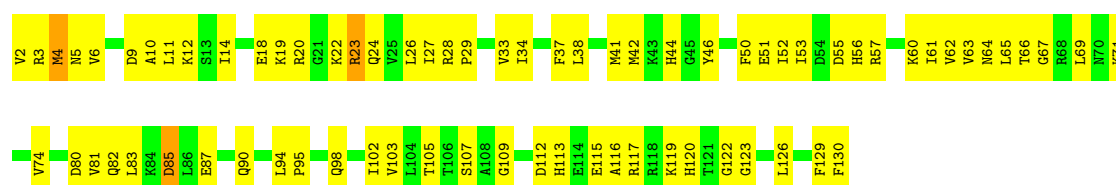
- Molecule 18: 40S ribosomal protein S15a

Chain sW: 35% 65%



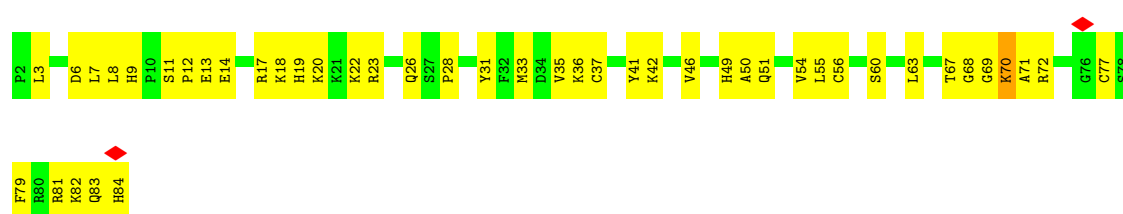
- Molecule 18: 40S ribosomal protein S15a

Chain SW: 43% 54%



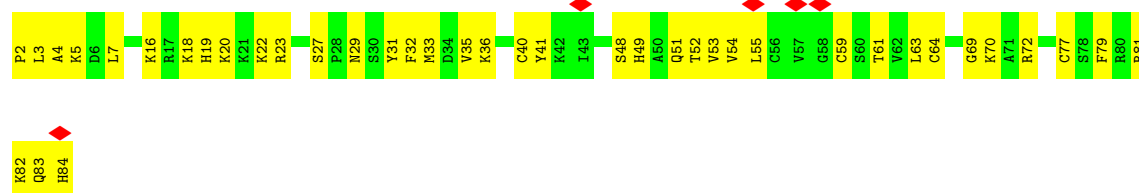
- Molecule 19: Small ribosomal subunit protein eS27

Chain sb: 46% 53%

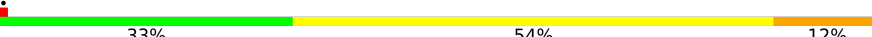


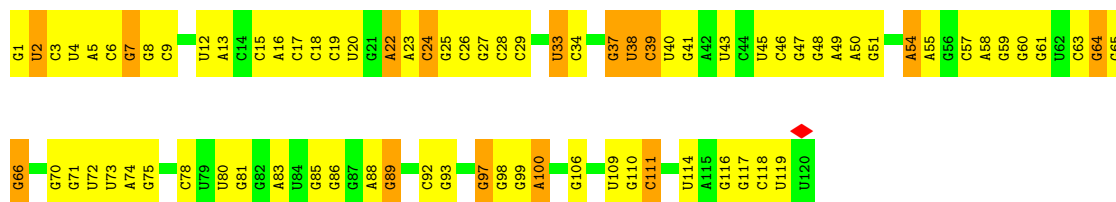
- Molecule 19: Small ribosomal subunit protein eS27

Chain Sb: 6% 52% 48%



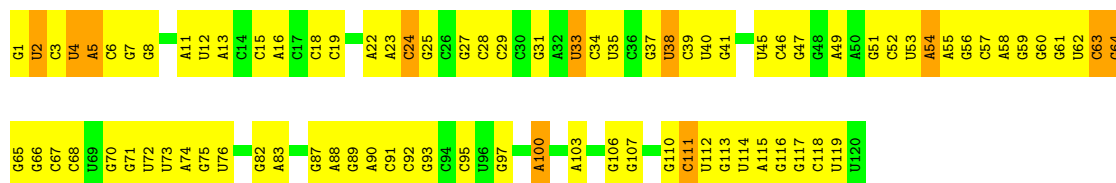
- Molecule 20: RNA (120-MER)5S rRNA [Homo sapiens]

Chain 17:  33% 54% 12%



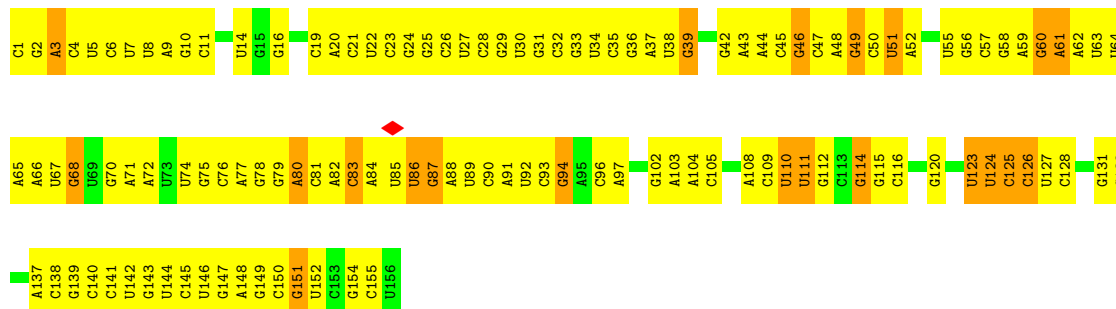
- Molecule 20: RNA (120-MER)5S rRNA [Homo sapiens]

Chain L7:  29% 62% 9%

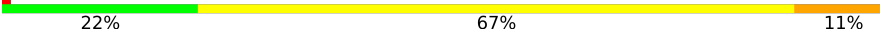


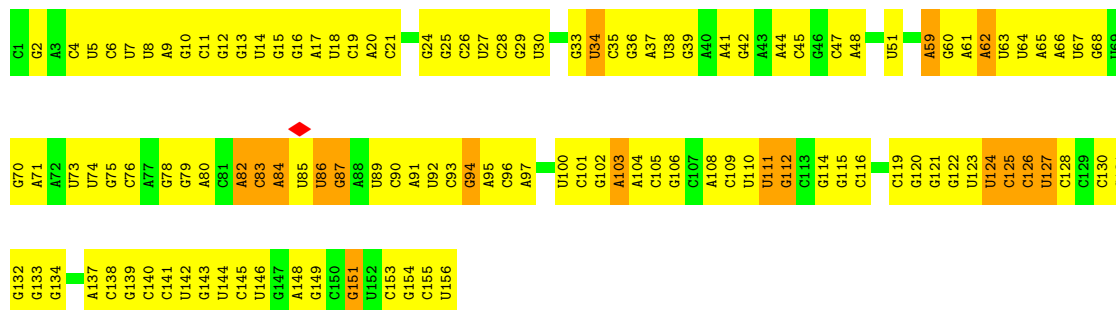
- Molecule 21: RNA (156-MER)5.8S rRNA [Homo sapiens]

Chain 18:  21% 66% 13%



- Molecule 21: RNA (156-MER)5.8S rRNA [Homo sapiens]

Chain L8:  22% 67% 11%

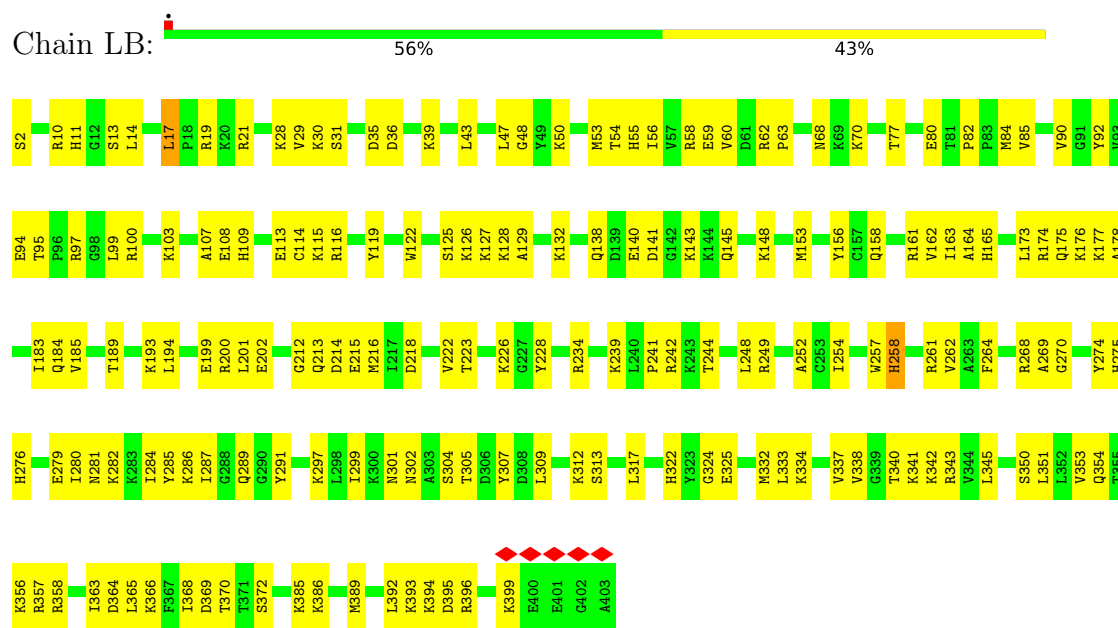


- Molecule 22: 60S ribosomal protein L8

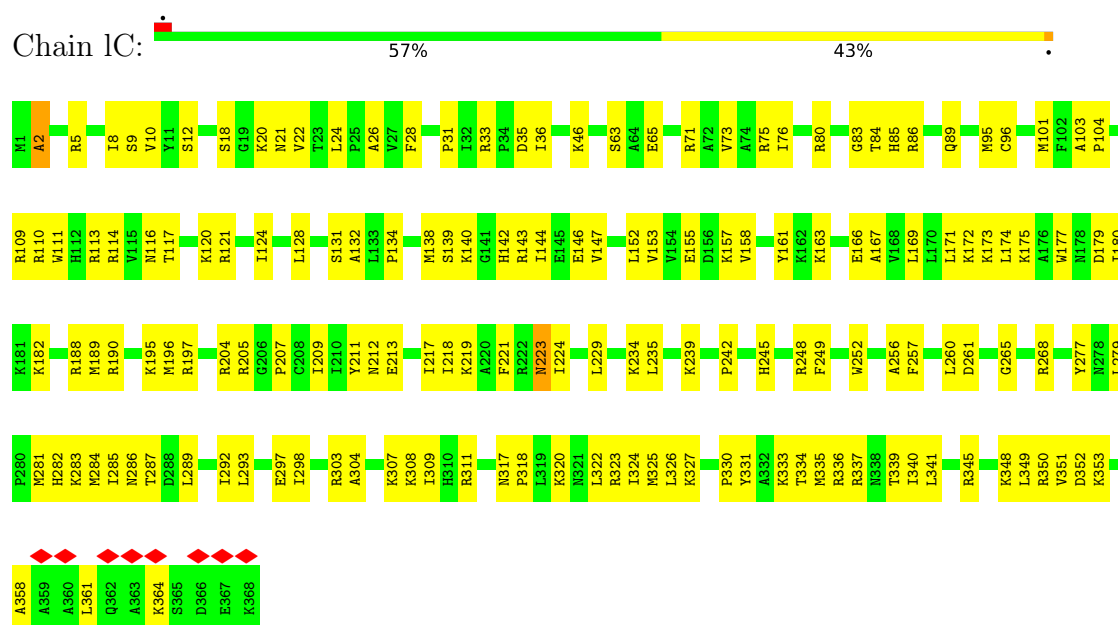
Chain 1A:  52% 48%



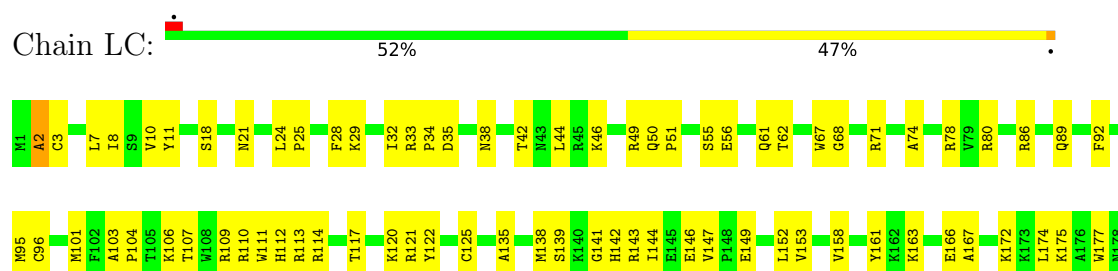
- Molecule 23: Large ribosomal subunit protein uL3

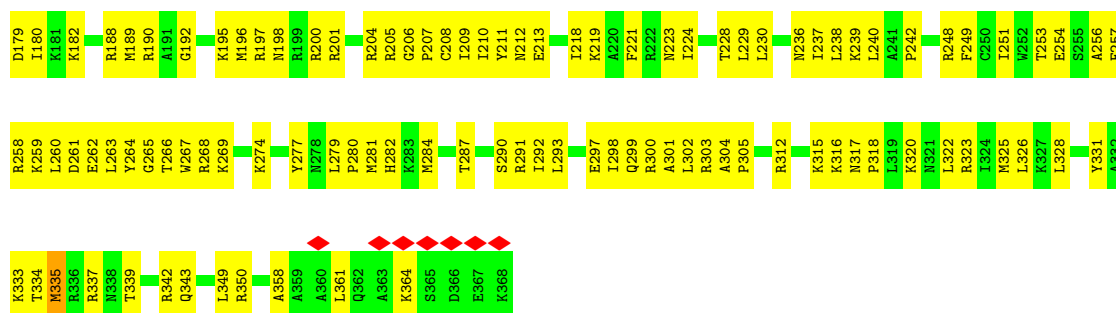


- Molecule 24: 60S ribosomal protein L4

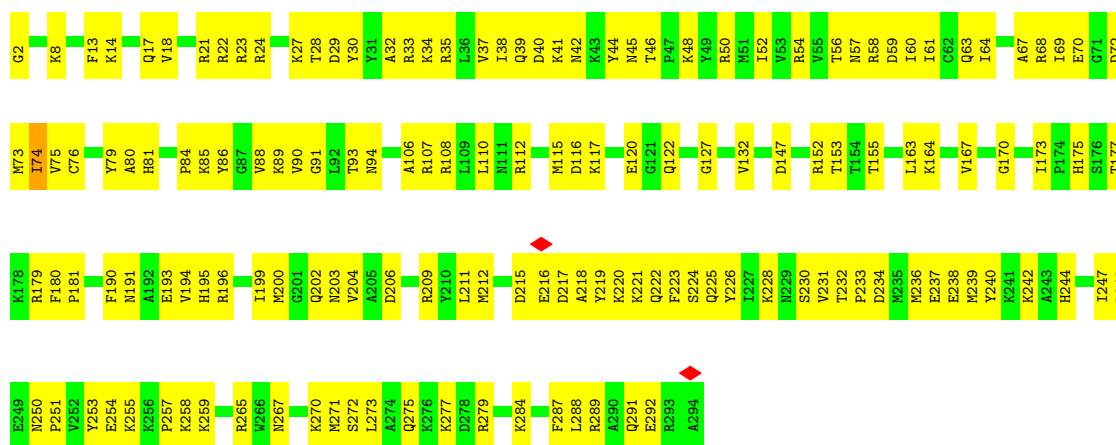


- Molecule 24: 60S ribosomal protein L4

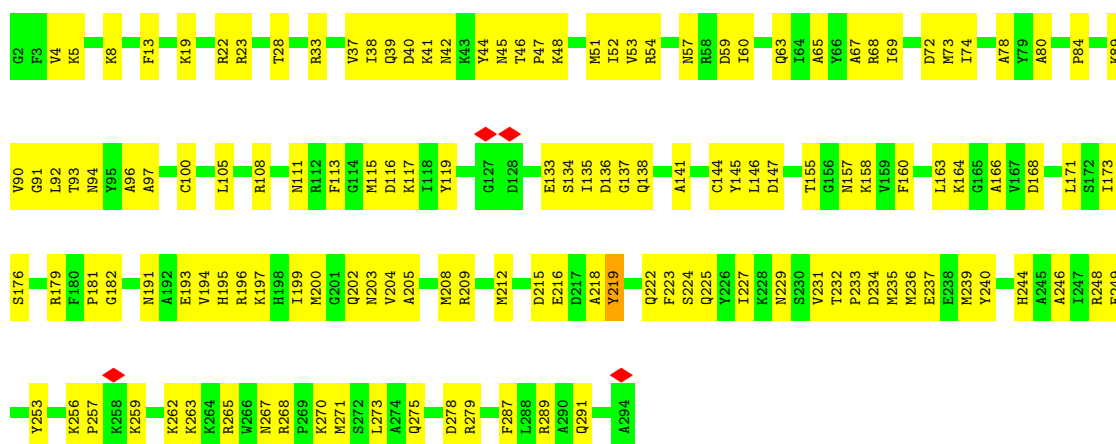




- Molecule 25: Large ribosomal subunit protein uL18

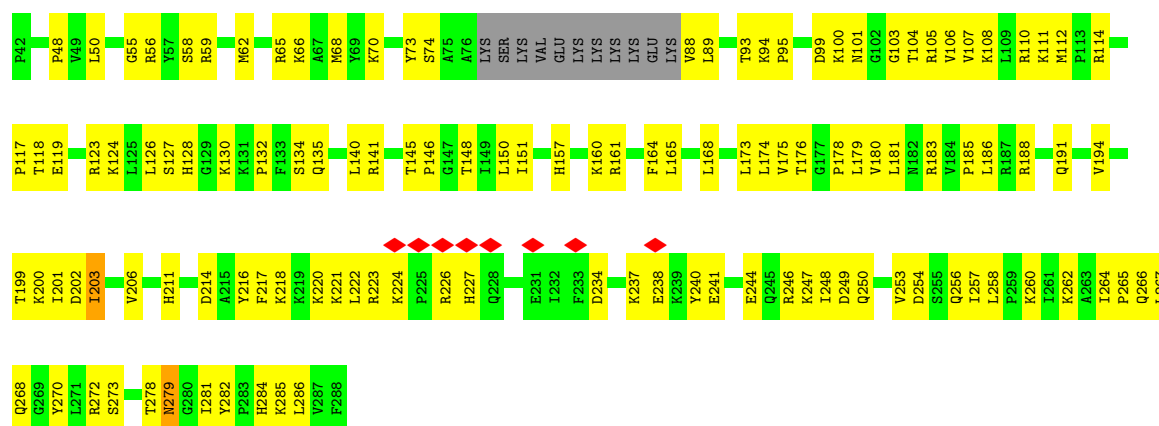


- Molecule 25: Large ribosomal subunit protein uL18

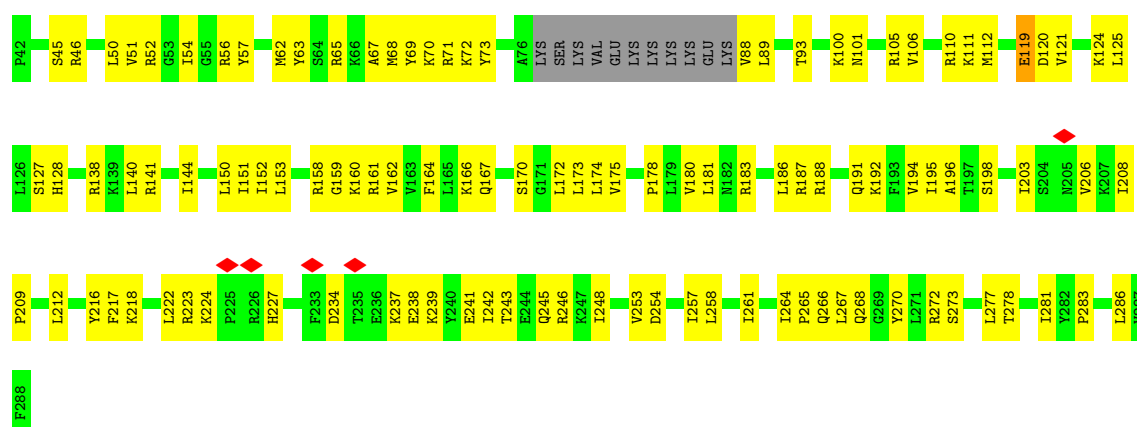


- Molecule 26: Large ribosomal subunit protein eL6

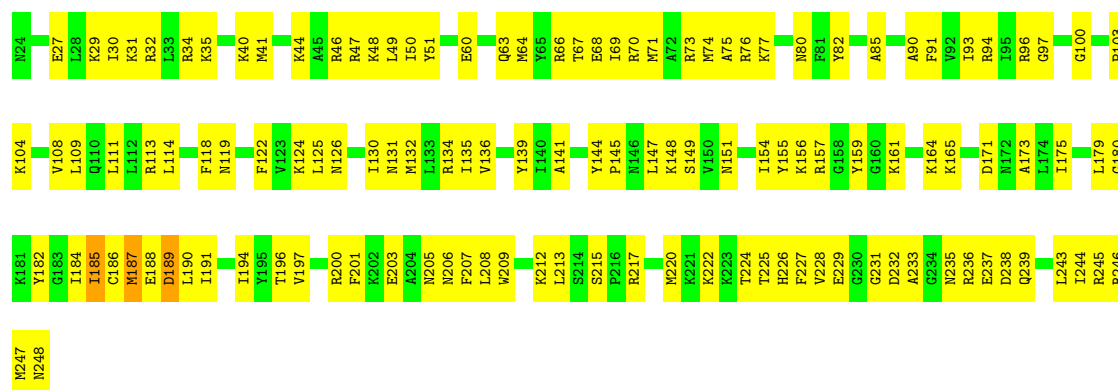




• Molecule 26: Large ribosomal subunit protein eL6

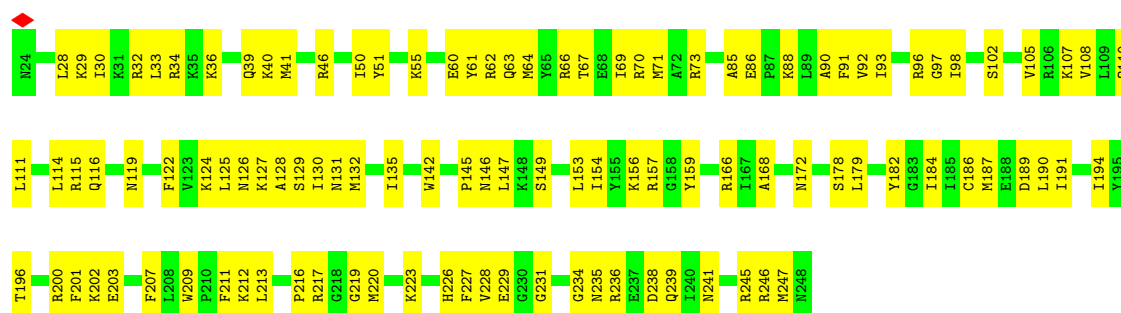


• Molecule 27: 60S ribosomal protein L7

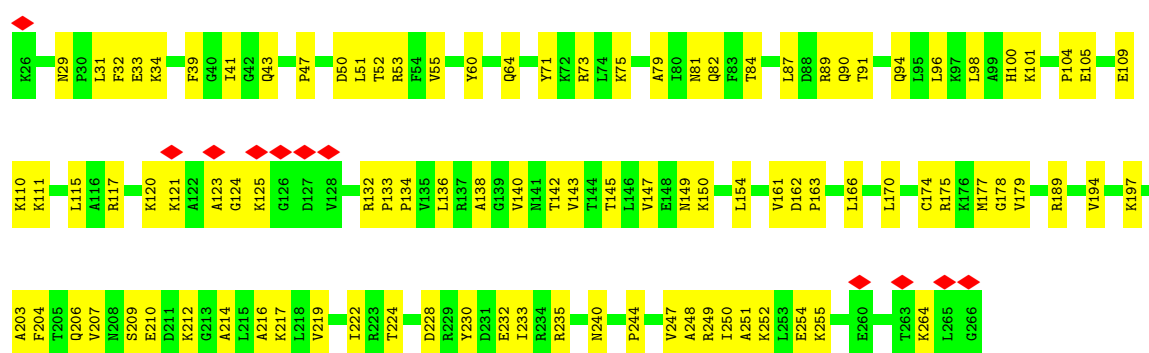


• Molecule 27: 60S ribosomal protein L7

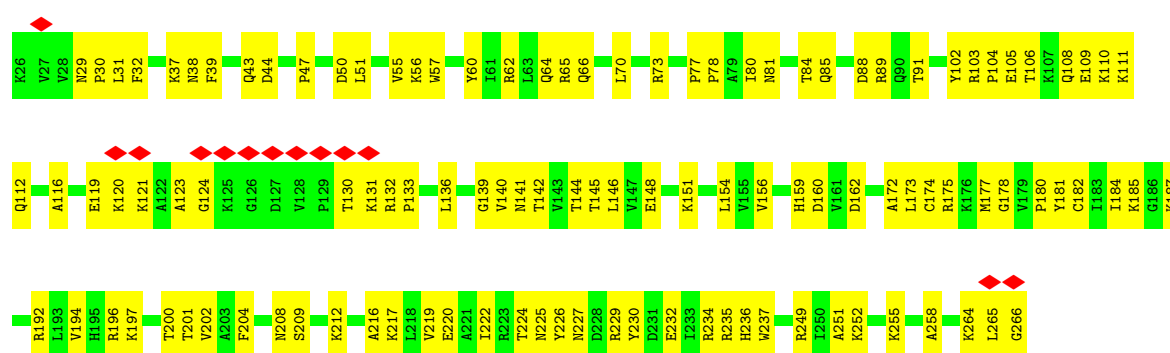




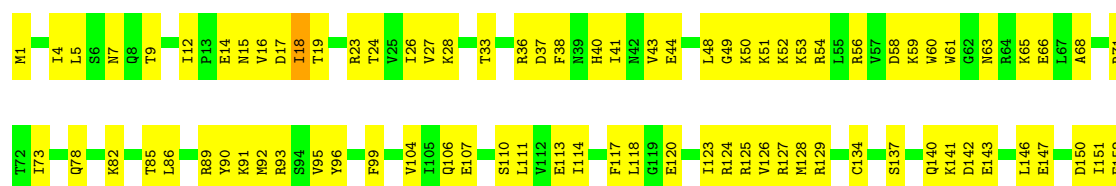
• Molecule 28: 60S ribosomal protein L7a



• Molecule 28: 60S ribosomal protein L7a

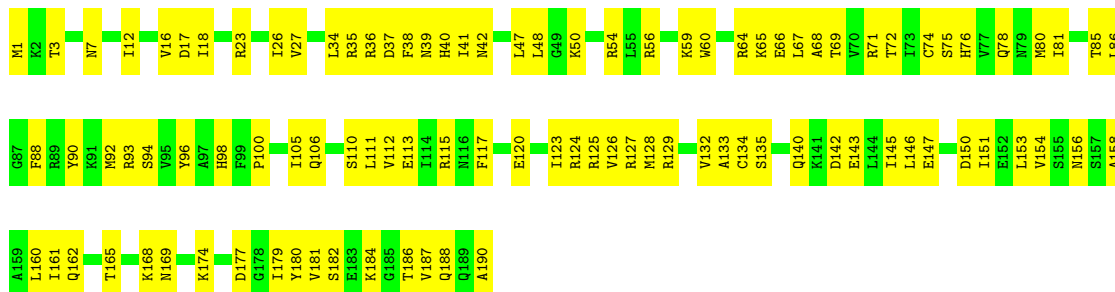


• Molecule 29: 60S ribosomal protein L9

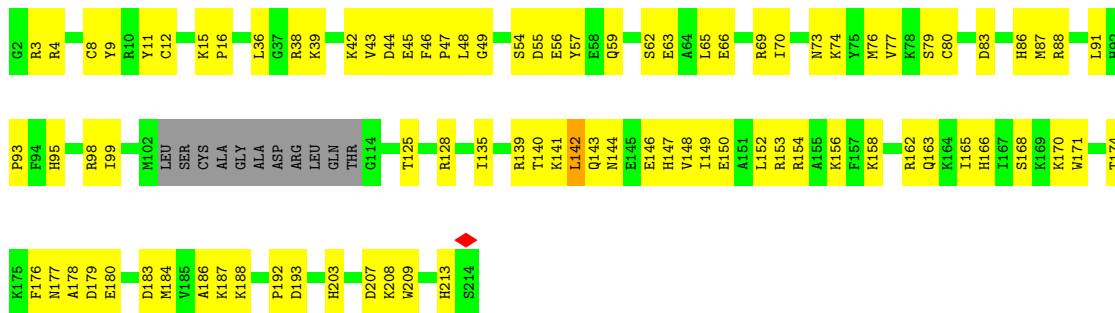




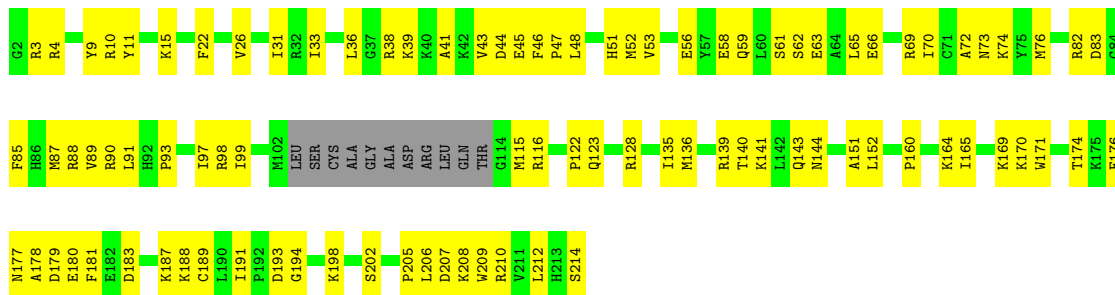
- Molecule 29: 60S ribosomal protein L9



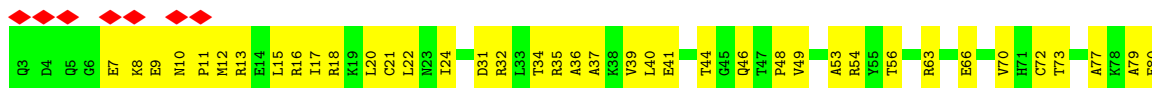
- Molecule 30: Ribosomal protein uL16-like

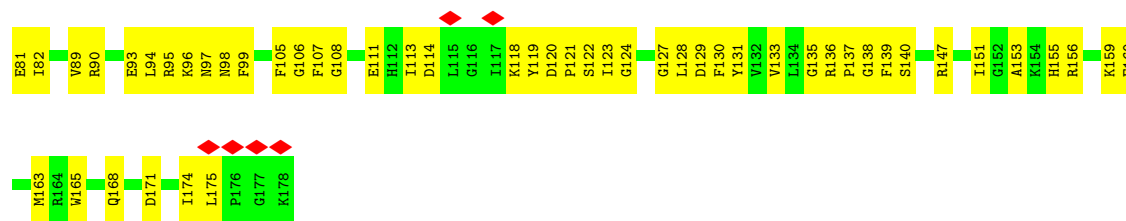


- Molecule 30: Ribosomal protein uL16-like

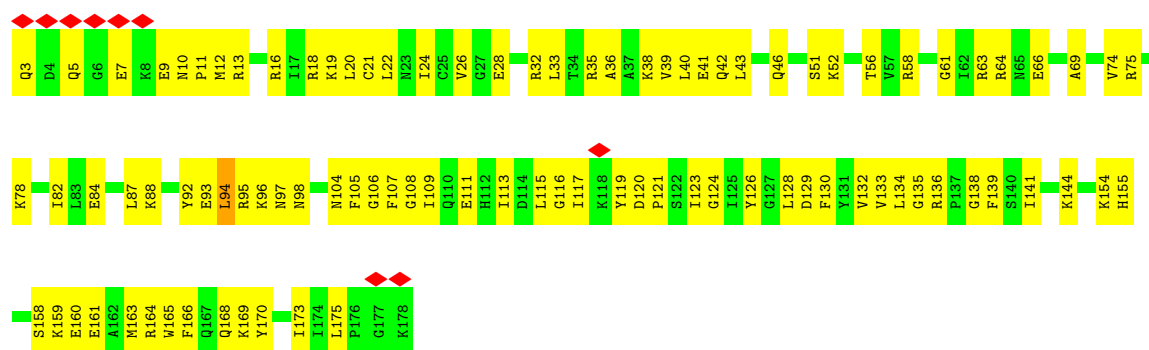


- Molecule 31: 60S ribosomal protein L11

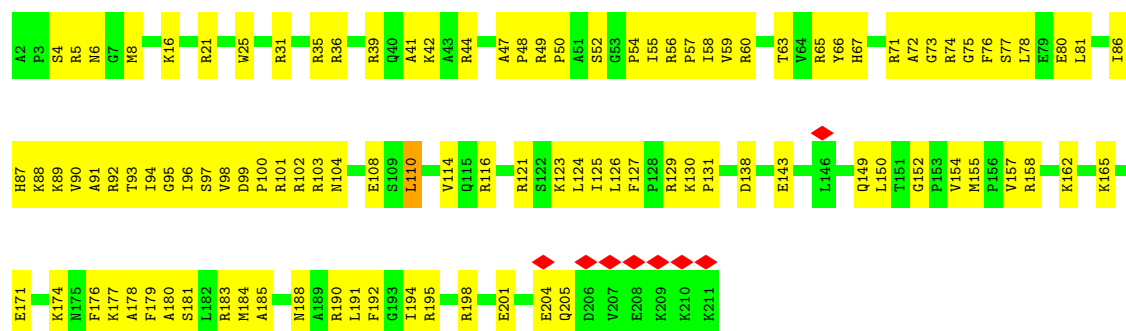




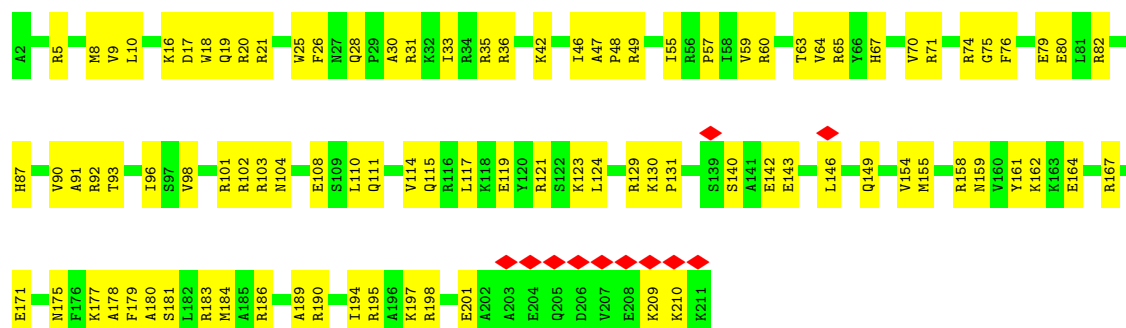
• Molecule 31: 60S ribosomal protein L11



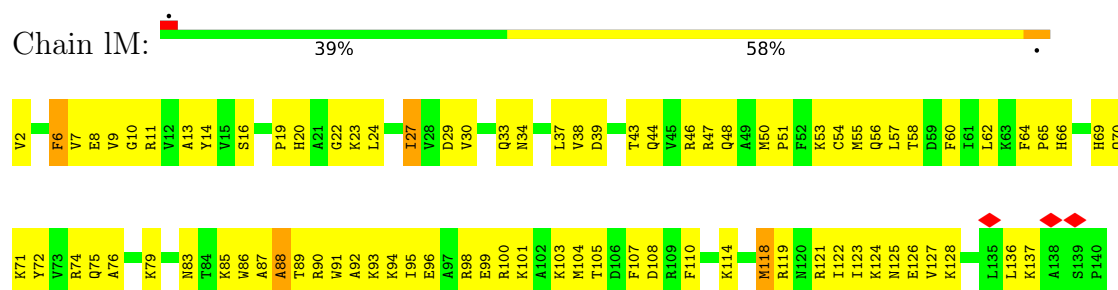
• Molecule 32: Large ribosomal subunit protein eL13



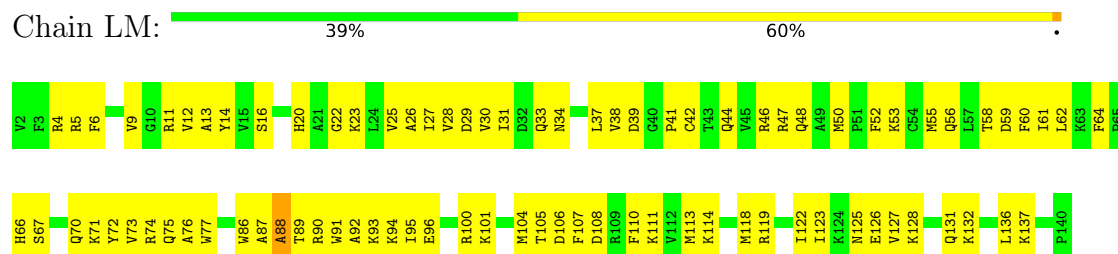
• Molecule 32: Large ribosomal subunit protein eL13



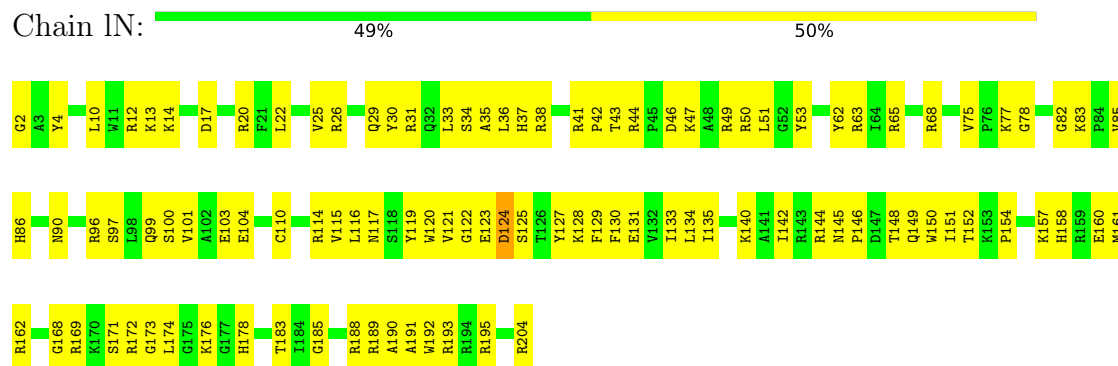
- Molecule 33: 60S ribosomal protein L14



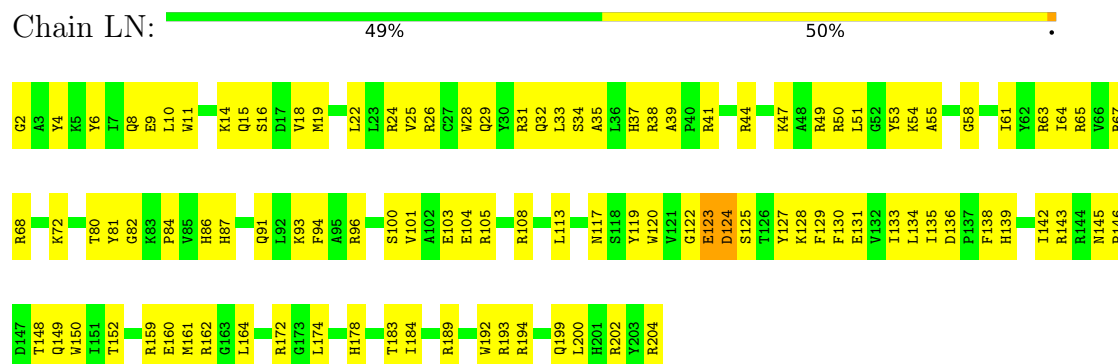
- Molecule 33: 60S ribosomal protein L14



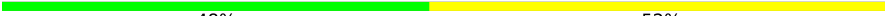
- Molecule 34: 60S ribosomal protein L15

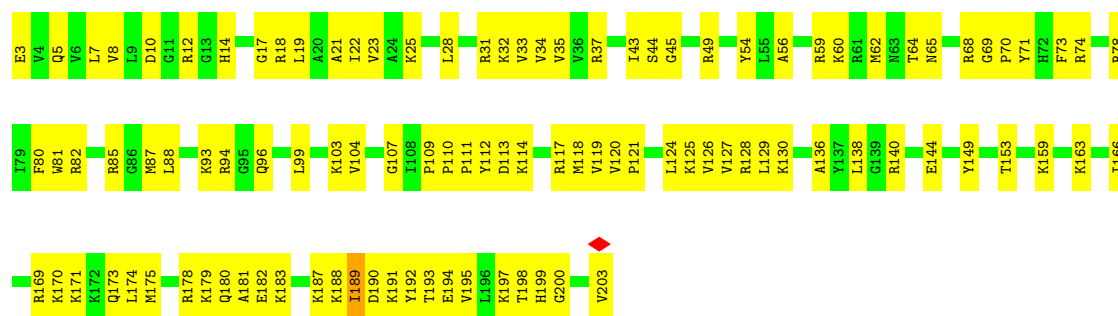


- Molecule 34: 60S ribosomal protein L15



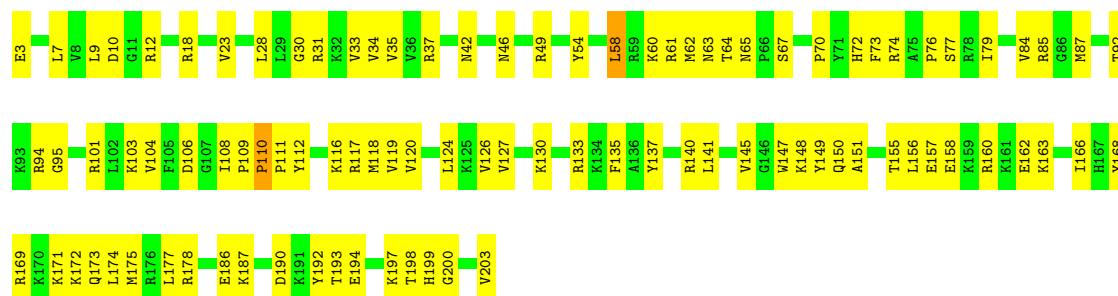
- Molecule 35: 60S ribosomal protein L13a

Chain IO:  48% 52%



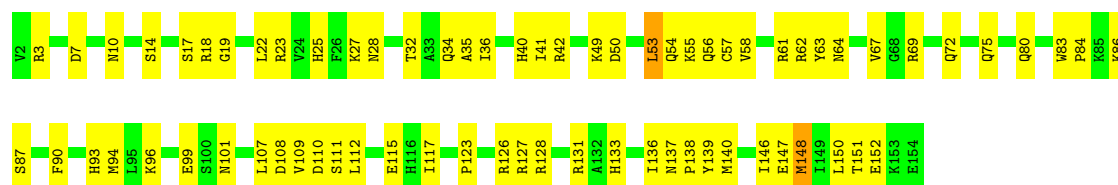
- Molecule 35: 60S ribosomal protein L13a

Chain LO:  52% 47%



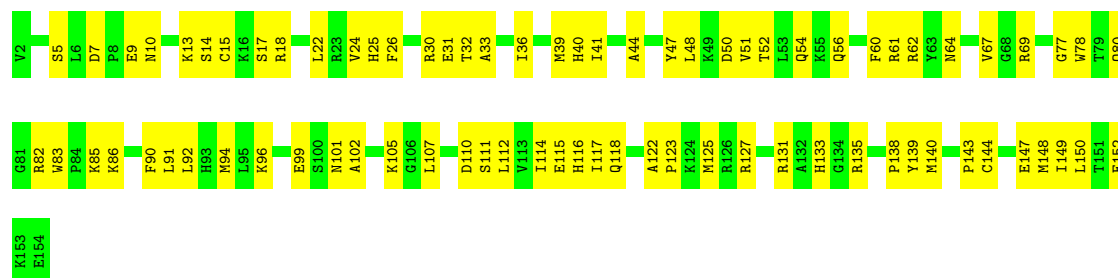
- Molecule 36: 60S ribosomal protein L17

Chain IP:  54% 45%



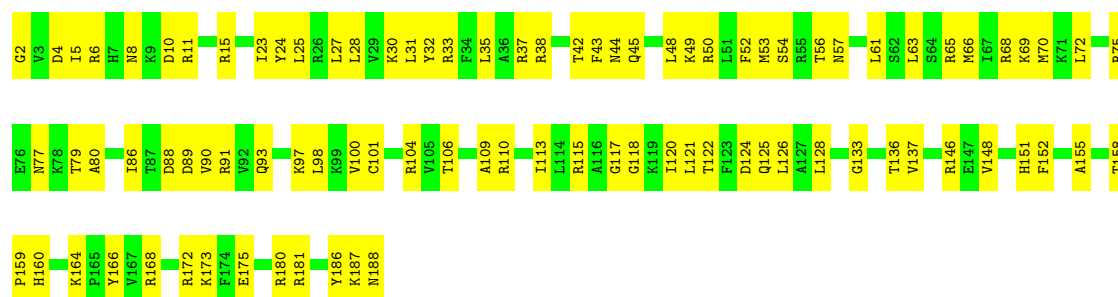
- Molecule 36: 60S ribosomal protein L17

Chain LP:  50% 50%



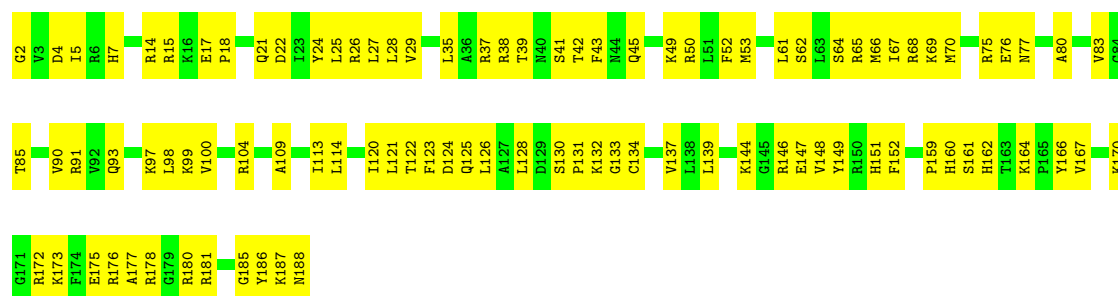
- Molecule 37: 60S ribosomal protein L18

Chain IQ:  51% 49%



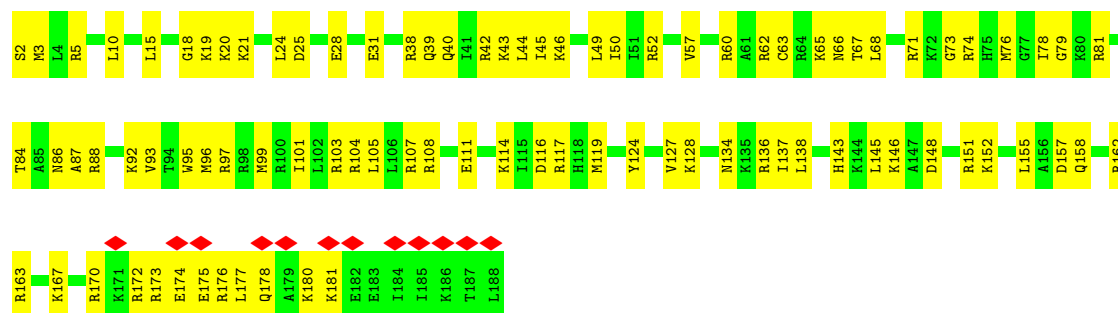
- Molecule 37: 60S ribosomal protein L18

Chain LQ:  49% 51%



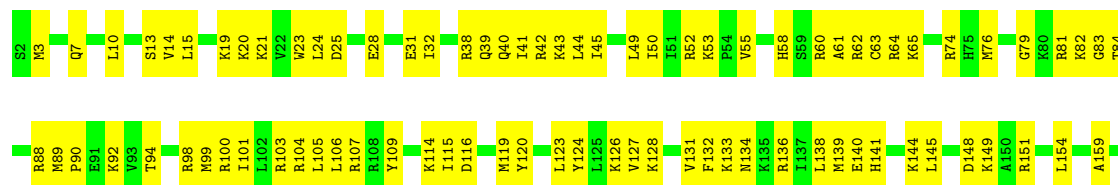
- Molecule 38: 60S ribosomal protein L19

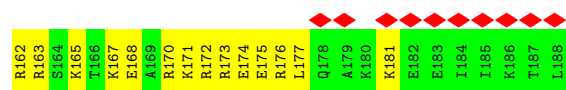
Chain IR:  6% 52% 48%



- Molecule 38: 60S ribosomal protein L19

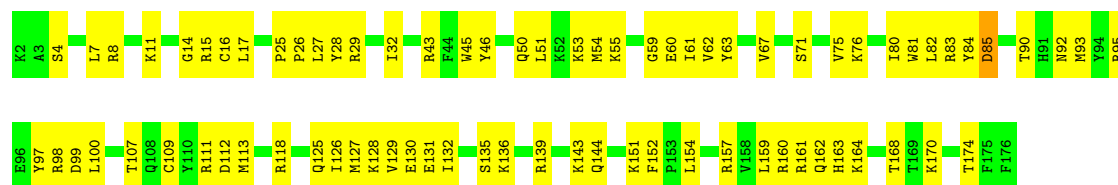
Chain LR:  5% 48% 52%





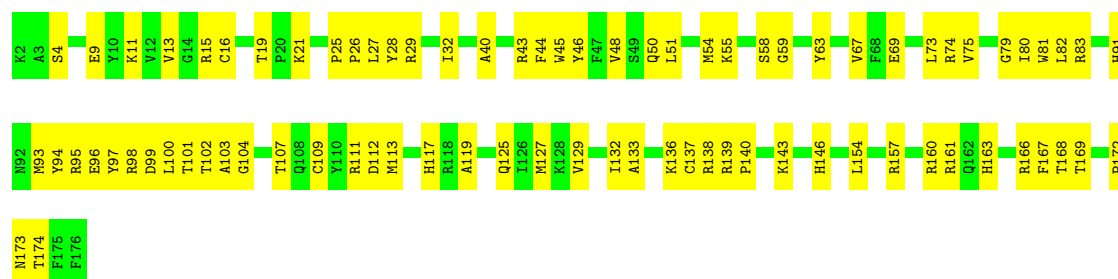
• Molecule 39: 60S ribosomal protein L18a

Chain IS: 56% 43%



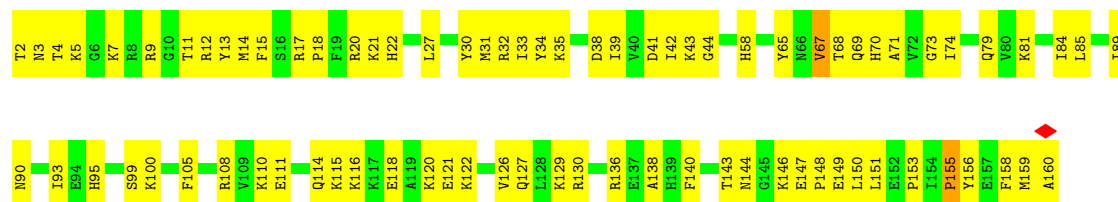
• Molecule 39: 60S ribosomal protein L18a

Chain LS: 54% 46%



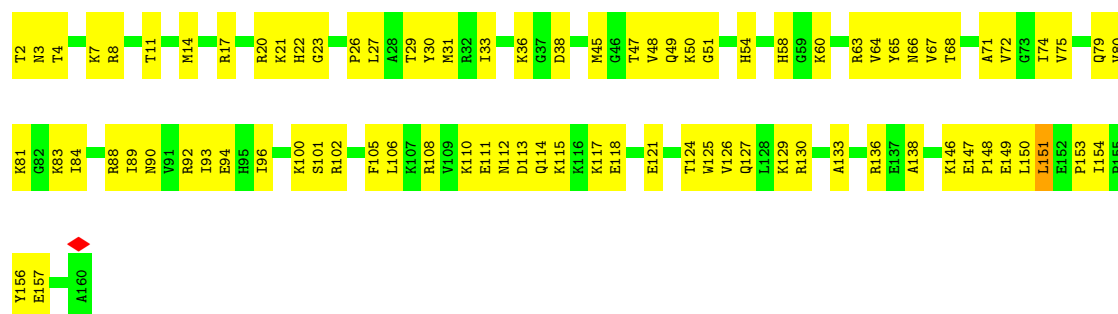
• Molecule 40: 60S ribosomal protein L21

Chain IT: 50% 49%

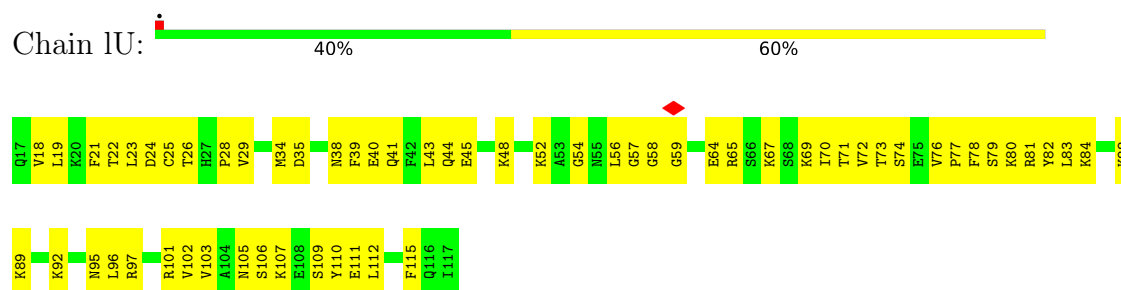


• Molecule 40: 60S ribosomal protein L21

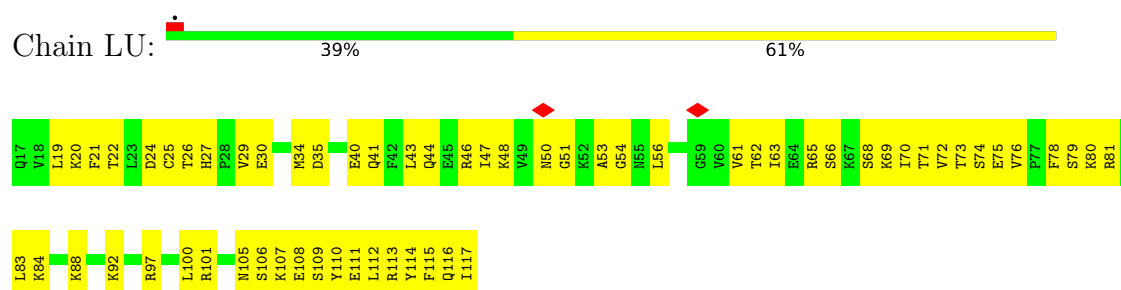
Chain LT: 47% 53%



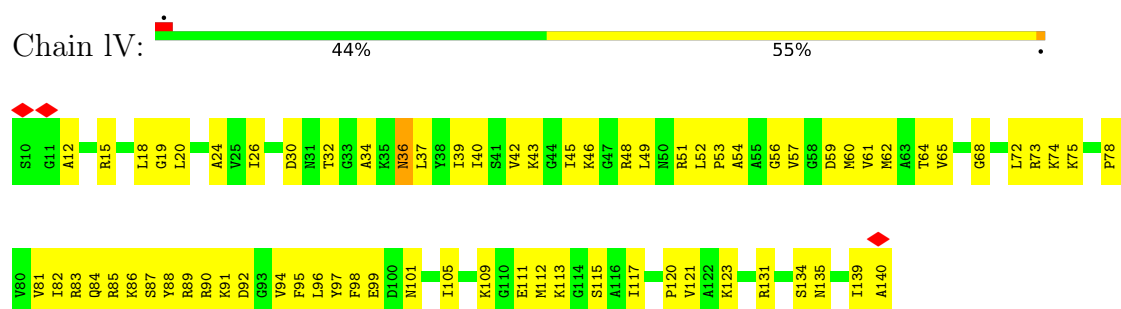
- Molecule 41: Heparin-binding protein HBp15



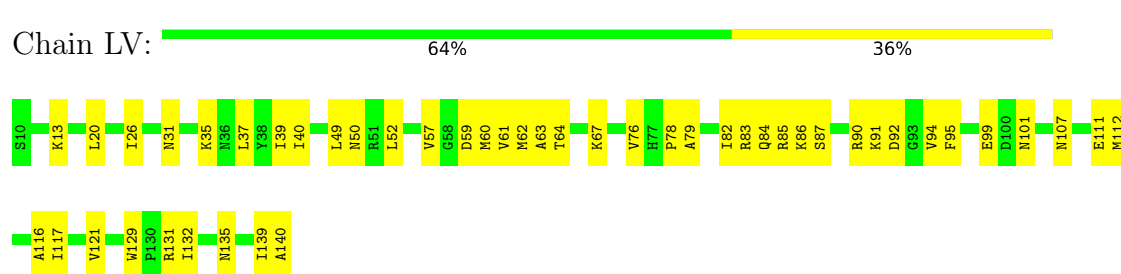
- Molecule 41: Heparin-binding protein HBp15



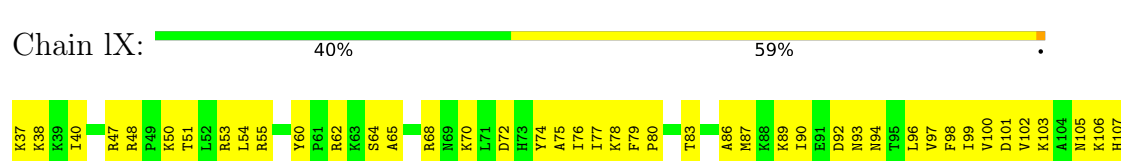
- Molecule 42: 60S ribosomal protein L23



- Molecule 42: 60S ribosomal protein L23



- Molecule 43: 60S ribosomal protein L23a

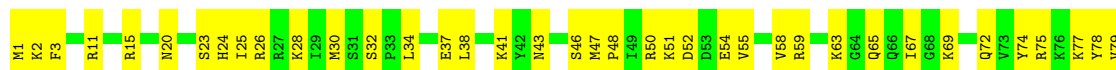




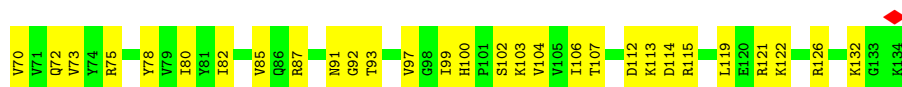
- Molecule 43: 60S ribosomal protein L23a



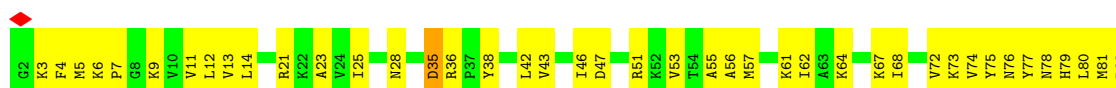
- Molecule 44: 60S ribosomal protein L26



- Molecule 44: 60S ribosomal protein L26

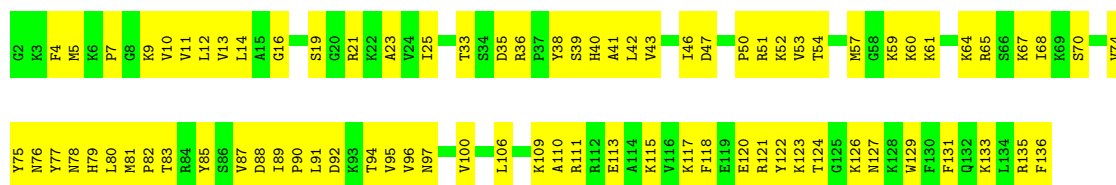


- Molecule 45: 60S ribosomal protein L27



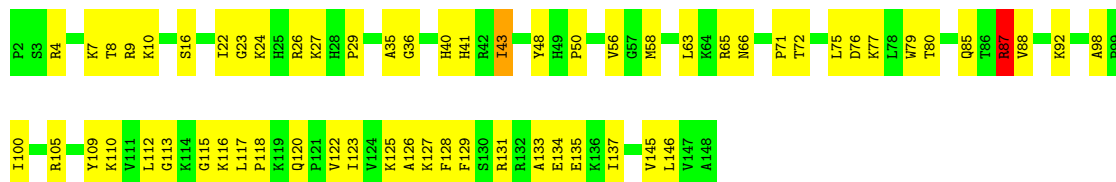
- Molecule 45: 60S ribosomal protein L27





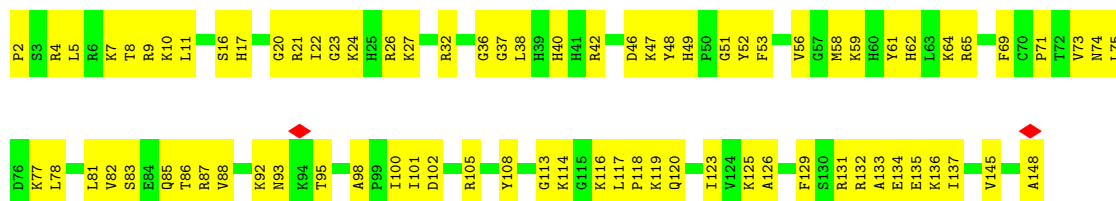
• Molecule 46: 60S ribosomal protein L27a

Chain la: 59% 40%



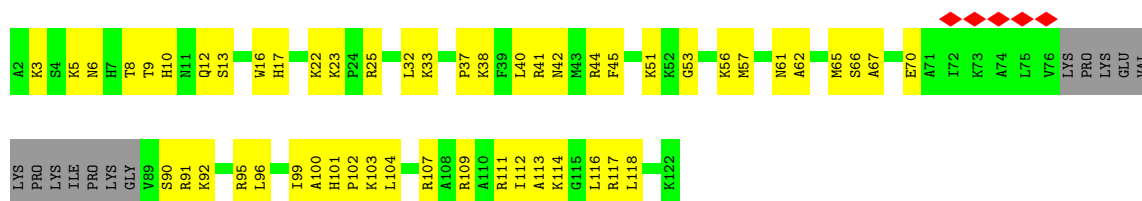
• Molecule 46: 60S ribosomal protein L27a

Chain La: 46% 54%



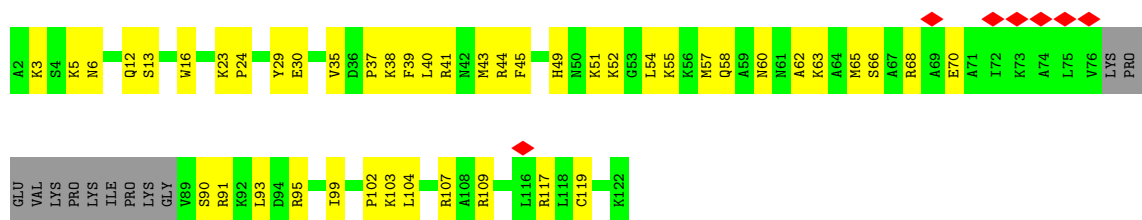
• Molecule 47: Large ribosomal subunit protein eL29

Chain lb: 47% 43% 10%



• Molecule 47: Large ribosomal subunit protein eL29

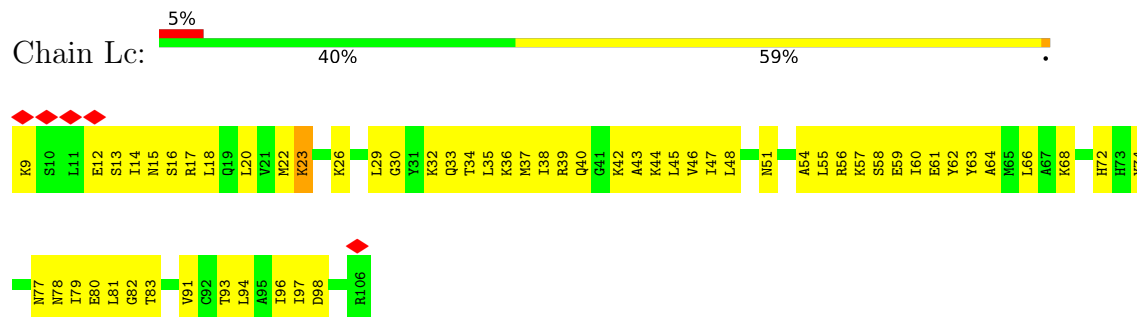
Chain Lb: 6% 53% 37% 10%



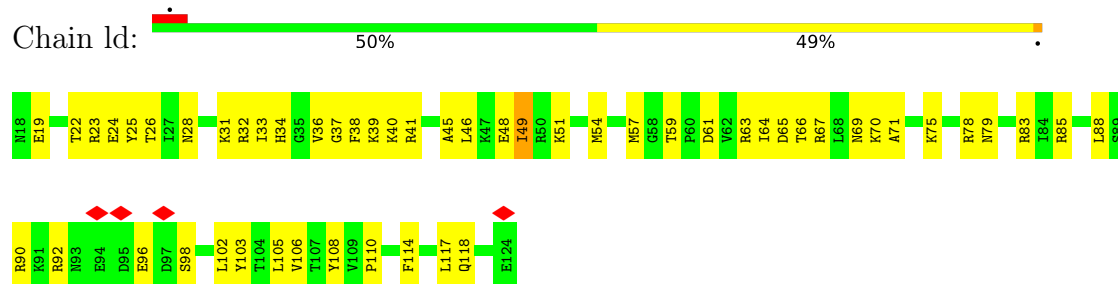
• Molecule 48: 60S ribosomal protein L30



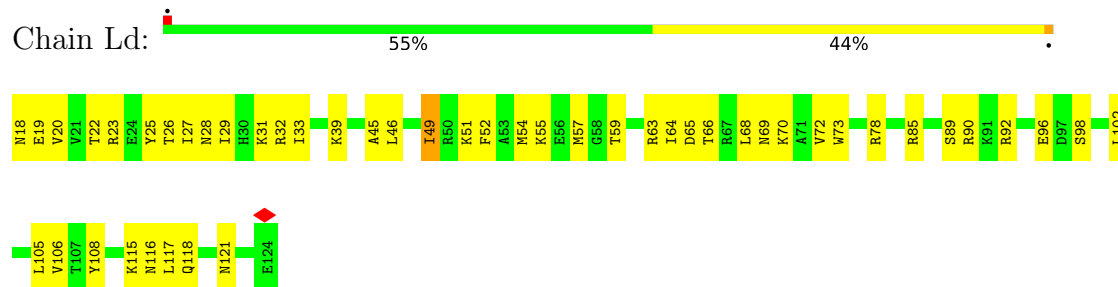
- Molecule 48: 60S ribosomal protein L30



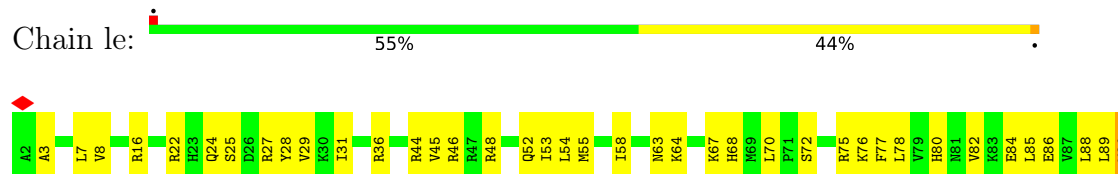
- Molecule 49: 60S ribosomal protein L31

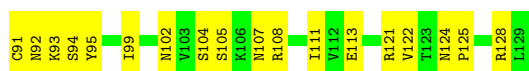


- Molecule 49: 60S ribosomal protein L31



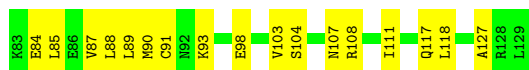
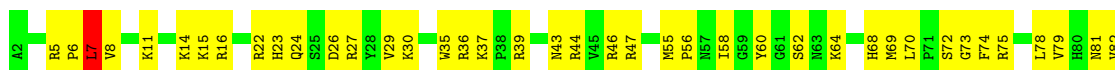
- Molecule 50: 60S ribosomal protein L32





- Molecule 50: 60S ribosomal protein L32

Chain Le: 55% 44%



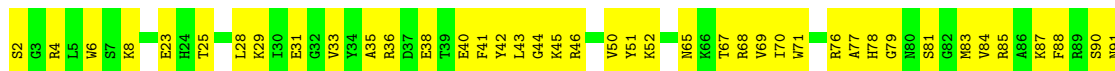
- Molecule 51: 60S ribosomal protein L35a

Chain lf: 53% 46%



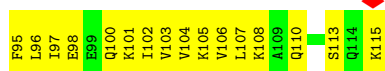
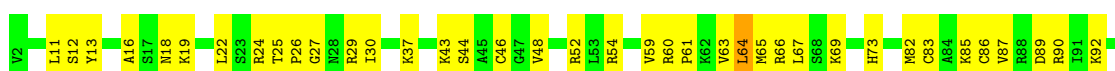
- Molecule 51: 60S ribosomal protein L35a

Chain Lf: 54% 45%



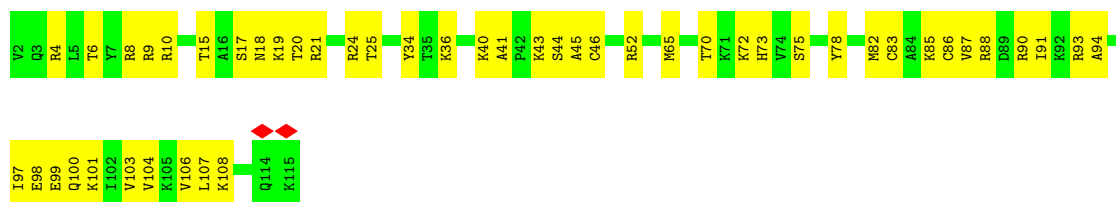
- Molecule 52: 60S ribosomal protein L34

Chain lg: 53% 46%



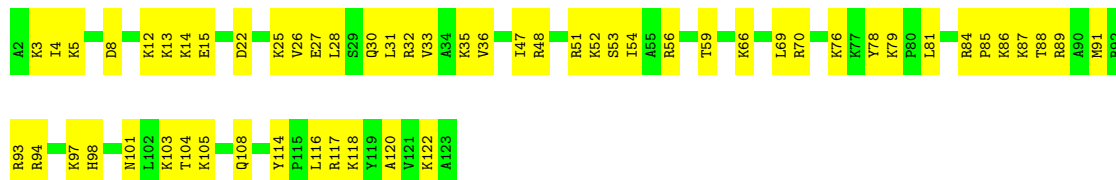
- Molecule 52: 60S ribosomal protein L34

Chain Lg: 58% 42%



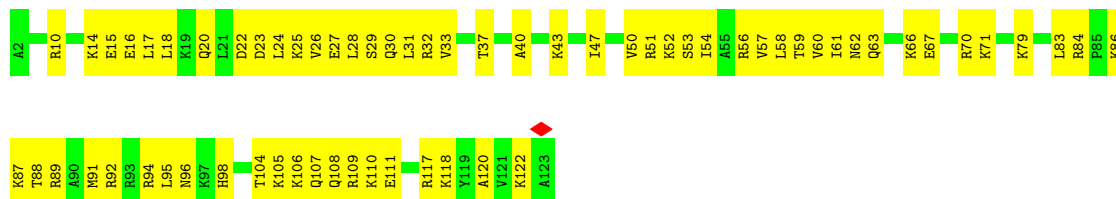
• Molecule 53: 60S ribosomal protein L35

Chain lh: 54% 46%



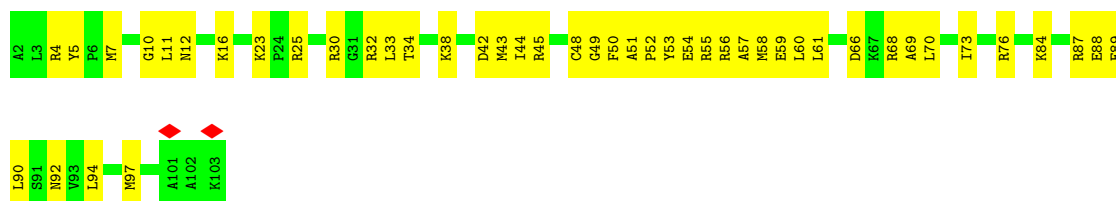
• Molecule 53: 60S ribosomal protein L35

Chain Lh: 47% 53%



• Molecule 54: 60S ribosomal protein L36

Chain li: 55% 45%

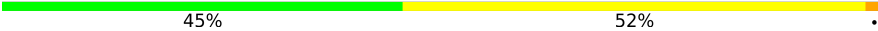


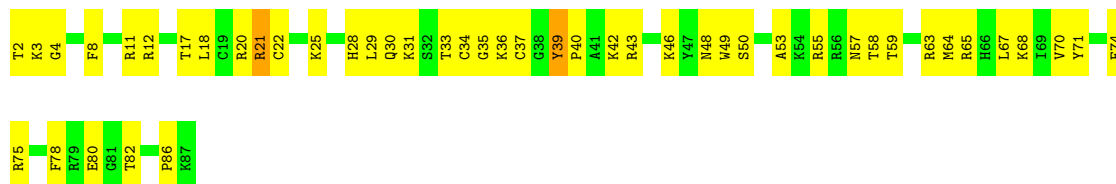
• Molecule 54: 60S ribosomal protein L36

Chain Li: 5% 47% 51%



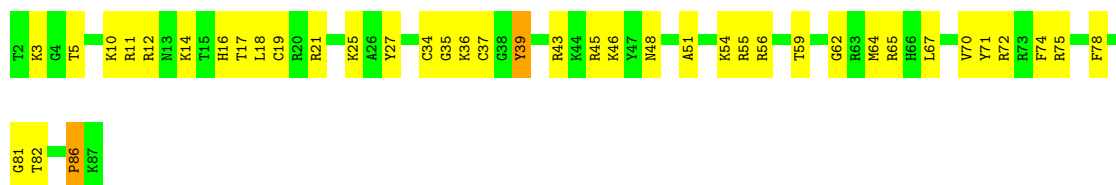
• Molecule 55: 60S ribosomal protein L37

Chain lj: 

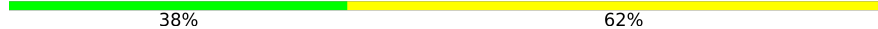


- Molecule 55: 60S ribosomal protein L37

Chain Lj: 



- Molecule 56: 60S ribosomal protein L38

Chain lk: 



- Molecule 56: 60S ribosomal protein L38

Chain Lk: 



- Molecule 57: 60S ribosomal protein L39

Chain ll: 



- Molecule 57: 60S ribosomal protein L39

Chain Ll: 



- Molecule 58: Large ribosomal subunit protein eL40



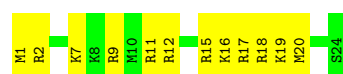
- Molecule 58: Large ribosomal subunit protein eL40



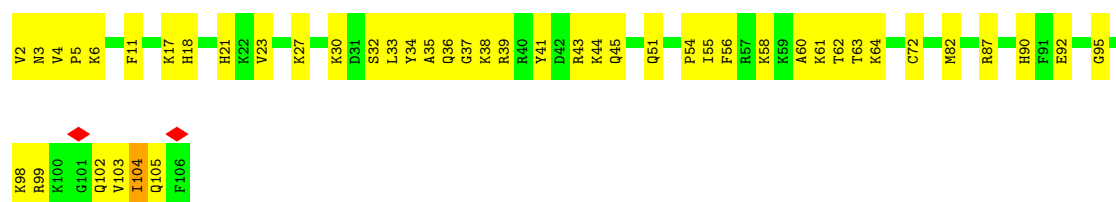
- Molecule 59: 60S ribosomal protein L41



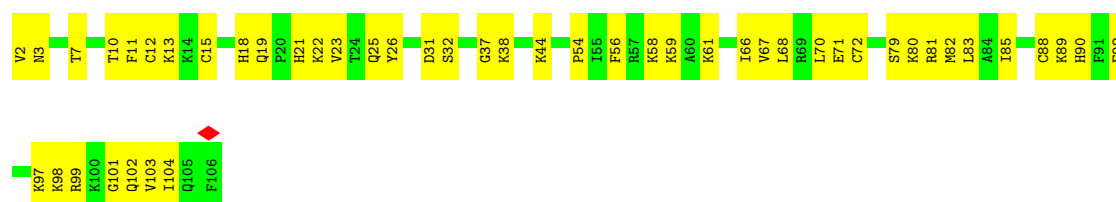
- Molecule 59: 60S ribosomal protein L41



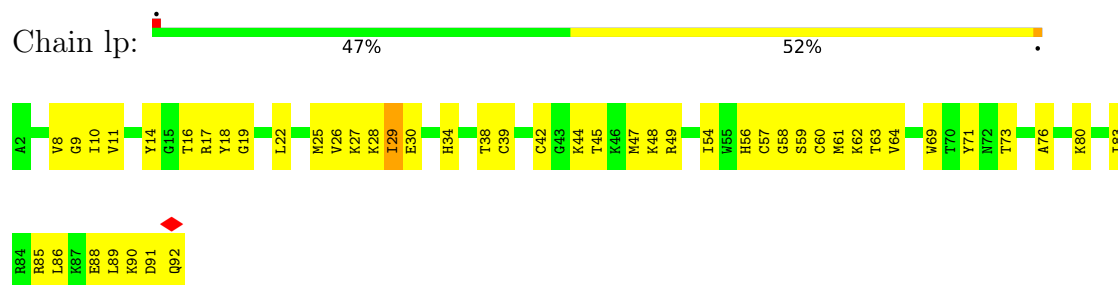
- Molecule 60: 60S ribosomal protein L36a



- Molecule 60: 60S ribosomal protein L36a



- Molecule 61: 60S ribosomal protein L37a



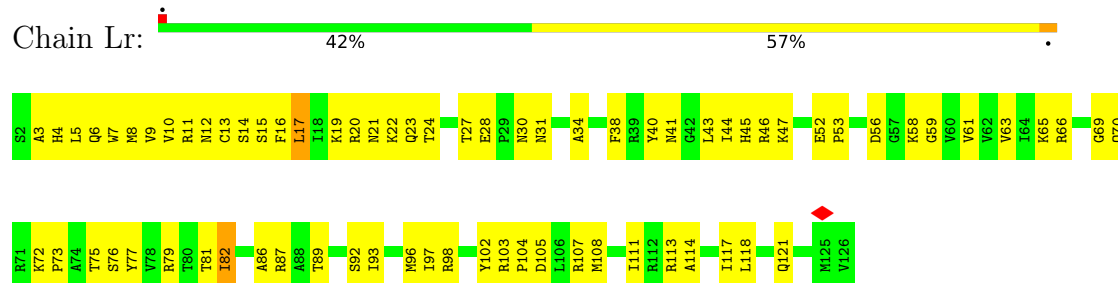
- Molecule 61: 60S ribosomal protein L37a



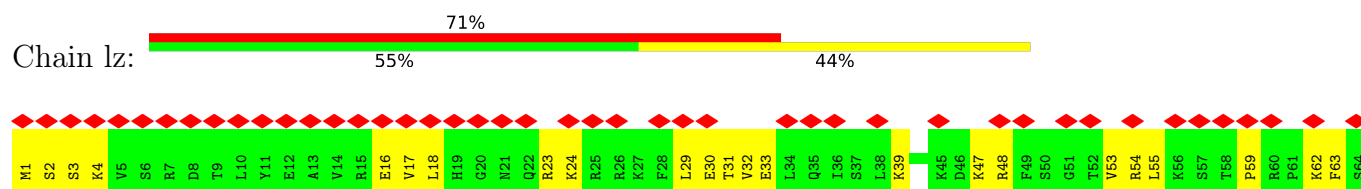
- Molecule 62: 60S ribosomal protein L28

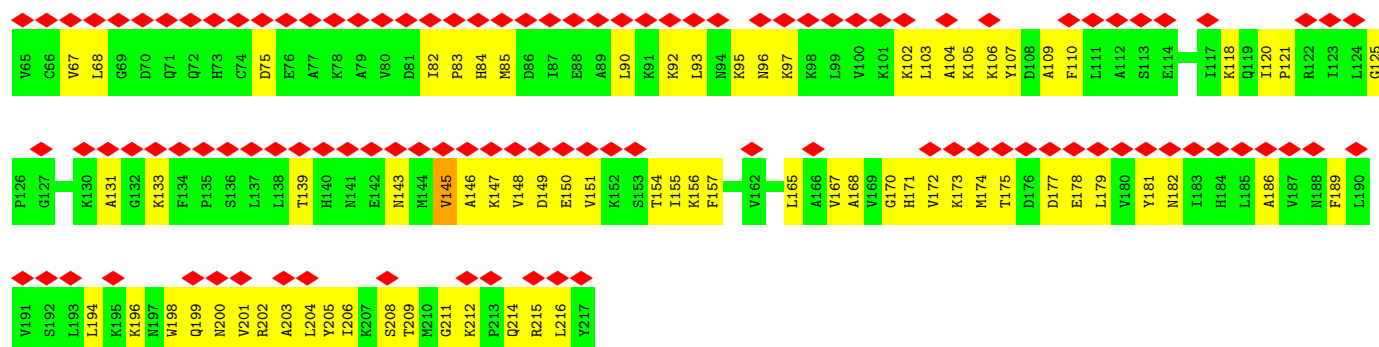


- Molecule 62: 60S ribosomal protein L28

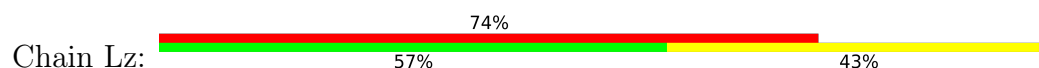


- Molecule 63: 60S ribosomal protein L10a





• Molecule 63: 60S ribosomal protein L10a

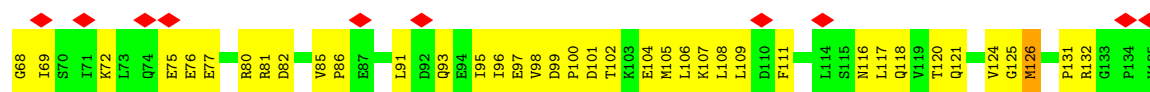


• Molecule 64: 40S ribosomal protein S17

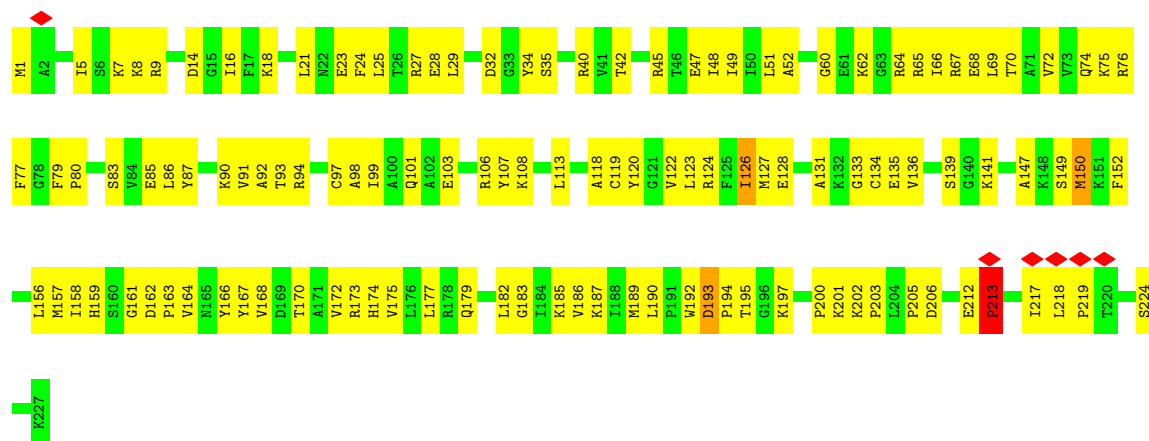


• Molecule 64: 40S ribosomal protein S17

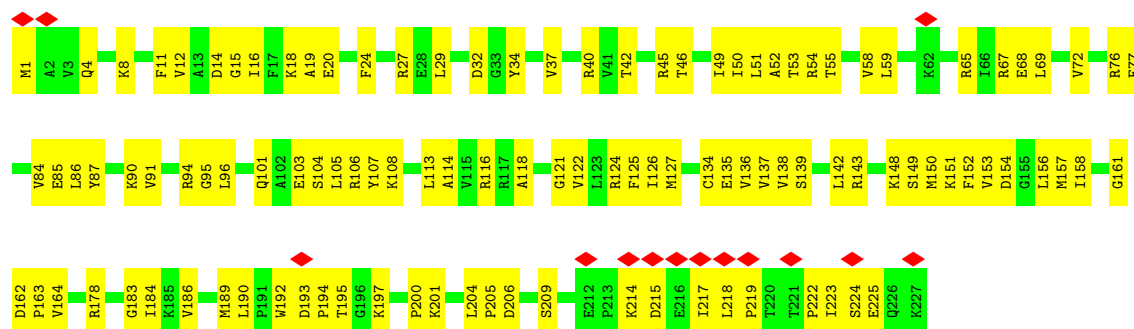




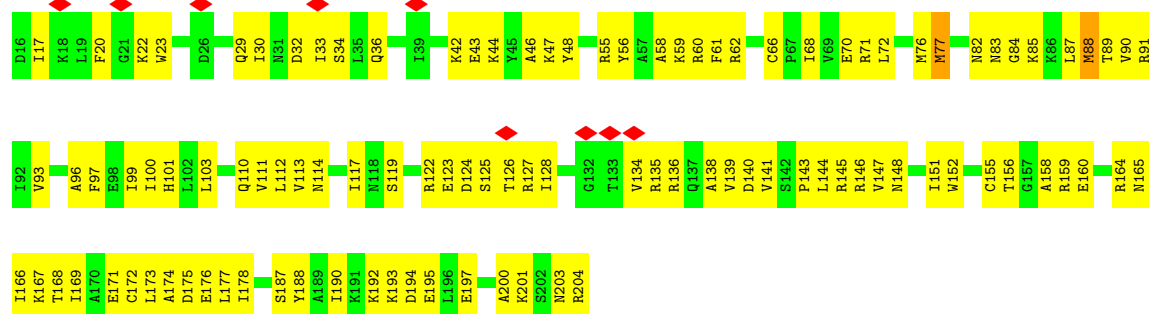
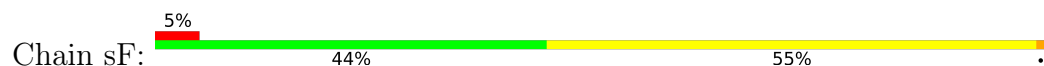
- Molecule 65: Small ribosomal subunit protein uS3



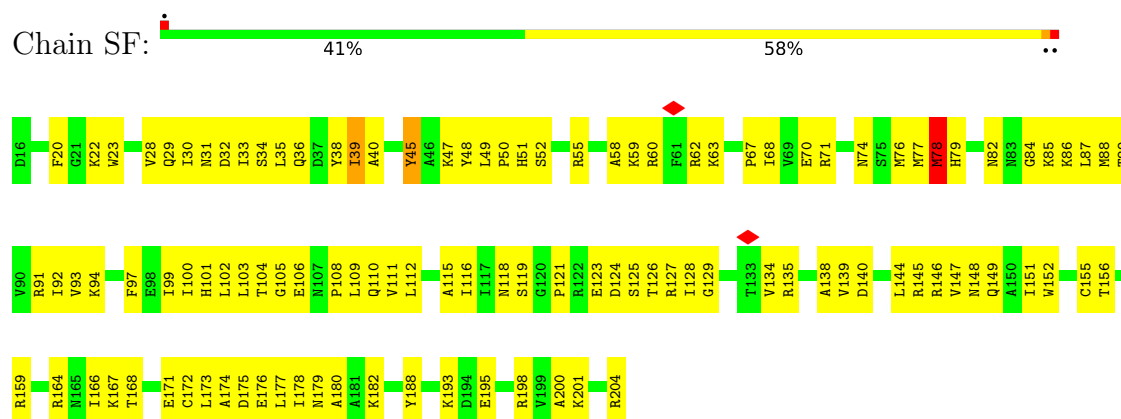
- Molecule 65: Small ribosomal subunit protein uS3



- Molecule 66: 40S ribosomal protein S5



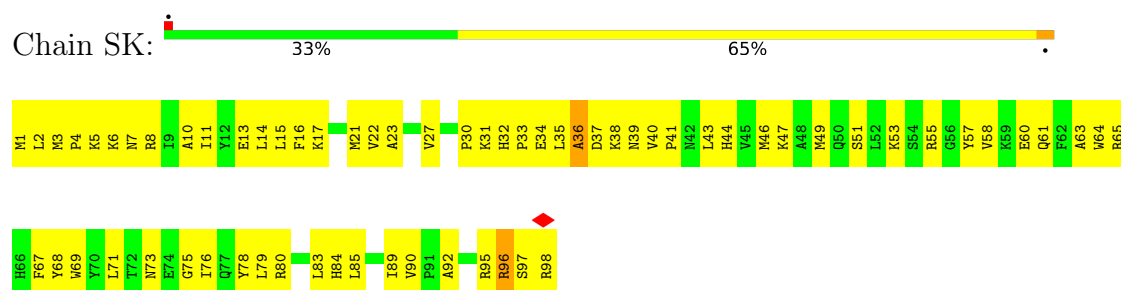
- Molecule 66: 40S ribosomal protein S5



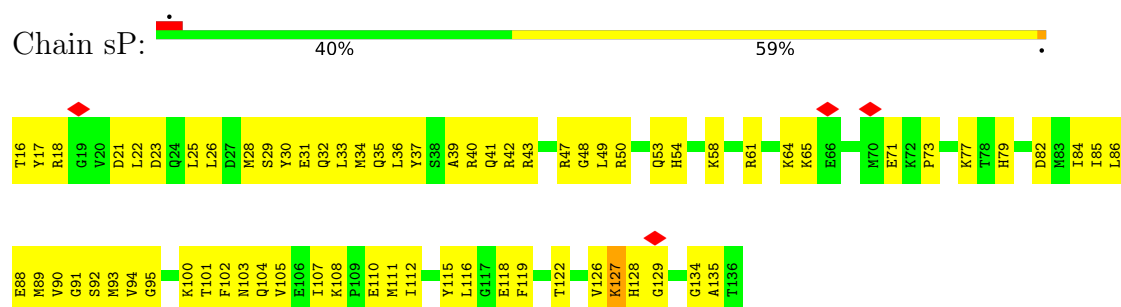
- Molecule 67: 40S ribosomal protein S10



- Molecule 67: 40S ribosomal protein S10

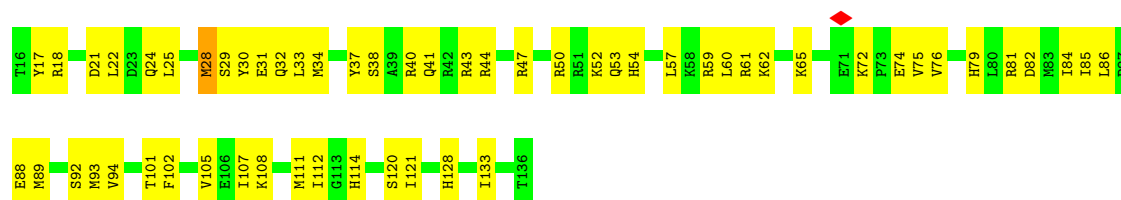


- Molecule 68: Small ribosomal subunit protein uS19



- Molecule 68: Small ribosomal subunit protein uS19

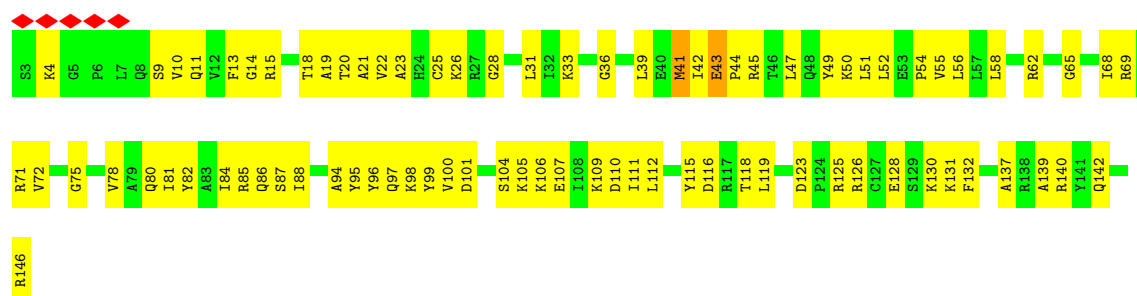




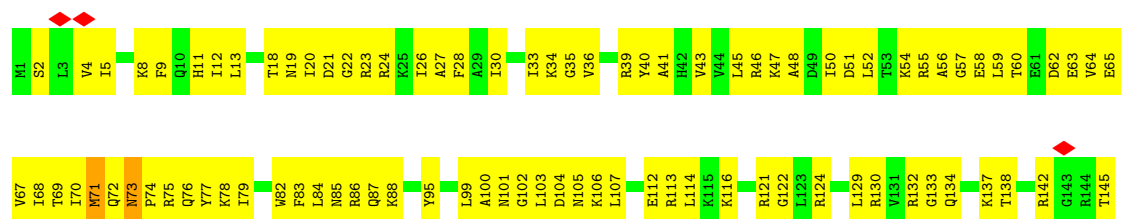
• Molecule 69: Small ribosomal subunit protein uS9



• Molecule 69: Small ribosomal subunit protein uS9

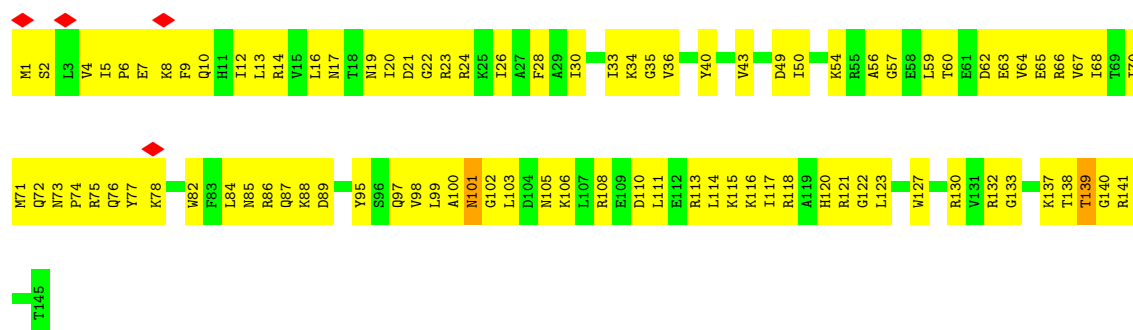


• Molecule 70: 40S ribosomal protein S18

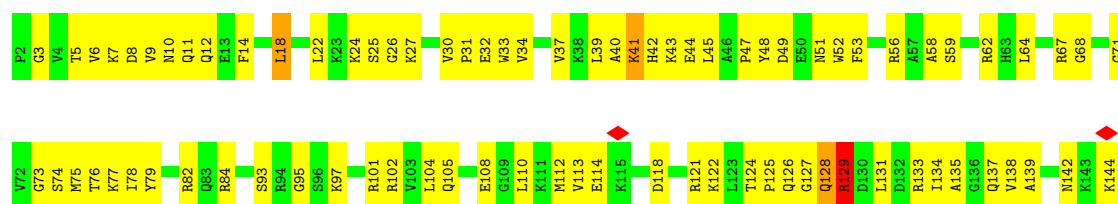


• Molecule 70: 40S ribosomal protein S18

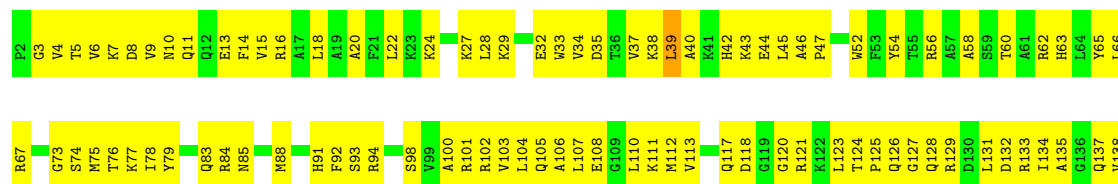




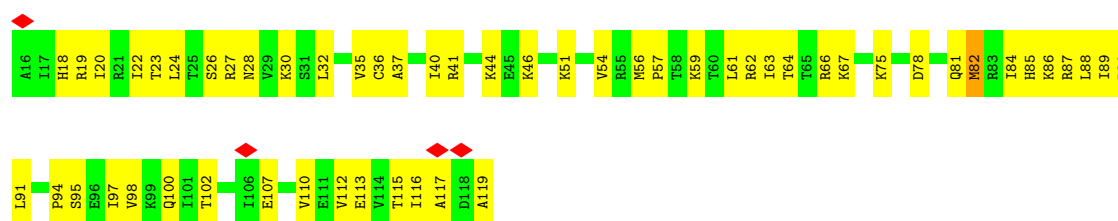
- Molecule 71: 40S ribosomal protein S19



- Molecule 71: 40S ribosomal protein S19

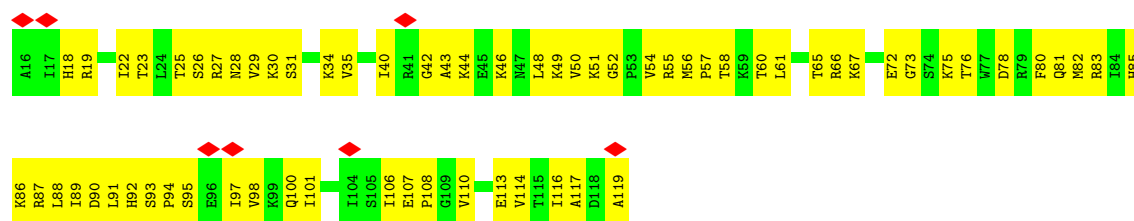


- Molecule 72: 40S ribosomal protein S20

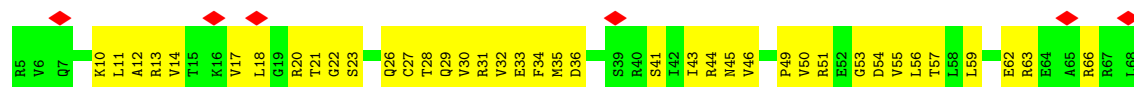


- Molecule 72: 40S ribosomal protein S20

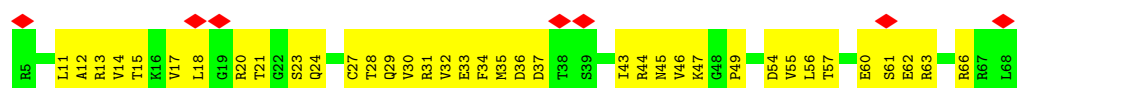
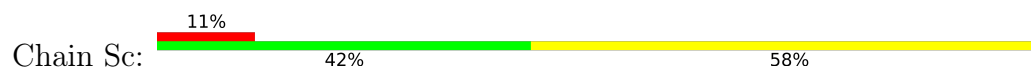




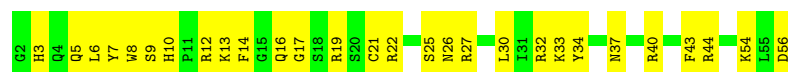
- Molecule 73: 40S ribosomal protein S28



- Molecule 73: 40S ribosomal protein S28



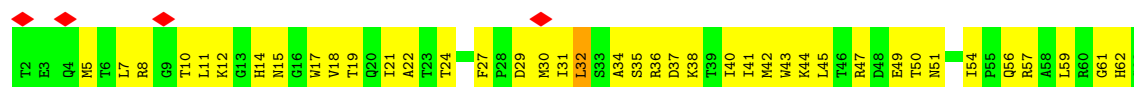
- Molecule 74: 40S ribosomal protein S29

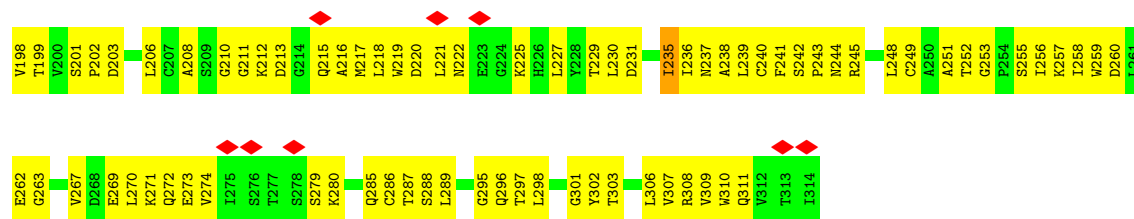


- Molecule 74: 40S ribosomal protein S29

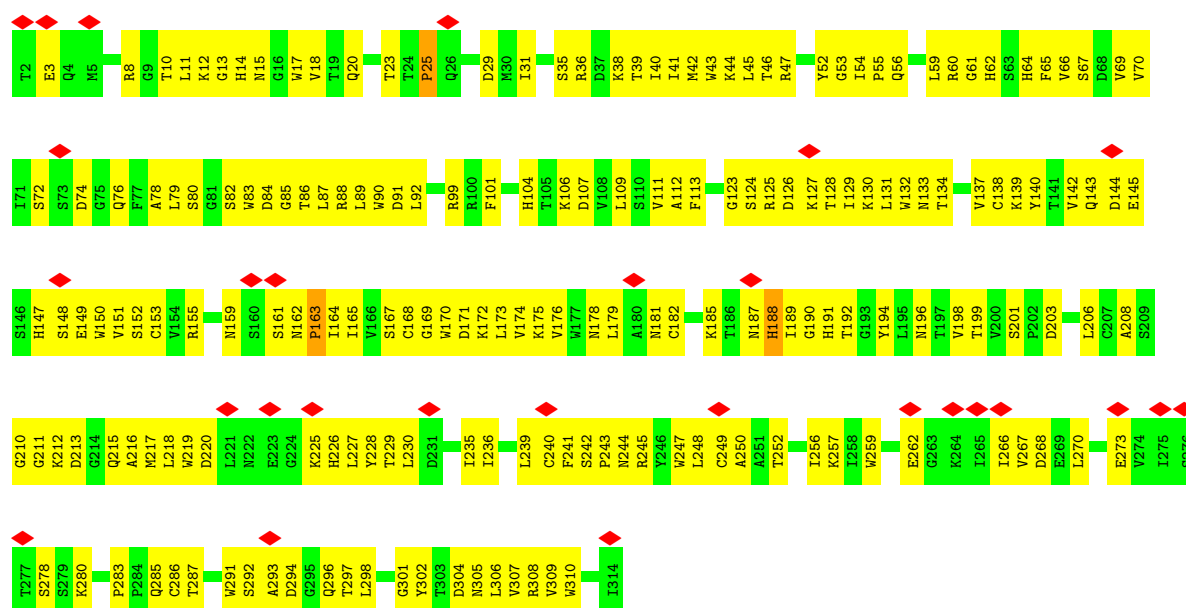


- Molecule 75: Receptor of activated protein C kinase 1

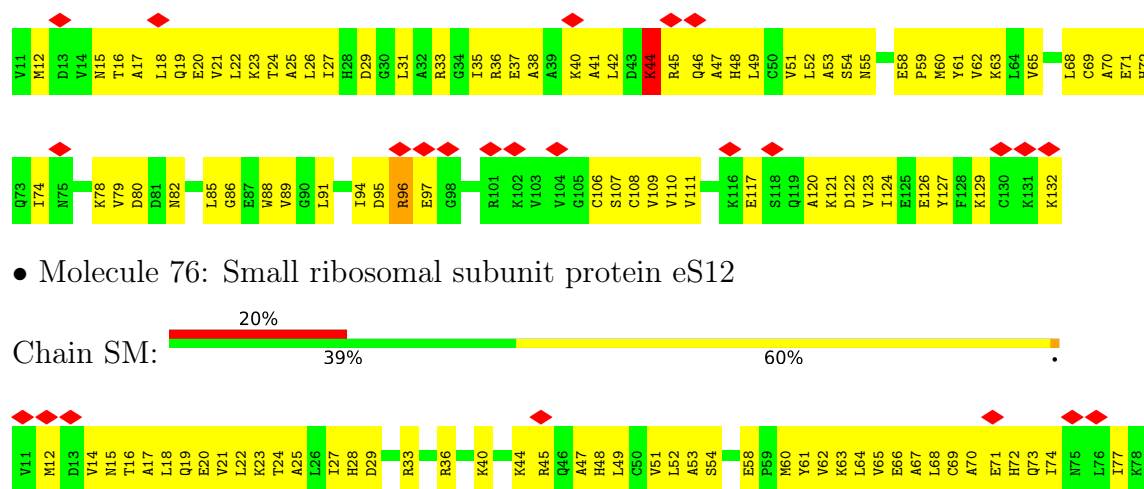




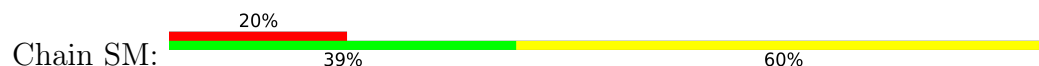
• Molecule 75: Receptor of activated protein C kinase 1

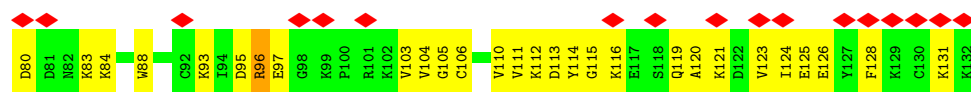


• Molecule 76: Small ribosomal subunit protein eS12

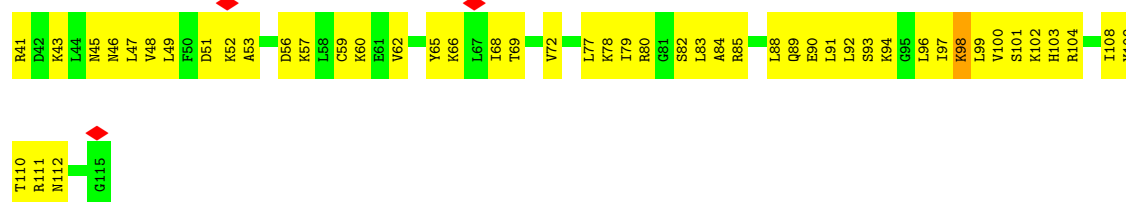
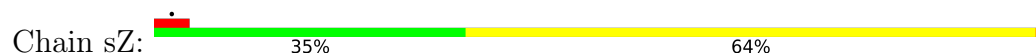


• Molecule 76: Small ribosomal subunit protein eS12

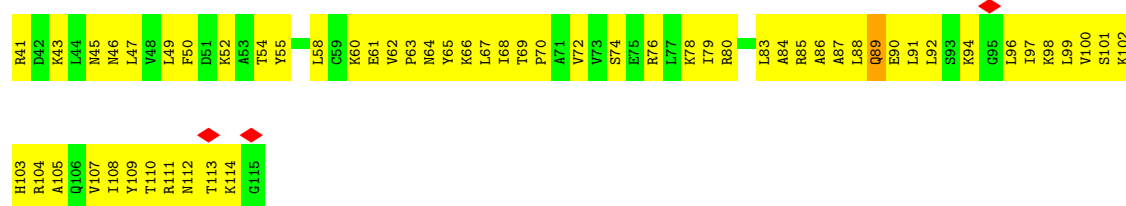




- Molecule 77: Small ribosomal subunit protein eS25



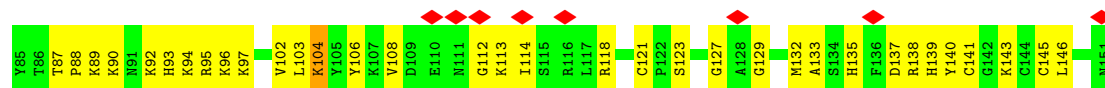
- Molecule 77: Small ribosomal subunit protein eS25



- Molecule 78: Ubiquitin-40S ribosomal protein S27a



- Molecule 78: Ubiquitin-40S ribosomal protein S27a

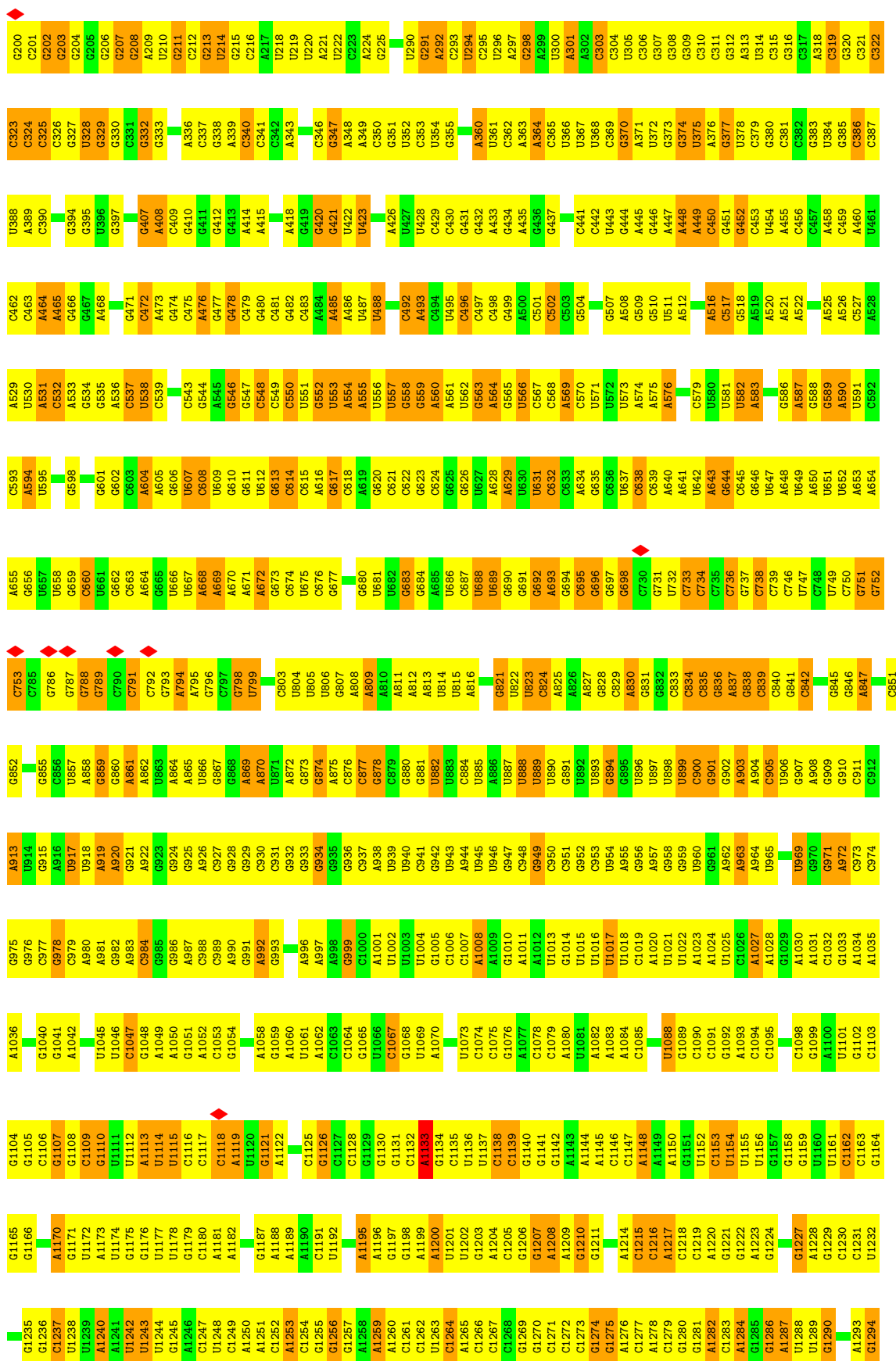


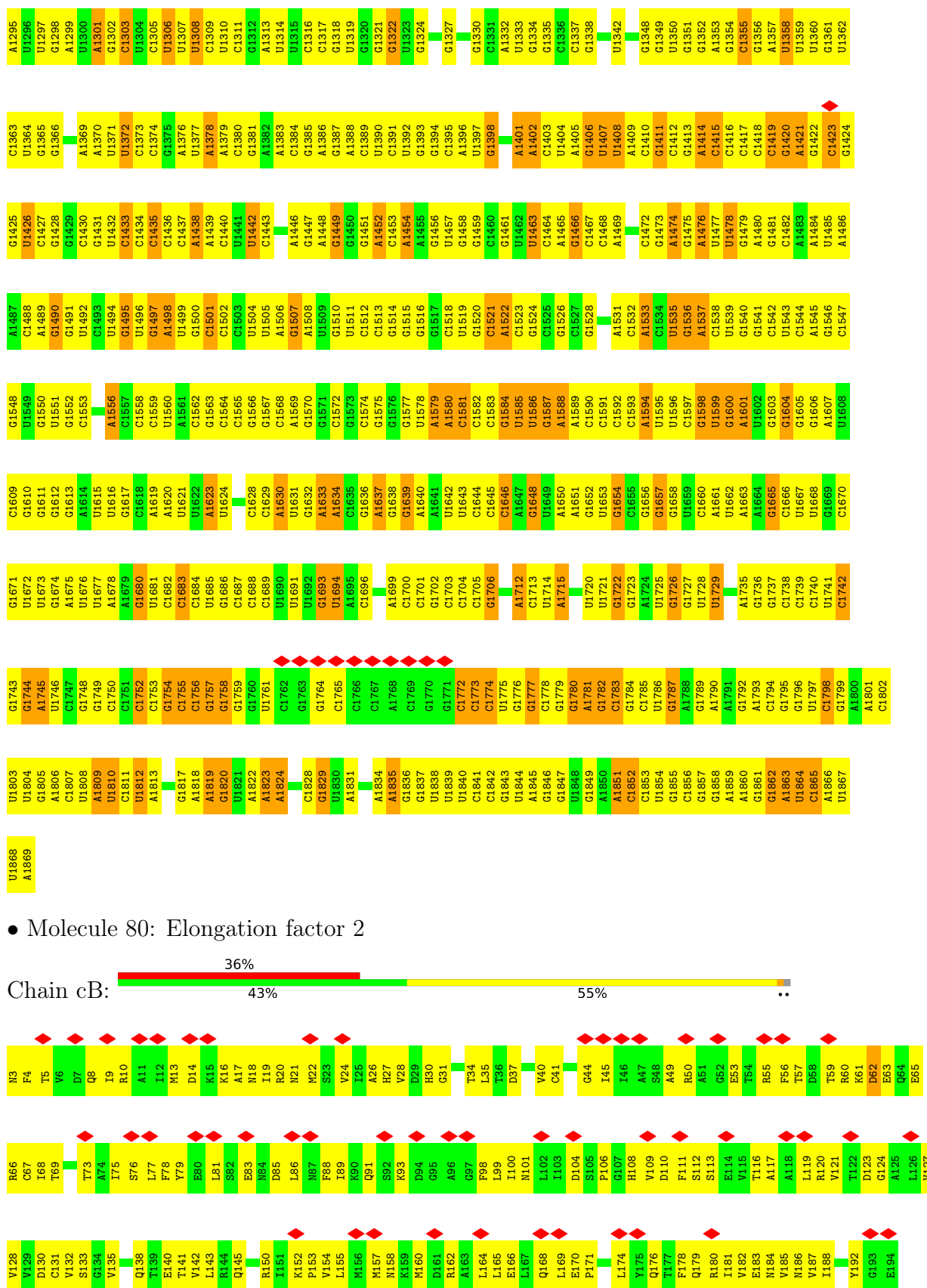
- Molecule 79: 18S rRNA [Homo sapiens]

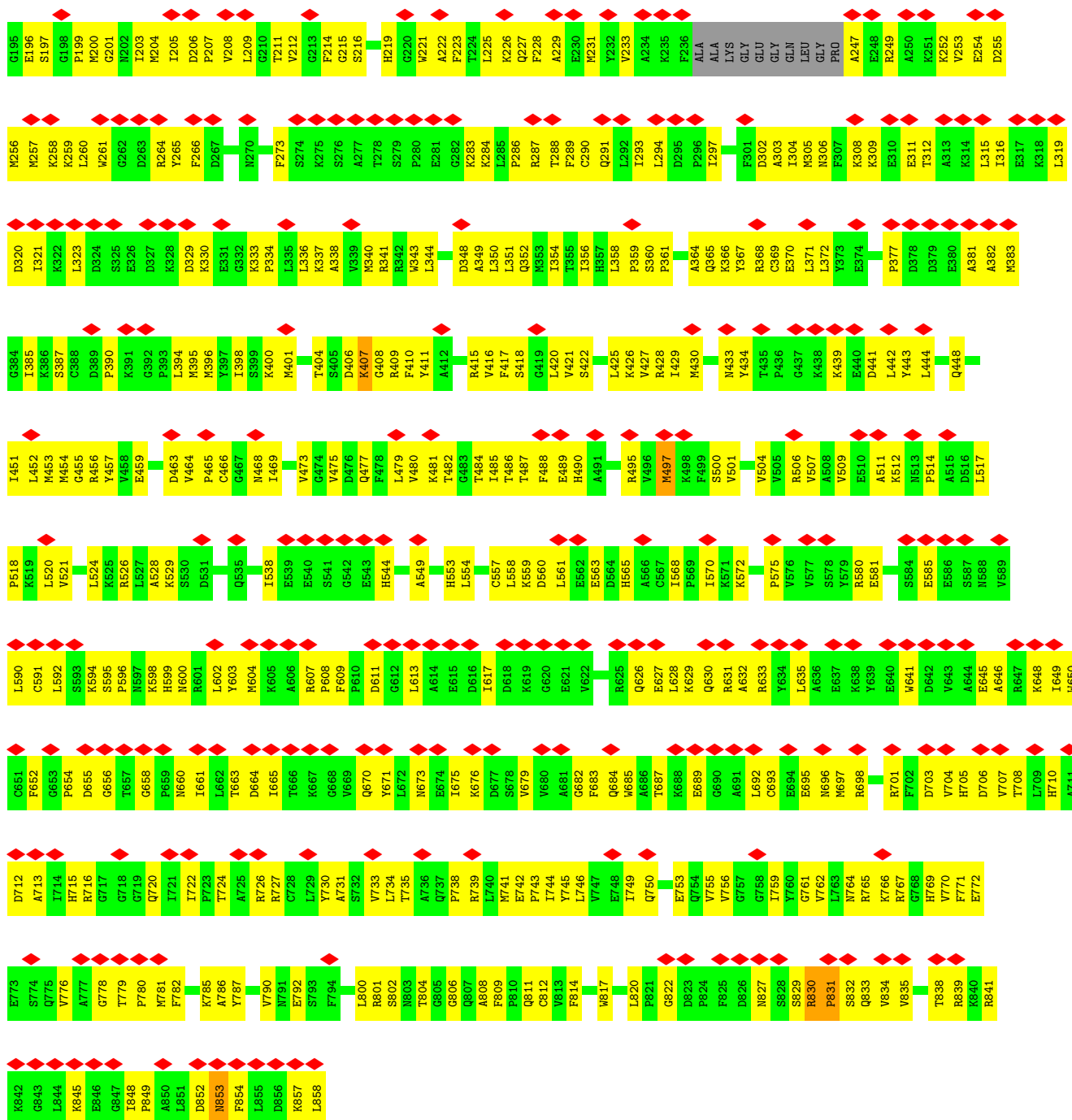


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U1155	C1095	A1027	A964	A903	G841	C739	G644	U581	A521	U461	C391	C326	G204	C142	
U1156	G1096		U965	A904	C842	C746	C645	U582	A522	C462	A392	C327	G205	G71	G71
U1157	G1097	G1033		C905	C843	U747	G646	U583	A523	C463	U393	U328	G206	U143	
U1158	G1098	A1034	U969	U906	U844	C748	U647	U584	U524	A464	G394	G329	G207	G145	C72
U1159	G1099	A1035	G970	U907	U845	C749	A648	C585	U525	A465	G395	G330	G208	G146	C73
U1160	A1100	A1036	G971	A908	G846	C750	U649	G586	A526	C466	U396	C331	A209	A147	G75
U1161	U1101	G1037	A972	G909	A847	G751	A650	U587	C527	C467	G397	G332	U210	U148	U76
G1162	C1102	U1038	C973	G910	U848	G752	U651	U588	A528	A468	A398	G333	G211	A149	A77
C1103	C1103	C1039	C974	A849	A849	C753	U652	G589	A529	A469	C399	G334	C212	A150	C78
G1104	C1104	C975	C975	C850	C850	C754	A653	A590	U530	C470			C213	C151	A79
G1105	G1105	G1041	G976	A913	C851	C755	A654	U591	A531	C471	C402	G338	U214	U152	G80
G1106	C1106	A1042	C977	U914	G852	G756	A655	C592	C532	C472	G403	A339	G215	G153	U81
G1107	G1107	G1043	G978	G915	C853	G757	G656	C593	A533	A473	G404	C340	C216	U154	G82
G1169	C1108	U1044	C979	A916	A854	G758	U657	U594	G534	C474		C341	A217	G155	A83
A1170	G1109	U1045	A980	U917	G855		U658	U595	G535	C475	G407	C342	U218	G156	A84
G1171	U1110	U1046	U981	U918	C856	C791	G659	U596	A536	A476	G408	A343	U219	U157	A85
U1172	G1111	C1047	G982	A919	U857	C792	C660		A537	C477	C409	U344	U220	A158	C86
A1173	U1112	G1048	A983	A920	A858	C793	U661	G600	U538	C478		U345	A221	U159	U87
U1174	A1113	A1049	C984	G921	C859	A794	G662	G601	C539	C479	A414	C346	U222	U160	C88
G1175	U1114	A1050	G985	A922	G860	A795		G602	U540	C480	A415	G347	C223	U161	C89
G1176	U1115	G1051	G986	G923	A861	G796	U666	C603	U541	C481	A416	A348	A224	G90	
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U1178	C1117	C1053	C988	G925	U863	G798	A668	C543	C543	C483	A418	C350		A164	
	C1118	G1054	C989	A926	A864	U799	A669	G506	G544	A484	G419	C351	G289	G165	U93
	A1119	A1055	A990	C927		U800	A670	U607	A545	A485	C420	U352	U290	G166	G94
	U1120	U1056	G991	G928	G867	U801	A671	C608	G546	A486	G421	U353	G291	G167	G95
	G1121	C1057	A992	G929	G868	A802	U672	U609	G547	U487		U354	G292	C168	
	A1122	A1058	G993	C930	A869	C803	G673	G610	C548	U488	A426	G355	C293	U169	U97
G1187	C1123	G1059		C931	A870	U804	C674	G611	C549	A489	U427	C356	U294	A170	C98
A1188	C1124	A1060	A996	G932	U871	U806	U675	U612	C550	C490	U428		C295	A171	
A1189	C1125	U1061	A997	G933	A872	U807	G676	G613	U551	C491	C429	U359	U296	U172	
G1190	G1126	A1062	A998	G934	G873	G807	G677	G614	G552	C492	C430	A360	A297	A173	
C1191	C1127	C1063	G999	G935	G874	A808	U678	U615	U553	A493	G431	U361	G298	C174	
U1192	C1128	C1064	C1000	G936	A875	A809	A679	A616	A554	C494	G432	C362	A299	A175	C106
U1193	G1129	G1065	A1001	C937	C876	A810	G680	G617	A555	U495	A433	A363	U300	U176	A107
A1194	G1130	U1066	U1002		G877	A811	U681	U618	U556	C496	G434	A364	A301	G177	G108
A1195	G1131	C1067	U1003	U940	G878	A812	U682	A619	U557	C497			A302	C178	U109
	C1132	G1068	U1004	C941	C879	A818	G683	G620	G558	C498	G437	U368	C303	C179	U110
G1198	A1133	U1069	G1005	G942	G880	G819	G684	G621	G559	C499		C369	C304	G180	
A1199	C1134		C1006	U943	G881	U820		C622	A560	A500	G440	G370	U305	A181	G113
A1200	C1135	U1073	C1007	A944	U882	U821	U688	G623	A561	C501	C441	A371	C306	G182	G114
U1201	U1136	C1074	A1008	U945	U883	G821	U689	G624	U562	C502	C442	U372	G307	U115	
U1202	U1137	C1075	U1009	U946	C884	U822	G690	G625	G563	C503	U443	G373	G308	U116	
G1203	C1138	G1076	G1010	G947	U885	U823	G691	G626	A564	G504	G444	G374	G309	G185	G117
A1204	C1139	A1077	A1011	C948		C824	G692	U627	G565	G505	A445	U375	C310	G186	
C1205	G1140	C1078	U1012	G949	U888	A825	A693	A628	U566	G506	G446	A376	C311	G187	C118
G1206	G1141	C1079	U1013	C950	U889	A826	G694	A629	C567	G507	A447	G377	G312	C188	
U1207	C1142	A1080	G1014	C951	U890	A827	C695	U630	C568	A508	U448	U378	G313	U189	G122
A1208	A1143		U1015	C952	G891	G828	G696	U631	A569	G509	A449	C379	U314	U124	
A1209	A1144	A1083	U1016	C953	U892	C829	G697		C570	G510	C450	G380	C315	G125	C126
G1210	A1145	A1084	U1017	U954	U893	A830	G698	A634	U571	U511	G451	C381	G316	C127	
G1211	C1146	C1085	U1018	A955	G894	G831	C730	G635	U572	A512	G452	C382	C317	C196	
G1212	C1147	G1086	G995	G956	C895	G832	G731	C636	U573	G513	C453	G383	A318	U197	G130
C1213	A1148	A1087	A1020	A957	U896	C833	U732	U637	A574	U514	U454	U384	G319	U198	
A1214	A1149	U1088	U1021	G958	U897	C834	C733	C638	A575	G515	A455	G385	C320	G131	
C1215	A1150	G1089	G959	G959	U898	C835	C734	C639	A576	A516	C456	C386	C321	U199	
C1216	G1151		A1023	G960	U899	C836	C735	A640	U577	C517	C457	C387	C322	G200	C138
A1217	U1152	G1092	A1024	G961	C900	A837	C736	A641	C578	G518	A458	C388	C323	C201	C139
C1218	C1153	A1093	U1025	A962	G901	C839	G737	U642	C579	A519		A389	C324	G202	C140

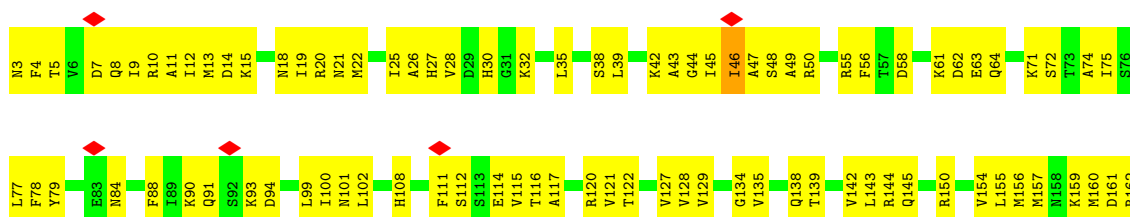


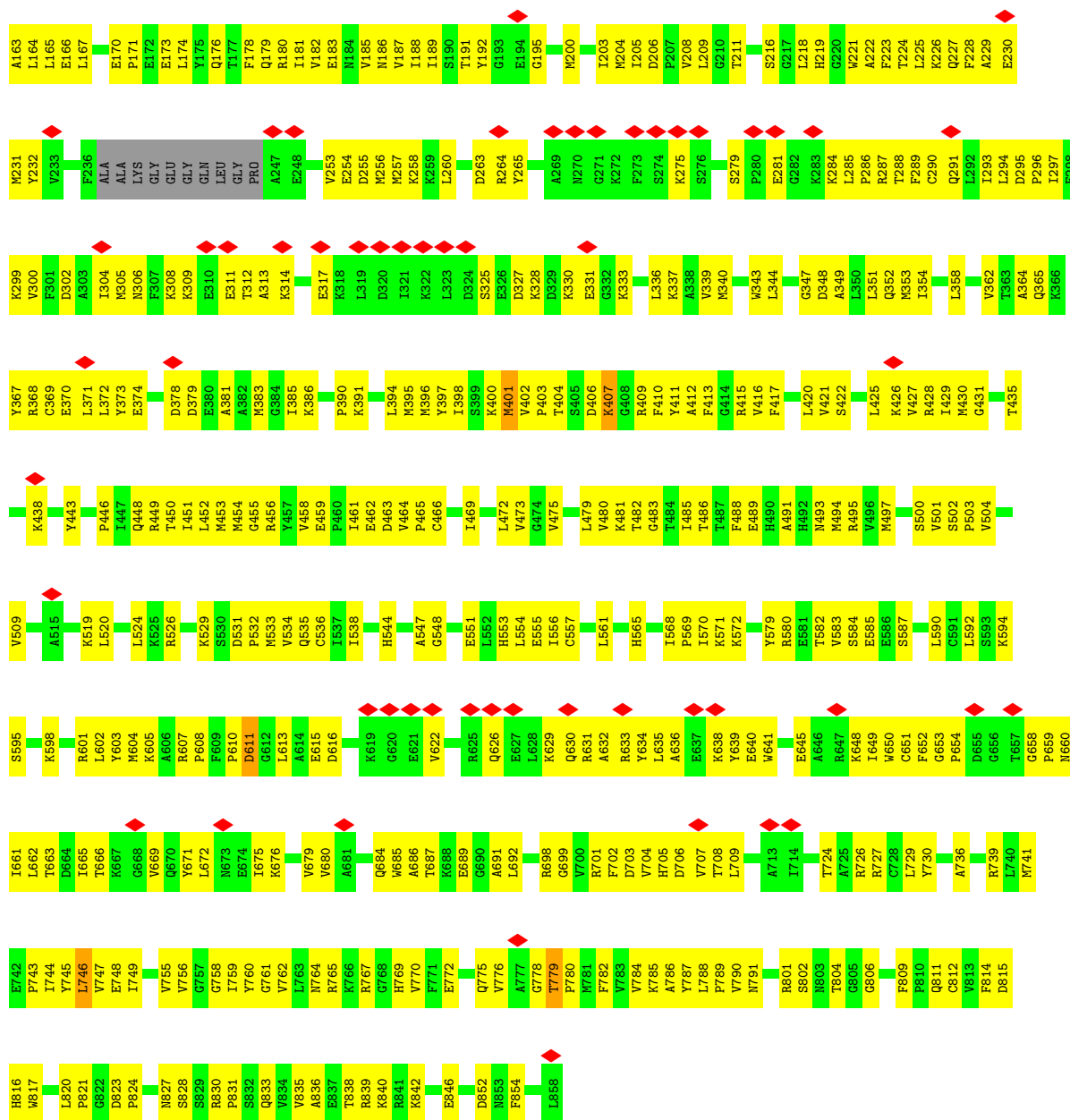




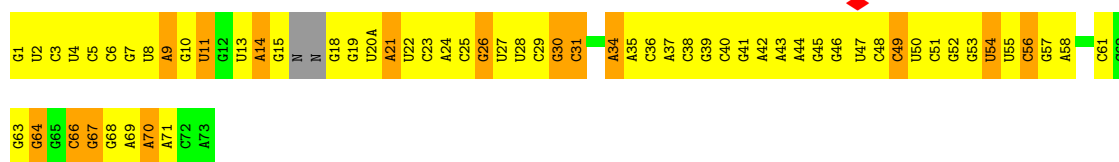
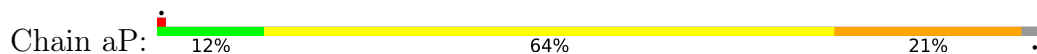


- Molecule 80: Elongation factor 2

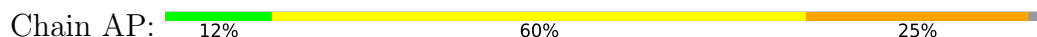


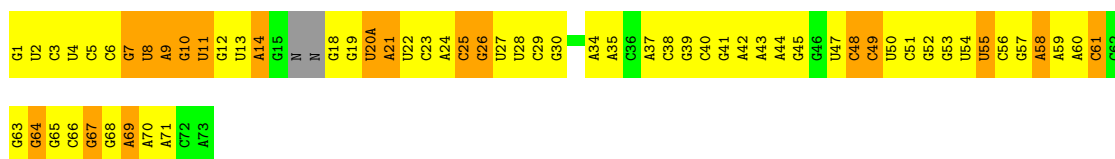


• Molecule 81: A/P site tRNA [Homo sapiens]

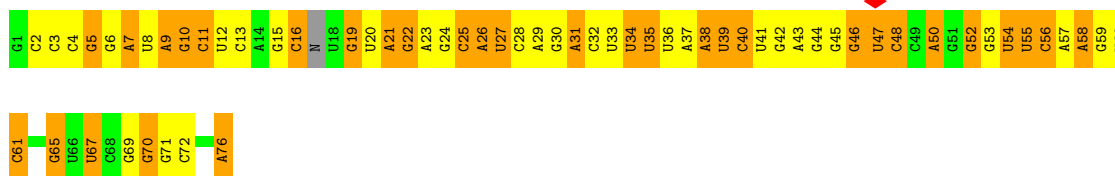
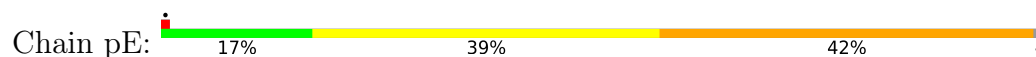


• Molecule 81: A/P site tRNA [Homo sapiens]

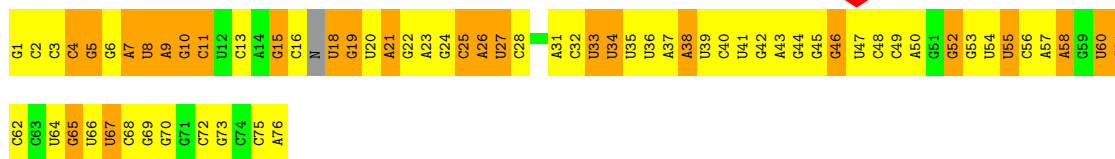
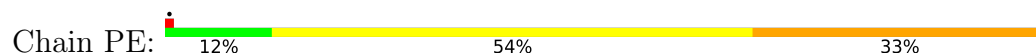




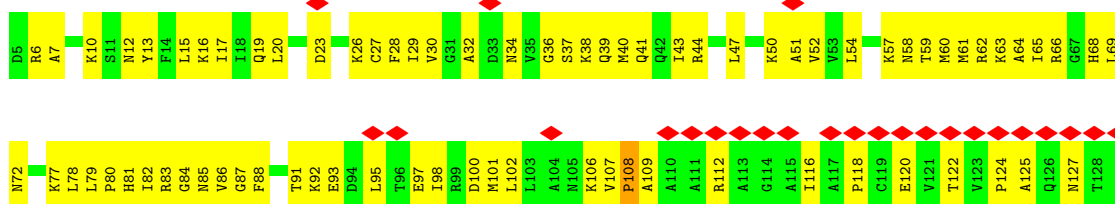
• Molecule 82: P/E site tRNA [Homo sapiens]



• Molecule 82: P/E site tRNA [Homo sapiens]

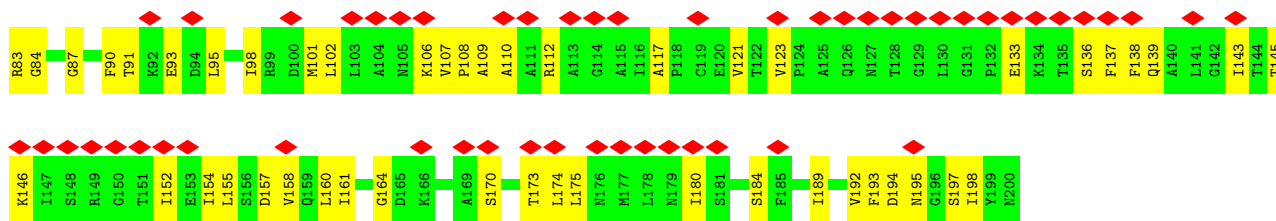


• Molecule 83: 60S acidic ribosomal protein P0

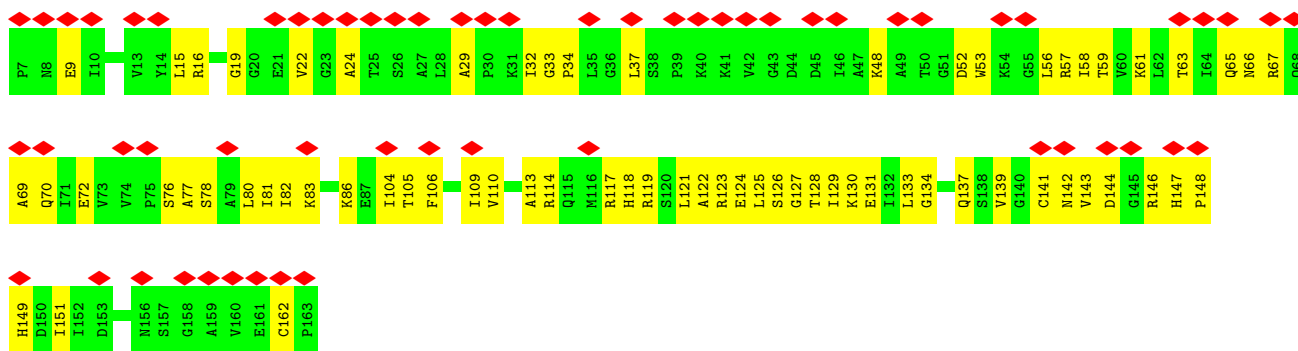
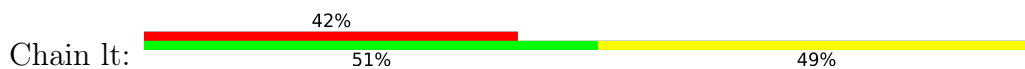


• Molecule 83: 60S acidic ribosomal protein P0

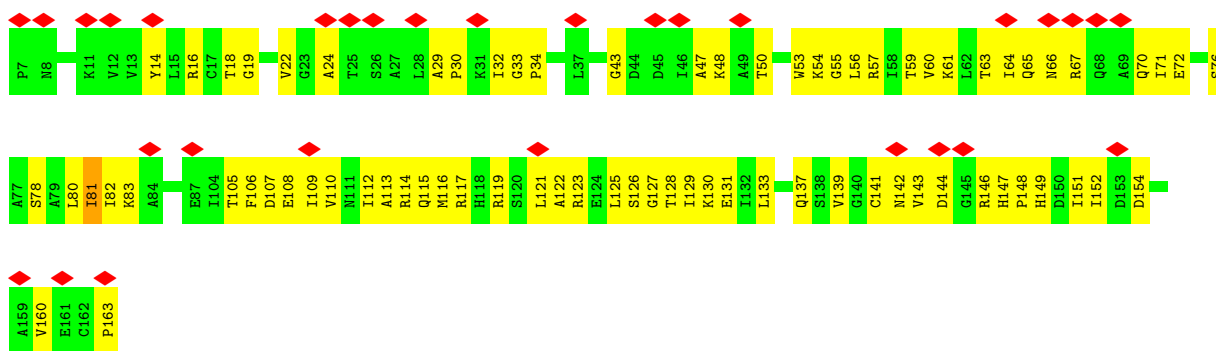




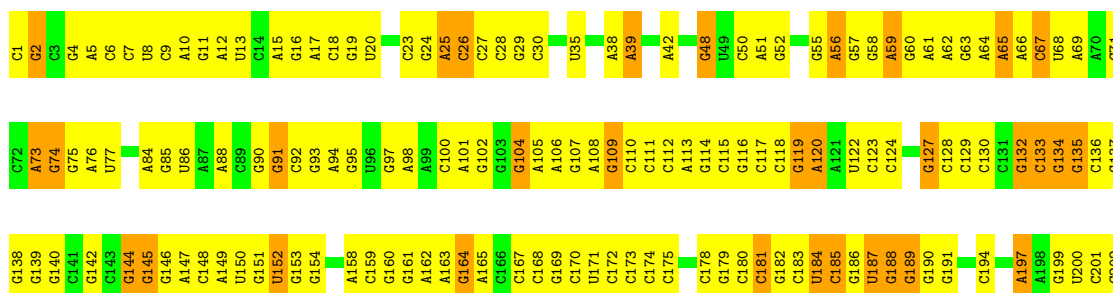
• Molecule 84: 60S ribosomal protein L12 [Homo sapiens]



• Molecule 84: 60S ribosomal protein L12 [Homo sapiens]



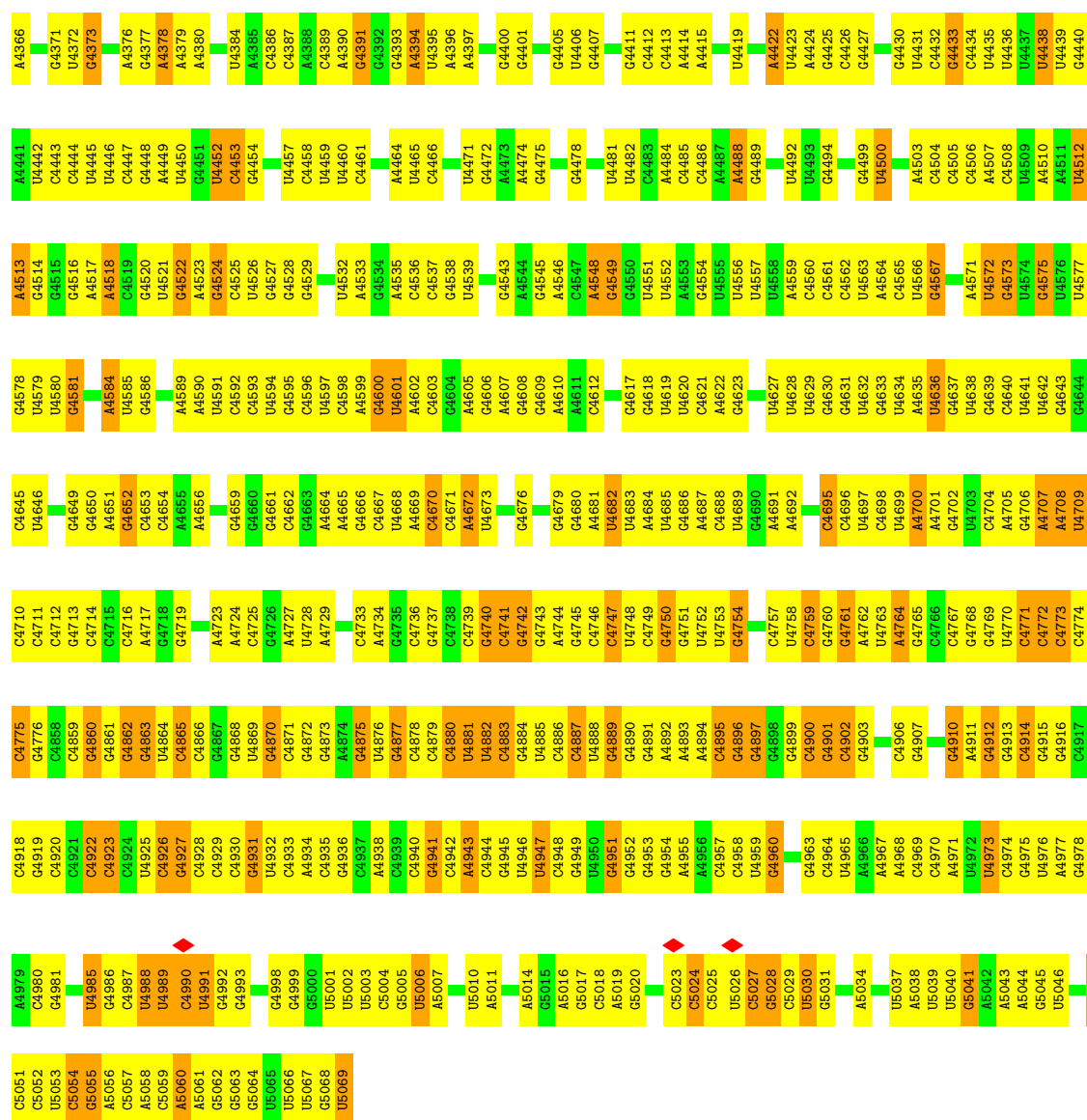
• Molecule 85: 28S rRNA [Homo sapiens]



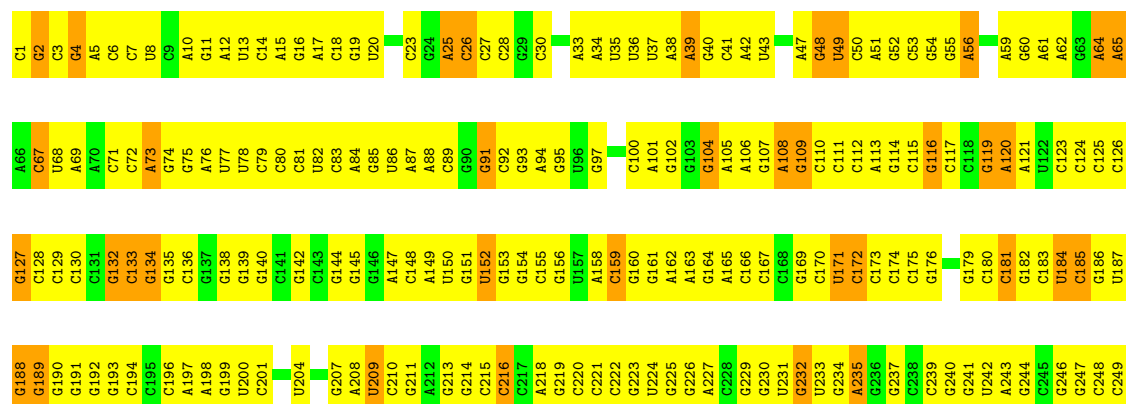
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G1562	G1563	C1480	C1481	C1411	A1345	C1280	C1202	C1076	C946	C737	G670	C486	A420	G342	U273	A209
A1564	A1565	G1482	G1483	C1413	C1346	G1281	C1203	A1077	C947	C738	G671	G488	G423	C343	C274	G210
A1566	A1567	C1484	C1485	C1414	U1348	G1283	C1204	C1079	C948	G740	C672	C489	U424	C344	C275	G211
C1566	C1567	G1486	G1487	C1415	G1349	G1284	G1205	C1080	C949	G741	G674	C490	U425	C345	G276	G212
G1570	G1571	A1490	A1491	C1416	U1285	U1286	C1206	C1081	C950	G742	C675	C491	A426	A347	G277	G213
U1572	U1573	C1488	C1489	C1417	C1350	C1287	C1207	C1082	C951	G743	G676	U492	A427	G348	G278	G214
G1574	G1575	A1492	A1493	C1418	U1351	U1289	U1208	U1083	C952	U750	G677	C493	G428	A349	G280	C216
G1576	G1577	C1490	C1491	C1419	C1352	G1288	C1209	C1084	A956	U751	C678	U494	G431	C350	U281	A217
U1579	U1580	A1494	A1495	A1420	A1354	G1289	G1211	C1085	C957	G752	C679	C495	C282	C351	C282	A218
G1582	G1583	C1496	C1497	C1421	C1355	G1290	G1212	C1086	C958	G753	G680	G496	G432	G352	G219	G220
C1586	C1587	U1498	U1499	C1422	C1356	G1291	G1213	C1087	G959	U754	G681	C498	A434	A353	C221	C221
U1588	U1589	A1500	A1501	C1423	C1357	G1292	C1214	C1088	A960	U755	C685	C499	U435	U356	U286	G222
C1590	C1591	C1430	C1431	C1424	G1358	G1293	C1215	G1089	C961	G758	G686	G500	C436	U357	U287	G223
G1592	G1593	U1432	U1433	C1425	G1359	G1294	C1216	C1090	C962	G759	G687	C501	G437	C358	U288	G224
A1596	A1597	C1434	C1435	C1426	G1360	C1295	G1217	C1091	C963	G760	U688	C502	G438	A359	U290	G225
G1600	G1601	U1436	U1437	C1427	G1361	U1297	G1218	C1092	C964	C903	U689	C503	G439	A360	U291	G226
C1604	C1605	C1438	C1439	C1428	C1362	C1298	G1219	C1093	G965	C904	C690	G504	U440	G364	A295	A227
U1606	U1607	U1440	U1441	C1429	C1363	C1301	G1220	C1094	A966	C905	C691	G505	U441	A296	A296	G229
G1610	G1611	C1442	C1443	C1430	G1364	C1302	G1221	C1095	C967	C906	C692	C506	G442	U297	G297	G230
C1612	C1613	U1444	U1445	C1431	G1365	C1303	G1222	C1096	C968	C907	A692	C507	G443	G368	G298	U231
U1616	U1617	C1446	C1447	C1432	G1366	C1304	G1223	C1097	C969	G908	C693	G508	G444	U370	C299	G232
G1618	G1619	U1448	U1449	C1433	C1367	C1305	G1224	C1098	C970	G909	C694	A509	U445	A371	A300	U233
C1620	C1621	C1450	C1451	C1434	G1368	C1306	G1225	C1099	C971	G910	C695	U510	C446	G372	G301	G234
U1622	U1623	U1452	U1453	C1435	G1369	C1307	G1226	C1100	C972	U911	C696	G509	C447	G373	A235	A235
A1623	A1624	C1454	C1455	C1436	C1370	C1308	G1227	C1101	C973	G912	G700	G510	G448	C302	C302	G236
G1625	G1626	U1456	U1457	C1437	G1371	C1309	G1228	C1102	C974	U913	G701	G511	G449	G303	C303	G237
C1626	C1627	C1458	C1459	C1438	G1372	C1310	G1229	C1103	C975	U914	U702	G512	G450	C304	C304	G238
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G1632	G1633	C1462	C1463	C1440	C1374	C1312	G1231	C1105	C977	G916	G704	G514	C452	A306	A306	G240
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U1637	U1638	U1468	U1469	C1443	C1377	C1315	G1234	C1108	C980	G919	G707	G517	C455	C309	C309	G247
G1639	G1640	C1470	C1471	C1444	G1378	C1316	G1235	C1109	C981	C920	G708	G518	C456	A385	A385	G248
A1641	A1642	U1472	U1473	C1445	C1379	C1317	G1236	C1110	C982	C921	G709	G519	C457	G387	G387	C249
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G1645	G1646	U1476	U1477	C1447	C1381	C1319	G1238	C1112	C984	C923	G711	G521	C459	G315	G315	G251
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U1649	U1650	U1480	U1481	C1449	C1383	C1321	G1240	C1114	C986	C925	G713	G523	C461	A318	A318	G253
G1651	G1652	C1482	C1483	C1450	G1384	C1322	G1241	C1115	C987	C926	G714	G524	C462	A319	A319	G254
C1653	C1654	U1484	U1485	C1451	C1385	C1323	G1242	C1116	C988	G927	G715	G525	C463	C323	C323	G255
U1655	U1656	C1486	C1487	C1452	G1386	C1324	G1243	C1117	C989	C928	G716	G526	C464	A324	A324	G256
G1657	G1658	U1488	U1489	C1453	C1387	C1325	G1244	C1118	C990	C929	G717	G527	C465	U325	U325	G257
C1659	C1660	C1490	C1491	C1454	G1388	C1326	G1245	C1119	C991	C930	G718	G528	C466	C326	C326	G258
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C1673	C1674	U1502	U1503	C1461	C1395	C1333	G1252	C1126	C998	C937	G725	G535	C473	A317	A317	G265
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G1677	G1678	U1506	U1507	C1463	C1397	C1335	G1254	C1128	C1000	C939	G727	G537	C475	A319	A319	G267
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U1681	U1682	U1510	U1511	C1465	C1399	C1337	G1256	C1130	C1002	C941	G729	G539	C477	U317	U317	G269
G1683	G1684	C1512	C1513	C1466	G1400	C1338	G1257	C1131	C1003	C942	G730	G540	C478	A335	A335	C271
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G1689	G1690	U1518	U1519	C1469	C1403	C1341	G1260	C1134	C1006	C945	G733	G543	C481	A338	A338	G272
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U1705	U1706	U1534	U1535	C1477	C1411	C1349	G1268	C1142	C1014	C953	G741	G551	C489	A405	A405	G280
G1707	G1708	C1536	C1537	C1478	G1412	C1350	G1269	C1143	C1015	C954	G742	G552	C490	A406	A406	G281
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C1715	C1716	C1544	C1545	C1482	G1416	C1354	G1273	C1147	C1019	C958	G746	G556	C494	A410	A410	G285
U1717	U1718	U1546	U1547	C1483	C1417	C1355	G1274	C1148	C1020	C959	G747	G557	C495	A411	A411	G286
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G1731	G1732	C1560	C1561	C1490	G1424	C1362	G1281	C1155	C1027	C966	G754	G564	C502	A418	A418	G293
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G2673	G2674	G2601	U2460	G2461	A2388	C2319	G2251	U2054	U1986	C1920	A1843	A1776	C1715	
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G2758	G2759	A2521	A2522	U2516	U2445	G2365	G2295	G2102	C2037					

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C2804	C2804	U2874	A3611	G3755	G3819	G3887	A3955	G4046	G4093	A4176	G4239	U4238	U4318	U4363	U4239	U4377	U4378
		G2876	U3688	A3756	G3820	A3888	G3956	G4047	G4094	A4177	G4240	U4239	U4319	U4364	U4240	U4378	U4379
		G2877	G3614	U3758	G3823	U3889	U3957	U4048	G4095	A4178	G4241	U4240	U4320	U4365	U4241	U4379	U4380
		G2878	G3615	A3759	A3824	C3892	U3958	U4049	G4096	A4179	U4242	U4241	U4321	U4366	U4242	U4380	U4381
		G2879	G3616	A3760	A3825	G3893	U3959	U4050	G4097	A4180	U4323	U4242	U4322	U4367	U4243	U4381	U4382
		U2880	U3617	A3761	G3826	G3894	A3960	C4051	G4098	U4181	G4244	U4243	U4323	U4368	U4244	U4382	U4383
		A2881	U3619	U3762	G3827	C3895	A3961	C4052	G4099	G4182	G4245	U4244	U4324	U4369	U4245	U4383	U4384
		G3619	U3695	U3763	A3828	G3897	A3962	U4053	G4100	G4183	A4250	U4245	U4325	U4370	U4246	U4384	U4385
		A3624	C3896	U3764	G3829	G3898	A3963	U4054	U4112	G4184	C4252	U4246	U4326	U4371	U4247	U4385	U4386
		G3625	U3697	G3765	A3830	G3899	U3964	U4055	U4113	G4185	A4253	U4247	U4327	U4372	U4248	U4386	U4387
		U3626	U3698	A3766	U3831	G3900	U3965	C4056	U4114	A4186	C4254	U4248	U4328	U4373	U4249	U4387	U4388
		U2886	G3626	C3767	U3832	A3901	A3966	U4058	U4115	A4187	A4255	U4249	U4329	U4374	U4250	U4388	U4389
			A3630	C3700	C3833	A3899	G3967	U4059	U4116	U4188	A4256	U4250	U4330	U4375	U4251	U4389	U4390
			U2889	G3701	C3834	A3902	U3968	U4060	U4117	U4189	A4257	U4251	U4331	U4376	U4252	U4390	U4391
			C2890	A3702	C3835	A3906	U3969	G4061	U4118	U4190	C4258	U4252	U4332	U4377	U4253	U4391	U4392
			U2891	G3703	A3836	G3907	G3970	U4062	U4119	G4191	C4259	U4253	U4333	U4378	U4254	U4392	U4393
			G3633	U3704	C3837	A3908	C3937	U4063	U4120	A4192	U4260	U4254	U4334	U4379	U4255	U4393	U4394
			A3634	G3705	U3838	C3909	U3839	C4064	U4121	G4193	C4261	U4255	U4335	U4380	U4256	U4394	U4395
			A3635	U3706	G3839	C3910	U3840	U4065	U4122	U4194	C4262	U4256	U4336	U4381	U4257	U4395	U4396
			U3637	C3707	U3841	C3911	G3973	G	U4123	U4195	C4263	U4257	U4337	U4382	U4258	U4396	U4397
				U3708	C3842	U3912	G	C	U4124	G4196	G4264	U4258	U4338	U4383	U4259	U4397	U4398
			U3641	C3709	C3843	U3915	C	C	A4127	U4197	U4265	U4259	U4339	U4384	U4260	U4398	U4399
			A3642	G3710	U3844	G3916	C	C	U4128	G4198	U4266	U4260	U4340	U4385	U4261	U4399	U4400
			A3643	A3711	U3845	A3917	C	C	U4129	U4068	U4267	U4261	U4130	U4386	U4262	U4400	U4401
			U3644	A3712	U3846	G3918	C	C	U4130	U4069	U4268	U4262	U4131	U4387	U4263	U4401	U4402
			A2632	U2901	A3645	C3919	G	C	U4131	U4070	U4269	U4263	U4132	U4388	U4264	U4402	U4403
			C2833	G2902	A3646	U3920	C	C	U4132	U4071	U4270	U4264	U4133	U4389	U4265	U4403	U4404
			A2835	C2903	A3647	U3921	G	C	U4133	U4072	U4271	U4265	U4134	U4390	U4266	U4404	U4405
			U2904	U2904	A3648	U3922	C	C	U4134	U4073	U4272	U4266	U4135	U4391	U4267	U4405	U4406
			C2905	C2905	A3649	G3923	C	C	U4135	U4074	U4273	U4267	U4136	U4392	U4268	U4406	U4407
			U2906	C2906	A3650	A3923	C	C	U4136	U4075	U4274	U4268	U4137	U4393	U4269	U4407	U4408
			G2838	G2907	A3651	C3924	G	C	U4137	U4076	U4275	U4269	U4138	U4394	U4270	U4408	U4409
			A2640	U2908	A3652	U3925	G	C	U4138	U4077	U4276	U4270	U4139	U4395	U4271	U4409	U4410
			U2908	U2908	A3653	C3926	U	C	U4139	U4078	U4277	U4271	U4140	U4396	U4272	U4410	U4411
			C2909	U2909	A3654	U3927	C	C	U4140	U4079	U4278	U4272	U4141	U4397	U4273	U4411	U4412
			U2910	C2910	G3654	A3928	C	C	U4141	U4080	U4279	U4273	U4142	U4398	U4274	U4412	U4413
			U2911	U2911	A3655	G3929	C	C	U4142	U4081	U4280	U4274	U4143	U4399	U4275	U4413	U4414
			G3585	C2912	A3656	G	C	C	U4143	U4082	U4281	U4275	U4144	U4400	U4276	U4414	U4415
			U3657	A3726	A3726		C	C	U4144	U4083	U4282	U4276	U4145	U4401	U4277	U4415	U4416
							C	C	U4145	U4084	U4283	U4277	U4146	U4402	U4278	U4416	U4417
							C	C	U4146	U4085	U4284	U4278	U4147	U4403	U4279	U4417	U4418
							C	C	U4147	U4086	U4285	U4279	U4148	U4404	U4280	U4418	U4419
							C	C	U4148	U4087	U4286	U4280	U4149	U4405	U4281	U4419	U4420
							C	C	U4149	U4088	U4287	U4281	U4150	U4406	U4282	U4420	U4421
							C	C	U4150	U4089	U4288	U4282	U4151	U4407	U4283	U4421	U4422
							C	C	U4151	U4090	U4289	U4283	U4152	U4408	U4284	U4422	U4423
							C	C	U4152	U4091	U4290	U4284	U4153	U4409	U4285	U4423	U4424
							C	C	U4153	U4092	U4291	U4285	U4154	U4410	U4286	U4424	U4425
							C	C	U4154	U4093	U4292	U4286	U4155	U4411	U4287	U4425	U4426
							C	C	U4155	U4094	U4293	U4287	U4156	U4412	U4288	U4426	U4427
							C	C	U4156	U4095	U4294	U4288	U4157	U4413	U4289	U4427	U4428
							C	C	U4157	U4096	U4295	U4289	U4158	U4414	U4290	U4428	U4429
							C	C	U4158	U4097	U4296	U4290	U4159	U4415	U4291	U4429	U4430
							C	C	U4159	U4098	U4297	U4291	U4160	U4416	U4292	U4430	U4431
							C	C	U4160	U4099	U4298	U4292	U4161	U4417	U4293	U4431	U4432
							C	C	U4161	U4100	U4299	U4293	U4162	U4418	U4294	U4432	U4433
							C	C	U4162	U4101	U4300	U4294	U4163	U4419	U4295	U4433	U4434
							C	C	U4163	U4102	U4301	U4295	U4164	U4420	U4296	U4434	U4435



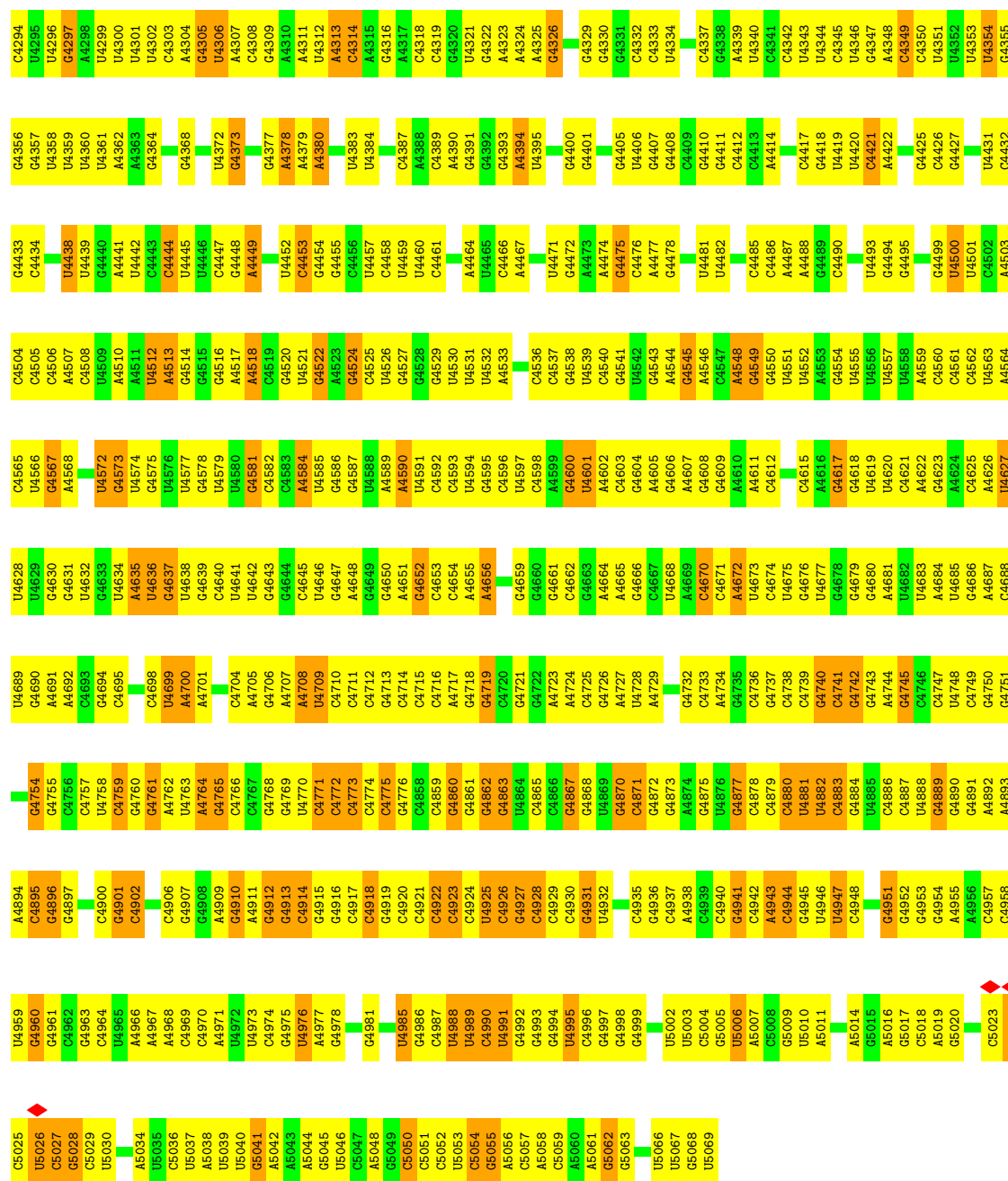
• Molecule 85: 28S rRNA [Homo sapiens]



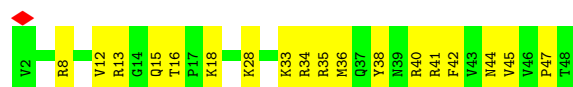


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G2541	G2542	G2543	G2544	G2545	G2546	G2547		G2552	G2553	G2554	G2555	G2556	G2557	G2558	G2559	G2560	G2561	G2562	G2563	G2564	G2565		G2568	G2569	G2570	G2571	G2572	G2573	G2574	G2575	G2576	G2577	G2578	G2579	G2580	G2581	G2582	G2583	G2584	G2585	G2586	G2587	G2588	G2589	G2590	G2591		G2594	G2595	G2596	G2597	G2598	G2599	G2600	G2601	G2602	G2603	G2604	G2605	G2606	G2607	G2608												
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A2341	A2342	A2343	A2344	A2345	A2346	A2347	A2348	A2349	A2350	A2351	A2352	A2353	A2354	G2358	G2359	A2360	G2361	A2362		A2367	A2368	A2369	G2372	G2373	G2374	G2375	G2376	G2377	G2378	G2379	G2380	A2381	A2382	G2383	G2384	G2385	G2386	G2387	G2388	A2389		G2392	G2393	G2394	A2395	G2396	G2397	G2398	G2399	G2400	A2401	G2402	G2403	A2404	G2405	G2406																		
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U1954	U1955	A1956	U1957		A1958	U1959		G1961	A1962		A1967		G1968	G1969		G1972	U1973	U1974	G1975	G1976	G1977	G1978	G1979	U1980	G1981	G1982	A1983	U1984	G1985	U1986		G1989	A1990	G1991	U1992	G1993	G1994	G1995	G1996		A1998	G1999	G2000	G2001	A2002	G2003	U2004	G2005	U2006	G2007		A2009	G2010	A2011	A2012	A2013	G2014		A2017	G2018	G2019													
U2020	G2021	G2022	G2023	G2024	A2025	G2026	U2027	G2028	U2029	A2030	G2031	U2032	A2033	G2034	G2035	G2036	G2037	U2038	G2039	A2040	A2041		U2044	G2045	G2046	U2047	U2048	G2049	G2050	G2051	U2054	G2055	G2056	G2057	G2058	G2059	G2060	U2061	G2062	G2063	G2064	G2065	G2066	G2067	G2068	A2069		G2072	G2073	G2074	G2075	G2076	G2077	G2078	G2079	U2080	G2081																	
G1818	G1819	G1820	G1821	G1822	G1823	G1824	G1825	G1826		G1831		G1832	G1833	G1834	G1835	G1836	A1837	G1838	G1839	G1840	G1841	G1842		A1843	G1844	U1845	G1846	G1847	G1848	U1849		G1852	G1853	G1854	G1855	G1856	G1857	A1858		U1862	G1863	G1864	G1865	G1866	A1867	G1868	G1869	G1870	A1871	G1872	G1873	G1874	G1875	U1876	G1877	G1878	G1879	G1880	G1881	G1882	G1883	G1884	G1885	G1886	G1887									
A1682	A1683	A1684	A1685	G1686		U1687	G1688	G1689	G1690	G1691		G1692	A1693		A1697	G1698	G1699	A1700	G1701	G1702	G1703	G1704	G1705	A1706	G1707	G1708	G1709	G1710	G1711	G1712	G1713	G1714	G1715	A1716	A1717	G1718	G1719	G1720	G1721	G1722	A1723	G1724	U1725	G1726	U1727	U1728		A1729	G1730	G1731	G1732	G1733	G1734	U1735	G1736	A1737	G1738	G1739	G1740	G1741	A1742		G1745	U1746	A1747	G1748	G1749	G1750	G1751	A1752	G1753			
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- Molecule 86: Small ribosomal subunit protein eS30

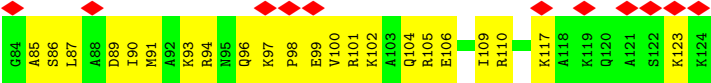


- Molecule 87: Ribosomal protein L24





• Molecule 87: Ribosomal protein L24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45867	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.580	Depositor
Minimum map value	-0.081	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.096	Depositor
Map size ($\text{\AA}$)	640.8, 640.8, 640.8	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.068, 1.068, 1.068	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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	CH	0.29	0/977	0.58	0/1306
1	cH	0.29	0/977	0.67	0/1306
2	SE	0.25	0/2118	0.46	2/2849 (0.1%)
2	sE	0.33	0/2118	0.58	3/2849 (0.1%)
3	SI	0.20	0/1715	0.43	0/2287
3	sI	0.22	0/1715	0.42	0/2287
4	SL	0.22	0/1268	0.44	0/1696
4	sL	0.37	0/1268	0.59	1/1696 (0.1%)
5	SX	0.23	0/1116	0.43	0/1490
5	sX	0.32	0/1116	0.54	1/1490 (0.1%)
6	SG	0.19	0/1946	0.42	0/2590
6	sG	0.25	0/1946	0.50	2/2590 (0.1%)
7	SJ	0.20	0/1550	0.46	0/2069
7	sJ	0.22	0/1550	0.45	0/2069
8	SY	0.20	0/1083	0.42	0/1438
8	sY	0.26	0/1083	0.49	0/1438
9	se	0.23	0/465	0.54	0/612
10	SA	0.25	0/1778	0.51	0/2416
10	sA	0.48	1/1778 (0.1%)	0.78	5/2416 (0.2%)
11	SB	0.22	0/1765	0.49	1/2362 (0.0%)
11	sB	0.39	0/1765	0.55	0/2362
12	SH	0.22	0/1519	0.50	1/2033 (0.0%)
12	sH	0.23	0/1519	0.52	0/2033
13	SV	0.23	0/643	0.50	0/860
13	sV	0.43	0/643	0.70	1/860 (0.1%)
14	Sa	0.35	1/836 (0.1%)	0.71	3/1121 (0.3%)
14	sa	0.34	0/836	0.56	1/1121 (0.1%)
15	SC	0.30	0/1762	0.55	0/2381
15	sC	0.30	0/1762	0.57	0/2381
16	SN	0.23	0/1232	0.45	0/1656
16	sN	0.31	0/1232	0.52	0/1656
17	SO	0.23	0/1062	0.59	2/1425 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	sO	0.27	0/1062	0.63	2/1425 (0.1%)
18	SW	0.28	0/1051	0.54	1/1406 (0.1%)
18	sW	0.31	0/1051	0.55	0/1406
19	Sb	0.23	0/665	0.50	0/891
19	sb	0.55	2/665 (0.3%)	0.88	3/891 (0.3%)
20	L7	0.19	0/2861	0.26	0/4459
20	l7	0.26	0/2861	0.30	0/4459
21	L8	0.19	0/3701	0.29	0/5766
21	l8	0.25	0/3701	0.30	0/5766
22	LA	0.29	0/1936	0.56	2/2596 (0.1%)
22	lA	0.33	0/1936	0.50	0/2596
23	LB	0.22	0/3306	0.43	0/4424
23	lB	0.28	0/3306	0.50	1/4424 (0.0%)
24	LC	0.40	3/2981 (0.1%)	0.59	4/4002 (0.1%)
24	lC	0.28	0/2981	0.50	2/4002 (0.0%)
25	LD	0.26	0/2428	0.52	2/3252 (0.1%)
25	lD	0.27	0/2428	0.48	0/3252
26	LE	0.18	0/1942	0.42	0/2606
26	lE	0.30	0/1942	0.50	1/2606 (0.0%)
27	LF	0.24	0/1905	0.43	0/2539
27	lF	0.29	0/1905	0.50	0/2539
28	LG	0.20	0/1960	0.44	0/2637
28	lG	0.28	0/1960	0.48	1/2637 (0.0%)
29	LH	0.19	0/1537	0.43	0/2066
29	lH	0.31	0/1537	0.52	0/2066
30	LI	0.25	0/1673	0.48	0/2233
30	lI	0.27	0/1673	0.48	0/2233
31	LJ	0.23	0/1433	0.54	0/1915
31	lJ	0.32	0/1433	0.59	0/1915
32	LL	0.20	0/1732	0.42	0/2315
32	lL	0.26	0/1732	0.46	0/2315
33	LM	0.25	0/1161	0.51	0/1554
33	lM	0.39	1/1161 (0.1%)	0.66	1/1554 (0.1%)
34	LN	0.22	0/1746	0.42	0/2338
34	lN	0.32	0/1746	0.48	0/2338
35	LO	0.23	0/1682	0.46	0/2250
35	lO	0.34	0/1682	0.54	0/2250
36	LP	0.22	0/1268	0.41	0/1701
36	lP	0.33	0/1268	0.50	0/1701
37	LQ	0.25	0/1537	0.48	0/2052
37	lQ	0.29	0/1537	0.45	0/2052
38	LR	0.20	0/1582	0.41	0/2091
38	lR	0.28	0/1582	0.47	0/2091

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	LS	0.21	0/1493	0.41	0/2003
39	IS	0.30	0/1493	0.50	0/2003
40	LT	0.26	0/1326	0.52	0/1770
40	IT	0.30	0/1326	0.58	1/1770 (0.1%)
41	LU	0.23	0/839	0.55	0/1126
41	IU	0.29	0/839	0.55	0/1126
42	LV	0.20	0/993	0.37	0/1332
42	IV	0.30	0/993	0.50	0/1332
43	LX	0.24	0/1002	0.48	0/1345
43	IX	0.29	0/1002	0.47	0/1345
44	LY	0.20	0/1132	0.41	0/1504
44	IY	0.24	0/1132	0.41	0/1504
45	LZ	0.21	0/1130	0.44	0/1507
45	IZ	0.35	0/1130	0.68	2/1507 (0.1%)
46	La	0.25	0/1191	0.47	0/1591
46	la	0.30	0/1191	0.49	1/1591 (0.1%)
47	Lb	0.25	0/889	0.56	0/1175
47	lb	0.31	0/889	0.55	0/1175
48	Lc	0.24	0/774	0.58	0/1038
48	lc	0.31	0/774	0.56	0/1038
49	Ld	0.21	0/903	0.44	0/1216
49	ld	0.28	0/903	0.46	0/1216
50	Le	0.26	0/1071	0.51	1/1429 (0.1%)
50	le	0.31	0/1071	0.48	1/1429 (0.1%)
51	Lf	0.18	0/895	0.40	0/1198
51	lf	0.29	0/895	0.52	0/1198
52	Lg	0.20	0/916	0.38	0/1220
52	lg	0.32	0/916	0.55	0/1220
53	Lh	0.26	0/1023	0.50	0/1351
53	lh	0.29	0/1023	0.47	0/1351
54	Li	0.41	0/843	0.73	2/1115 (0.2%)
54	li	0.26	0/843	0.51	0/1115
55	Lj	0.27	0/720	0.57	2/952 (0.2%)
55	lj	0.34	0/720	0.60	2/952 (0.2%)
56	Lk	0.23	0/575	0.49	0/761
56	lk	0.27	0/575	0.51	0/761
57	Ll	0.18	0/454	0.40	0/599
57	ll	0.32	0/454	0.60	2/599 (0.3%)
58	Lm	0.21	0/435	0.47	0/575
58	lm	0.25	0/435	0.47	0/575
59	Ln	0.23	0/231	0.55	0/294
59	ln	0.28	0/231	0.58	0/294
60	Lo	0.19	0/876	0.45	0/1156

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
60	lo	0.29	0/876	0.57	2/1156 (0.2%)
61	Lp	0.23	0/718	0.47	0/953
61	lp	0.33	0/718	0.52	1/953 (0.1%)
62	Lr	0.26	0/1017	0.50	0/1364
62	lr	0.41	0/1017	0.58	0/1364
63	Lz	0.18	0/1769	0.49	0/2371
63	lz	0.18	0/1769	0.49	0/2371
64	SR	0.32	0/1105	0.65	2/1484 (0.1%)
64	sR	0.71	2/1105 (0.2%)	1.15	6/1484 (0.4%)
65	SD	0.24	0/1793	0.46	0/2414
65	sD	0.81	5/1793 (0.3%)	0.96	6/2414 (0.2%)
66	SF	0.25	0/1516	0.56	2/2037 (0.1%)
66	sF	0.34	0/1516	0.59	3/2037 (0.1%)
67	SK	0.29	0/851	0.66	0/1147
67	sK	0.32	0/851	0.66	0/1147
68	SP	0.23	0/1003	0.53	0/1342
68	sP	0.28	0/1003	0.62	0/1342
69	SQ	0.28	1/1160 (0.1%)	0.64	2/1553 (0.1%)
69	sQ	0.32	0/1160	0.63	1/1553 (0.1%)
70	SS	0.24	0/1216	0.54	2/1628 (0.1%)
70	sS	0.28	0/1216	0.58	1/1628 (0.1%)
71	ST	0.26	0/1131	0.55	0/1515
71	sT	0.32	0/1131	0.59	1/1515 (0.1%)
72	SU	0.23	0/831	0.50	0/1115
72	sU	0.32	0/831	0.55	1/1115 (0.1%)
73	Sc	0.20	0/508	0.51	0/680
73	sc	0.32	0/508	0.62	0/680
74	Sd	0.21	0/470	0.51	0/623
74	sd	0.27	0/470	0.46	0/623
75	Sg	0.43	3/2493 (0.1%)	0.81	5/3394 (0.1%)
75	sg	0.26	0/2493	0.53	0/3394
76	SM	0.25	0/950	0.53	0/1275
76	sM	0.30	0/950	0.67	2/1275 (0.2%)
77	SZ	0.30	0/604	0.73	1/810 (0.1%)
77	sZ	0.34	0/604	0.69	1/810 (0.1%)
78	Sf	0.17	0/560	0.46	0/745
78	sf	0.21	0/560	0.52	0/745
79	S2	0.19	0/41243	0.30	1/64259 (0.0%)
79	s2	0.24	0/41241	0.34	0/64251
80	CB	0.25	0/6734	0.49	2/9094 (0.0%)
80	cB	0.59	6/6734 (0.1%)	0.74	13/9094 (0.1%)
81	AP	0.14	0/1692	0.26	0/2634
81	aP	0.17	0/1692	0.29	0/2634

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
82	PE	0.17	0/1778	0.36	0/2767
82	pE	0.21	0/1778	0.38	0/2767
83	Ls	0.19	0/1519	0.47	1/2052 (0.0%)
83	ls	0.28	0/1519	0.63	3/2052 (0.1%)
84	Lt	0.23	0/1058	0.57	0/1430
84	lt	0.20	0/1058	0.53	0/1430
85	L5	0.31	18/88929 (0.0%)	0.35	32/138727 (0.0%)
85	l5	0.25	0/88929	0.33	0/138727
86	Se	0.19	0/382	0.43	0/504
87	LW	0.19	0/979	0.39	0/1295
87	IW	0.27	0/979	0.46	0/1295
All	All	0.28	43/492435 (0.0%)	0.43	148/721182 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	cH	0	1
5	SX	0	1
5	sX	0	1
12	SH	0	1
12	sH	0	1
22	lA	0	1
23	LB	0	2
23	lB	0	2
31	LJ	0	1
33	LM	0	2
33	lM	0	2
35	LO	0	1
35	lO	0	1
46	la	0	1
51	Lf	0	1
51	lf	0	1
55	Lj	0	1
55	lj	0	1
64	sR	0	4
66	SF	0	1
68	sP	0	1
69	SQ	0	1
69	sQ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
71	ST	0	1
71	sT	0	1
All	All	0	32

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	L5	4105	A	C1'-N9	33.51	1.98	1.48
80	cB	849	PRO	CG-CD	-31.82	0.42	1.50
85	L5	4102	C	N1-C2	23.76	1.87	1.40
85	L5	4102	C	N3-C4	23.13	1.80	1.33
85	L5	4102	C	C2-N3	23.11	1.81	1.35

The worst 5 of 148 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	cB	831	PRO	CB-CG-CD	-33.15	0.03	106.10
85	L5	4105	A	C8-N9-C4	-22.64	37.87	105.80
75	Sg	163	PRO	N-CD-CG	-22.52	69.42	103.20
64	sR	134	PRO	N-CD-CG	-20.29	72.76	103.20
65	sD	213	PRO	CB-CG-CD	-19.43	43.92	106.10

There are no chirality outliers.

5 of 32 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	cH	51	GLN	Peptide
22	lA	13	GLY	Peptide
23	lB	17	LEU	Peptide
12	sH	15	LYS	Peptide
5	sX	126	ALA	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CH	968	0	1013	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	cH	968	0	1013	109	0
2	SE	2076	0	2177	162	0
2	sE	2076	0	2177	149	0
3	SI	1686	0	1772	116	0
3	sI	1686	0	1772	106	0
4	SL	1247	0	1323	97	0
4	sL	1247	0	1323	114	0
5	SX	1098	0	1167	80	0
5	sX	1098	0	1167	82	0
6	SG	1923	0	2089	159	0
6	sG	1923	0	2089	199	0
7	SJ	1525	0	1640	120	0
7	sJ	1525	0	1640	108	0
8	SY	1065	0	1142	92	0
8	sY	1065	0	1142	101	0
9	se	459	0	503	64	0
10	SA	1741	0	1746	161	0
10	sA	1741	0	1746	190	0
11	SB	1738	0	1809	149	0
11	sB	1738	0	1809	157	0
12	SH	1497	0	1590	132	0
12	sH	1497	0	1590	114	0
13	SV	636	0	637	60	0
13	sV	636	0	637	85	0
14	Sa	821	0	870	90	0
14	sa	821	0	870	65	0
15	SC	1725	0	1813	130	0
15	sC	1725	0	1813	152	0
16	SN	1208	0	1294	78	0
16	sN	1208	0	1294	88	0
17	SO	1049	0	1073	94	0
17	sO	1049	0	1073	94	0
18	SW	1034	0	1080	98	0
18	sW	1034	0	1080	102	0
19	Sb	651	0	672	40	0
19	sb	651	0	672	67	0
20	L7	2561	0	1295	89	0
20	l7	2561	0	1294	99	0
21	L8	3314	0	1683	149	0
21	l8	3314	0	1682	144	0
22	LA	1898	0	1993	133	0
22	lA	1898	0	1993	134	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	LB	3238	0	3376	169	0
23	lB	3238	0	3376	160	0
24	LC	2927	0	3104	201	0
24	lC	2927	0	3104	156	0
25	LD	2382	0	2410	154	0
25	lD	2382	0	2410	168	0
26	LE	1904	0	2055	127	0
26	lE	1904	0	2055	153	0
27	LF	1870	0	1996	124	0
27	lF	1870	0	1996	149	0
28	LG	1927	0	2074	110	0
28	lG	1927	0	2074	99	0
29	LH	1518	0	1601	85	0
29	lH	1518	0	1601	118	0
30	LI	1634	0	1671	101	0
30	lI	1634	0	1671	79	0
31	LJ	1410	0	1441	97	0
31	lJ	1410	0	1441	96	0
32	LL	1701	0	1818	104	0
32	lL	1701	0	1818	111	0
33	LM	1138	0	1204	95	0
33	lM	1138	0	1204	106	0
34	LN	1701	0	1749	125	0
34	lN	1701	0	1749	143	0
35	LO	1650	0	1794	108	0
35	lO	1650	0	1794	116	0
36	LP	1242	0	1269	74	0
36	lP	1242	0	1269	80	0
37	LQ	1513	0	1628	104	0
37	lQ	1513	0	1628	99	0
38	LR	1566	0	1729	109	0
38	lR	1566	0	1729	86	0
39	LS	1453	0	1490	90	0
39	lS	1453	0	1490	94	0
40	LT	1298	0	1366	98	0
40	lT	1298	0	1366	106	0
41	LU	825	0	850	63	0
41	lU	825	0	850	83	0
42	LV	979	0	1039	39	0
42	lV	979	0	1039	86	0
43	LX	985	0	1066	73	0
43	lX	985	0	1066	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	LY	1115	0	1205	73	0
44	lY	1115	0	1205	66	0
45	LZ	1107	0	1182	82	0
45	lZ	1107	0	1182	79	0
46	La	1162	0	1213	92	0
46	la	1162	0	1213	61	0
47	Lb	876	0	948	56	0
47	lb	876	0	948	65	0
48	Lc	764	0	804	58	0
48	lc	764	0	804	62	0
49	Ld	888	0	930	44	0
49	ld	888	0	930	51	0
50	Le	1053	0	1146	59	0
50	le	1053	0	1147	55	0
51	Lf	876	0	912	55	0
51	lf	876	0	912	53	0
52	Lg	906	0	998	47	0
52	lg	906	0	998	67	0
53	Lh	1015	0	1148	73	0
53	lh	1015	0	1148	78	0
54	Li	832	0	917	81	0
54	li	832	0	917	46	0
55	Lj	705	0	737	72	0
55	lj	705	0	736	67	0
56	Lk	569	0	637	39	0
56	lk	569	0	637	50	0
57	Ll	444	0	483	16	0
57	ll	444	0	483	33	0
58	Lm	429	0	465	25	0
58	lm	429	0	465	31	0
59	Ln	230	0	276	21	0
59	ln	230	0	276	22	0
60	Lo	862	0	929	53	0
60	lo	862	0	930	57	0
61	Lp	708	0	756	51	0
61	lp	708	0	756	51	0
62	Lr	1002	0	1068	84	0
62	lr	1002	0	1068	83	0
63	Lz	1741	0	1854	92	0
63	lz	1741	0	1854	93	0
64	SR	1090	0	1149	91	0
64	sR	1090	0	1149	245	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
65	SD	1765	0	1865	111	0
65	sD	1765	0	1865	131	0
66	SF	1495	0	1549	148	0
66	sF	1495	0	1549	130	0
67	SK	827	0	854	78	0
67	sK	827	0	854	97	0
68	SP	985	0	1031	61	0
68	sP	985	0	1031	79	0
69	SQ	1142	0	1213	83	0
69	sQ	1142	0	1213	122	0
70	SS	1198	0	1261	109	0
70	sS	1198	0	1261	120	0
71	ST	1112	0	1146	116	0
71	sT	1112	0	1146	121	0
72	SU	821	0	883	77	0
72	sU	821	0	883	57	0
73	Sc	506	0	536	57	0
73	sc	506	0	536	64	0
74	Sd	459	0	452	52	0
74	sd	459	0	452	51	0
75	Sg	2436	0	2393	199	0
75	sg	2436	0	2393	214	0
76	SM	940	0	965	81	0
76	sM	940	0	965	89	0
77	SZ	598	0	656	73	0
77	sZ	598	0	656	75	0
78	Sf	548	0	555	36	0
78	sf	548	0	555	32	0
79	S2	36898	0	18603	1606	0
79	s2	36898	0	18603	1960	0
80	CB	6605	0	6679	456	0
80	cB	6605	0	6679	504	0
81	AP	1514	0	770	62	0
81	aP	1514	0	770	66	0
82	PE	1593	0	810	57	0
82	pE	1593	0	810	69	0
83	Ls	1496	0	1540	76	0
83	ls	1496	0	1540	98	0
84	Lt	1046	0	1076	94	0
84	lt	1046	0	1076	66	0
85	L5	79496	0	40159	3416	0
85	l5	79496	0	40159	2938	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	Se	378	0	420	27	0
87	LW	965	0	1029	59	0
87	lW	965	0	1029	81	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
88	lg	1	0	0	0	0
88	lj	1	0	0	0	0
88	lm	1	0	0	0	0
88	lo	1	0	0	0	0
88	lp	1	0	0	0	0
88	sa	1	0	0	0	0
89	L5	213	0	0	0	0
89	L7	3	0	0	0	0
89	L8	5	0	0	0	0
89	LA	1	0	0	0	0
89	LP	1	0	0	0	0
89	LV	1	0	0	0	0
89	Le	1	0	0	0	0
89	Lj	1	0	0	0	0
89	S2	29	0	0	0	0
89	l5	212	0	0	0	0
89	l7	3	0	0	0	0
89	l8	5	0	0	0	0
89	lA	1	0	0	0	0
89	lB	1	0	0	0	0
89	le	2	0	0	0	0
89	lg	1	0	0	0	0
89	lj	1	0	0	0	0
89	s2	29	0	0	0	0
All	All	459641	0	345702	22392	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 28.

The worst 5 of 22392 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:L5:4102:C:C4	85:L5:4102:C:C5	1.83	1.59
85:L5:4102:C:C6	85:L5:4102:C:N1	1.78	1.51
85:L5:4102:C:C2	85:L5:4105:A:N9	1.77	1.50
85:L5:4102:C:C4	85:L5:4102:C:N3	1.80	1.49
85:L5:4102:C:C2	85:L5:4102:C:N3	1.82	1.47

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CH	123/125 (98%)	109 (89%)	12 (10%)	2 (2%)	7	36
1	cH	123/125 (98%)	106 (86%)	16 (13%)	1 (1%)	16	50
2	SE	260/262 (99%)	246 (95%)	14 (5%)	0	100	100
2	sE	260/262 (99%)	243 (94%)	16 (6%)	1 (0%)	30	62
3	SI	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
3	sI	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
4	SL	151/153 (99%)	137 (91%)	14 (9%)	0	100	100
4	sL	151/153 (99%)	136 (90%)	15 (10%)	0	100	100
5	SX	139/141 (99%)	124 (89%)	14 (10%)	1 (1%)	18	52
5	sX	139/141 (99%)	121 (87%)	17 (12%)	1 (1%)	18	52
6	SG	235/237 (99%)	219 (93%)	16 (7%)	0	100	100
6	sG	235/237 (99%)	220 (94%)	14 (6%)	1 (0%)	30	62
7	SJ	183/185 (99%)	168 (92%)	15 (8%)	0	100	100
7	sJ	183/185 (99%)	171 (93%)	12 (7%)	0	100	100
8	SY	129/131 (98%)	116 (90%)	13 (10%)	0	100	100
8	sY	129/131 (98%)	117 (91%)	12 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	se	56/58 (97%)	47 (84%)	9 (16%)	0	100	100
10	SA	219/221 (99%)	201 (92%)	18 (8%)	0	100	100
10	sA	219/221 (99%)	196 (90%)	23 (10%)	0	100	100
11	SB	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
11	sB	212/214 (99%)	199 (94%)	13 (6%)	0	100	100
12	SH	182/189 (96%)	159 (87%)	23 (13%)	0	100	100
12	sH	182/189 (96%)	156 (86%)	26 (14%)	0	100	100
13	SV	81/83 (98%)	74 (91%)	7 (9%)	0	100	100
13	sV	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
14	Sa	100/102 (98%)	81 (81%)	18 (18%)	1 (1%)	12	45
14	sa	100/102 (98%)	90 (90%)	10 (10%)	0	100	100
15	SC	220/222 (99%)	202 (92%)	18 (8%)	0	100	100
15	sC	220/222 (99%)	203 (92%)	17 (8%)	0	100	100
16	SN	148/150 (99%)	142 (96%)	6 (4%)	0	100	100
16	sN	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
17	SO	138/140 (99%)	125 (91%)	13 (9%)	0	100	100
17	sO	138/140 (99%)	124 (90%)	14 (10%)	0	100	100
18	SW	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
18	sW	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
19	Sb	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
19	sb	81/83 (98%)	69 (85%)	12 (15%)	0	100	100
22	LA	246/248 (99%)	219 (89%)	27 (11%)	0	100	100
22	lA	246/248 (99%)	225 (92%)	21 (8%)	0	100	100
23	LB	400/402 (100%)	364 (91%)	36 (9%)	0	100	100
23	lB	400/402 (100%)	371 (93%)	29 (7%)	0	100	100
24	LC	366/368 (100%)	347 (95%)	19 (5%)	0	100	100
24	lC	366/368 (100%)	340 (93%)	26 (7%)	0	100	100
25	LD	291/293 (99%)	279 (96%)	12 (4%)	0	100	100
25	lD	291/293 (99%)	271 (93%)	20 (7%)	0	100	100
26	LE	232/247 (94%)	212 (91%)	20 (9%)	0	100	100
26	lE	232/247 (94%)	210 (90%)	22 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	LF	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
27	IF	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
28	LG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
28	IG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
29	LH	188/190 (99%)	174 (93%)	14 (7%)	0	100	100
29	IH	188/190 (99%)	173 (92%)	15 (8%)	0	100	100
30	LI	198/213 (93%)	183 (92%)	15 (8%)	0	100	100
30	II	198/213 (93%)	188 (95%)	10 (5%)	0	100	100
31	LJ	174/176 (99%)	158 (91%)	16 (9%)	0	100	100
31	IJ	174/176 (99%)	155 (89%)	19 (11%)	0	100	100
32	LL	208/210 (99%)	190 (91%)	18 (9%)	0	100	100
32	IL	208/210 (99%)	191 (92%)	17 (8%)	0	100	100
33	LM	137/139 (99%)	127 (93%)	9 (7%)	1 (1%)	18	52
33	IM	137/139 (99%)	126 (92%)	10 (7%)	1 (1%)	18	52
34	LN	201/203 (99%)	184 (92%)	16 (8%)	1 (0%)	24	59
34	IN	201/203 (99%)	190 (94%)	10 (5%)	1 (0%)	24	59
35	LO	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
35	IO	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
36	LP	151/153 (99%)	140 (93%)	11 (7%)	0	100	100
36	IP	151/153 (99%)	138 (91%)	13 (9%)	0	100	100
37	LQ	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
37	IQ	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
38	LR	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
38	IR	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
39	LS	173/175 (99%)	160 (92%)	13 (8%)	0	100	100
39	IS	173/175 (99%)	159 (92%)	14 (8%)	0	100	100
40	LT	157/159 (99%)	149 (95%)	8 (5%)	0	100	100
40	IT	157/159 (99%)	143 (91%)	14 (9%)	0	100	100
41	LU	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
41	IU	99/101 (98%)	81 (82%)	18 (18%)	0	100	100
42	LV	129/131 (98%)	121 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	IV	129/131 (98%)	119 (92%)	10 (8%)	0	100	100
43	LX	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
43	IX	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
44	LY	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
44	IY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
45	LZ	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
45	IZ	133/135 (98%)	120 (90%)	13 (10%)	0	100	100
46	La	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
46	la	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
47	Lb	105/121 (87%)	95 (90%)	10 (10%)	0	100	100
47	lb	105/121 (87%)	94 (90%)	11 (10%)	0	100	100
48	Lc	96/98 (98%)	89 (93%)	7 (7%)	0	100	100
48	lc	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
49	Ld	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
49	ld	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
50	Le	126/128 (98%)	119 (94%)	7 (6%)	0	100	100
50	le	126/128 (98%)	116 (92%)	10 (8%)	0	100	100
51	Lf	107/109 (98%)	97 (91%)	10 (9%)	0	100	100
51	lf	107/109 (98%)	97 (91%)	10 (9%)	0	100	100
52	Lg	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
52	lg	112/114 (98%)	100 (89%)	12 (11%)	0	100	100
53	Lh	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
53	lh	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
54	Li	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
54	li	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
55	Lj	84/86 (98%)	76 (90%)	8 (10%)	0	100	100
55	lj	84/86 (98%)	73 (87%)	11 (13%)	0	100	100
56	Lk	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
56	lk	67/69 (97%)	64 (96%)	3 (4%)	0	100	100
57	Ll	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
57	ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	Lm	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
58	lm	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
59	Ln	22/24 (92%)	22 (100%)	0	0	100	100
59	ln	22/24 (92%)	22 (100%)	0	0	100	100
60	Lo	103/105 (98%)	94 (91%)	9 (9%)	0	100	100
60	lo	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
61	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
61	lp	89/91 (98%)	82 (92%)	7 (8%)	0	100	100
62	Lr	123/125 (98%)	116 (94%)	7 (6%)	0	100	100
62	lr	123/125 (98%)	110 (89%)	13 (11%)	0	100	100
63	Lz	215/217 (99%)	166 (77%)	49 (23%)	0	100	100
63	lz	215/217 (99%)	172 (80%)	43 (20%)	0	100	100
64	SR	133/135 (98%)	114 (86%)	18 (14%)	1 (1%)	16	50
64	sR	133/135 (98%)	106 (80%)	25 (19%)	2 (2%)	8	37
65	SD	225/227 (99%)	208 (92%)	17 (8%)	0	100	100
65	sD	225/227 (99%)	205 (91%)	19 (8%)	1 (0%)	30	62
66	SF	187/189 (99%)	159 (85%)	28 (15%)	0	100	100
66	sF	187/189 (99%)	165 (88%)	22 (12%)	0	100	100
67	SK	96/98 (98%)	85 (88%)	9 (9%)	2 (2%)	5	31
67	sK	96/98 (98%)	85 (88%)	10 (10%)	1 (1%)	12	45
68	SP	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
68	sP	119/121 (98%)	109 (92%)	10 (8%)	0	100	100
69	SQ	142/144 (99%)	121 (85%)	20 (14%)	1 (1%)	18	52
69	sQ	142/144 (99%)	122 (86%)	19 (13%)	1 (1%)	18	52
70	SS	143/145 (99%)	132 (92%)	11 (8%)	0	100	100
70	sS	143/145 (99%)	131 (92%)	12 (8%)	0	100	100
71	ST	141/143 (99%)	127 (90%)	13 (9%)	1 (1%)	18	52
71	sT	141/143 (99%)	128 (91%)	12 (8%)	1 (1%)	18	52
72	SU	102/104 (98%)	91 (89%)	11 (11%)	0	100	100
72	sU	102/104 (98%)	93 (91%)	9 (9%)	0	100	100
73	Sc	62/64 (97%)	51 (82%)	11 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	sc	62/64 (97%)	50 (81%)	12 (19%)	0	100	100
74	Sd	53/55 (96%)	49 (92%)	4 (8%)	0	100	100
74	sd	53/55 (96%)	48 (91%)	5 (9%)	0	100	100
75	Sg	311/313 (99%)	275 (88%)	36 (12%)	0	100	100
75	sg	311/313 (99%)	274 (88%)	37 (12%)	0	100	100
76	SM	120/122 (98%)	101 (84%)	18 (15%)	1 (1%)	16	50
76	sM	120/122 (98%)	109 (91%)	10 (8%)	1 (1%)	16	50
77	SZ	73/75 (97%)	58 (80%)	15 (20%)	0	100	100
77	sZ	73/75 (97%)	62 (85%)	11 (15%)	0	100	100
78	Sf	65/67 (97%)	55 (85%)	10 (15%)	0	100	100
78	sf	65/67 (97%)	55 (85%)	10 (15%)	0	100	100
80	CB	842/856 (98%)	782 (93%)	57 (7%)	3 (0%)	30	62
80	cB	842/856 (98%)	782 (93%)	57 (7%)	3 (0%)	30	62
83	Ls	194/196 (99%)	184 (95%)	10 (5%)	0	100	100
83	ls	194/196 (99%)	176 (91%)	18 (9%)	0	100	100
84	Lt	137/141 (97%)	103 (75%)	32 (23%)	2 (2%)	8	37
84	lt	137/141 (97%)	104 (76%)	31 (23%)	2 (2%)	8	37
86	Se	45/47 (96%)	43 (96%)	2 (4%)	0	100	100
87	LW	114/124 (92%)	109 (96%)	5 (4%)	0	100	100
87	IW	114/124 (92%)	112 (98%)	2 (2%)	0	100	100
All	All	25645/26099 (98%)	23469 (92%)	2141 (8%)	35 (0%)	49	79

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	sG	217	MET
67	sK	96	ARG
80	cB	779	THR
80	CB	407	LYS
80	CB	779	THR

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CH	100/100 (100%)	100 (100%)	0	100	100
1	cH	100/100 (100%)	100 (100%)	0	100	100
2	SE	224/224 (100%)	223 (100%)	1 (0%)	84	86
2	sE	224/224 (100%)	224 (100%)	0	100	100
3	SI	178/178 (100%)	178 (100%)	0	100	100
3	sI	178/178 (100%)	178 (100%)	0	100	100
4	SL	137/137 (100%)	135 (98%)	2 (2%)	57	76
4	sL	137/137 (100%)	136 (99%)	1 (1%)	76	83
5	SX	113/113 (100%)	113 (100%)	0	100	100
5	sX	113/113 (100%)	112 (99%)	1 (1%)	70	81
6	SG	207/207 (100%)	206 (100%)	1 (0%)	81	85
6	sG	207/207 (100%)	207 (100%)	0	100	100
7	SJ	161/161 (100%)	161 (100%)	0	100	100
7	sJ	161/161 (100%)	161 (100%)	0	100	100
8	SY	113/113 (100%)	113 (100%)	0	100	100
8	sY	113/113 (100%)	112 (99%)	1 (1%)	70	81
9	se	47/47 (100%)	47 (100%)	0	100	100
10	SA	183/183 (100%)	183 (100%)	0	100	100
10	sA	183/183 (100%)	182 (100%)	1 (0%)	81	85
11	SB	195/195 (100%)	194 (100%)	1 (0%)	81	85
11	sB	195/195 (100%)	193 (99%)	2 (1%)	68	80
12	SH	166/169 (98%)	166 (100%)	0	100	100
12	sH	166/169 (98%)	164 (99%)	2 (1%)	63	79
13	SV	67/67 (100%)	67 (100%)	0	100	100
13	sV	67/67 (100%)	67 (100%)	0	100	100
14	Sa	89/89 (100%)	88 (99%)	1 (1%)	65	79
14	sa	89/89 (100%)	87 (98%)	2 (2%)	45	71
15	SC	188/188 (100%)	187 (100%)	1 (0%)	81	85
15	sC	188/188 (100%)	186 (99%)	2 (1%)	65	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	SN	130/130 (100%)	130 (100%)	0	100	100
16	sN	130/130 (100%)	129 (99%)	1 (1%)	73	82
17	SO	110/110 (100%)	110 (100%)	0	100	100
17	sO	110/110 (100%)	110 (100%)	0	100	100
18	SW	112/112 (100%)	110 (98%)	2 (2%)	51	74
18	sW	112/112 (100%)	112 (100%)	0	100	100
19	Sb	75/75 (100%)	75 (100%)	0	100	100
19	sb	75/75 (100%)	75 (100%)	0	100	100
22	LA	190/190 (100%)	190 (100%)	0	100	100
22	lA	190/190 (100%)	190 (100%)	0	100	100
23	LB	348/348 (100%)	348 (100%)	0	100	100
23	lB	348/348 (100%)	347 (100%)	1 (0%)	86	88
24	LC	306/306 (100%)	306 (100%)	0	100	100
24	lC	306/306 (100%)	305 (100%)	1 (0%)	86	88
25	LD	246/247 (100%)	245 (100%)	1 (0%)	84	86
25	lD	246/247 (100%)	245 (100%)	1 (0%)	84	86
26	LE	209/220 (95%)	208 (100%)	1 (0%)	81	85
26	lE	209/220 (95%)	208 (100%)	1 (0%)	81	85
27	LF	194/194 (100%)	194 (100%)	0	100	100
27	lF	194/194 (100%)	191 (98%)	3 (2%)	57	76
28	LG	203/205 (99%)	202 (100%)	1 (0%)	81	85
28	lG	203/205 (99%)	203 (100%)	0	100	100
29	LH	169/169 (100%)	169 (100%)	0	100	100
29	lH	169/169 (100%)	168 (99%)	1 (1%)	78	84
30	LI	172/180 (96%)	171 (99%)	1 (1%)	78	84
30	lI	172/180 (96%)	171 (99%)	1 (1%)	78	84
31	LJ	148/148 (100%)	147 (99%)	1 (1%)	76	83
31	lJ	148/148 (100%)	147 (99%)	1 (1%)	76	83
32	LL	176/176 (100%)	176 (100%)	0	100	100
32	lL	176/176 (100%)	175 (99%)	1 (1%)	78	84
33	LM	118/118 (100%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	IM	118/118 (100%)	116 (98%)	2 (2%)	53	75
34	LN	171/171 (100%)	170 (99%)	1 (1%)	78	84
34	IN	171/171 (100%)	171 (100%)	0	100	100
35	LO	173/173 (100%)	172 (99%)	1 (1%)	78	84
35	IO	173/173 (100%)	172 (99%)	1 (1%)	78	84
36	LP	134/134 (100%)	134 (100%)	0	100	100
36	IP	134/134 (100%)	132 (98%)	2 (2%)	57	76
37	LQ	164/164 (100%)	164 (100%)	0	100	100
37	IQ	164/164 (100%)	164 (100%)	0	100	100
38	LR	166/166 (100%)	166 (100%)	0	100	100
38	IR	166/166 (100%)	166 (100%)	0	100	100
39	LS	156/156 (100%)	156 (100%)	0	100	100
39	IS	156/156 (100%)	155 (99%)	1 (1%)	78	84
40	LT	139/139 (100%)	138 (99%)	1 (1%)	76	83
40	IT	139/139 (100%)	138 (99%)	1 (1%)	76	83
41	LU	91/91 (100%)	90 (99%)	1 (1%)	65	79
41	IU	91/91 (100%)	91 (100%)	0	100	100
42	LV	101/101 (100%)	101 (100%)	0	100	100
42	IV	101/101 (100%)	100 (99%)	1 (1%)	68	80
43	LX	108/108 (100%)	107 (99%)	1 (1%)	70	81
43	IX	108/108 (100%)	107 (99%)	1 (1%)	70	81
44	LY	124/124 (100%)	124 (100%)	0	100	100
44	IY	124/124 (100%)	124 (100%)	0	100	100
45	LZ	117/117 (100%)	117 (100%)	0	100	100
45	IZ	117/117 (100%)	114 (97%)	3 (3%)	40	69
46	La	120/120 (100%)	120 (100%)	0	100	100
46	la	120/120 (100%)	118 (98%)	2 (2%)	53	75
47	Lb	88/101 (87%)	88 (100%)	0	100	100
47	lb	88/101 (87%)	88 (100%)	0	100	100
48	Lc	83/83 (100%)	82 (99%)	1 (1%)	63	79
48	lc	83/83 (100%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	Ld	98/98 (100%)	97 (99%)	1 (1%)	68	80
49	ld	98/98 (100%)	97 (99%)	1 (1%)	68	80
50	Le	114/114 (100%)	113 (99%)	1 (1%)	70	81
50	le	114/114 (100%)	113 (99%)	1 (1%)	70	81
51	Lf	88/88 (100%)	88 (100%)	0	100	100
51	lf	88/88 (100%)	87 (99%)	1 (1%)	65	79
52	Lg	98/98 (100%)	98 (100%)	0	100	100
52	lg	98/98 (100%)	97 (99%)	1 (1%)	68	80
53	Lh	109/109 (100%)	109 (100%)	0	100	100
53	lh	109/109 (100%)	109 (100%)	0	100	100
54	Li	86/86 (100%)	85 (99%)	1 (1%)	63	79
54	li	86/86 (100%)	86 (100%)	0	100	100
55	Lj	73/73 (100%)	73 (100%)	0	100	100
55	lj	73/73 (100%)	73 (100%)	0	100	100
56	Lk	64/64 (100%)	64 (100%)	0	100	100
56	lk	64/64 (100%)	64 (100%)	0	100	100
57	Ll	47/47 (100%)	47 (100%)	0	100	100
57	ll	47/47 (100%)	47 (100%)	0	100	100
58	Lm	48/48 (100%)	47 (98%)	1 (2%)	47	71
58	lm	48/48 (100%)	48 (100%)	0	100	100
59	Ln	23/23 (100%)	23 (100%)	0	100	100
59	ln	23/23 (100%)	23 (100%)	0	100	100
60	Lo	93/93 (100%)	93 (100%)	0	100	100
60	lo	93/93 (100%)	93 (100%)	0	100	100
61	Lp	74/74 (100%)	74 (100%)	0	100	100
61	lp	74/74 (100%)	74 (100%)	0	100	100
62	Lr	109/109 (100%)	107 (98%)	2 (2%)	51	74
62	lr	109/109 (100%)	109 (100%)	0	100	100
63	Lz	195/196 (100%)	195 (100%)	0	100	100
63	lz	195/196 (100%)	194 (100%)	1 (0%)	81	85
64	SR	122/122 (100%)	122 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
64	sR	122/122 (100%)	122 (100%)	0	100	100
65	SD	190/190 (100%)	190 (100%)	0	100	100
65	sD	190/190 (100%)	187 (98%)	3 (2%)	55	75
66	SF	159/159 (100%)	157 (99%)	2 (1%)	61	78
66	sF	159/159 (100%)	159 (100%)	0	100	100
67	SK	89/89 (100%)	88 (99%)	1 (1%)	65	79
67	sK	89/89 (100%)	89 (100%)	0	100	100
68	SP	107/107 (100%)	105 (98%)	2 (2%)	50	73
68	sP	107/107 (100%)	107 (100%)	0	100	100
69	SQ	119/119 (100%)	119 (100%)	0	100	100
69	sQ	119/119 (100%)	117 (98%)	2 (2%)	53	75
70	SS	126/126 (100%)	124 (98%)	2 (2%)	55	75
70	sS	126/126 (100%)	125 (99%)	1 (1%)	73	82
71	ST	113/113 (100%)	113 (100%)	0	100	100
71	sT	113/113 (100%)	111 (98%)	2 (2%)	51	74
72	SU	94/94 (100%)	93 (99%)	1 (1%)	65	79
72	sU	94/94 (100%)	94 (100%)	0	100	100
73	Sc	57/57 (100%)	57 (100%)	0	100	100
73	sc	57/57 (100%)	57 (100%)	0	100	100
74	Sd	48/48 (100%)	48 (100%)	0	100	100
74	sd	48/48 (100%)	48 (100%)	0	100	100
75	Sg	272/272 (100%)	271 (100%)	1 (0%)	84	86
75	sg	272/272 (100%)	268 (98%)	4 (2%)	57	76
76	SM	102/104 (98%)	102 (100%)	0	100	100
76	sM	102/104 (98%)	101 (99%)	1 (1%)	68	80
77	SZ	66/66 (100%)	66 (100%)	0	100	100
77	sZ	66/66 (100%)	66 (100%)	0	100	100
78	Sf	60/60 (100%)	59 (98%)	1 (2%)	53	75
78	sf	60/60 (100%)	60 (100%)	0	100	100
80	CB	722/728 (99%)	719 (100%)	3 (0%)	84	86
80	cB	722/728 (99%)	720 (100%)	2 (0%)	86	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
83	Ls	162/164 (99%)	162 (100%)	0	100	100
83	ls	162/164 (99%)	162 (100%)	0	100	100
84	Lt	112/115 (97%)	111 (99%)	1 (1%)	70	81
84	lt	112/115 (97%)	112 (100%)	0	100	100
86	Se	39/39 (100%)	39 (100%)	0	100	100
87	LW	97/103 (94%)	97 (100%)	0	100	100
87	IW	97/103 (94%)	95 (98%)	2 (2%)	47	71
All	All	22282/22398 (100%)	22182 (100%)	100 (0%)	81	86

5 of 100 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
80	cB	853	ASN
26	LE	119	GLU
87	IW	32	LEU
80	CB	520	LEU
11	SB	43	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 248 such sidechains are listed below:

Mol	Chain	Res	Type
75	sg	143	GLN
46	La	34	ASN
5	SX	97	ASN
44	LY	96	HIS
65	SD	101	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	L7	119/120 (99%)	15 (12%)	0
20	l7	119/120 (99%)	16 (13%)	0
21	L8	155/156 (99%)	28 (18%)	0
21	l8	155/156 (99%)	35 (22%)	0
79	S2	1714/1740 (98%)	495 (28%)	12 (0%)
79	s2	1712/1740 (98%)	546 (31%)	0
81	AP	69/73 (94%)	25 (36%)	1 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
81	aP	69/73 (94%)	25 (36%)	0
82	PE	74/76 (97%)	40 (54%)	3 (4%)
82	pE	73/76 (96%)	35 (47%)	0
85	L5	3696/3740 (98%)	969 (26%)	34 (0%)
85	l5	3696/3740 (98%)	929 (25%)	0
All	All	11651/11810 (98%)	3158 (27%)	50 (0%)

5 of 3158 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	l7	2	U
20	l7	7	G
20	l7	22	A
20	l7	24	C
20	l7	33	U

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
85	L5	4111	U
79	S2	307	G
82	PE	34	U
85	L5	4112	C
85	L5	4699	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 522 ligands modelled in this entry, 522 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
85	L5	10
85	l5	10
79	s2	7
79	S2	5
84	Lt	1
84	lt	1

The worst 5 of 34 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	753:C	O3'	785:C	P	27.80
1	s2	753:C	O3'	785:C	P	27.36
1	L5	2910:G	O3'	3584:C	P	20.89
1	l5	2910:G	O3'	3584:C	P	20.75
1	l5	760:G	O3'	903:C	P	17.11

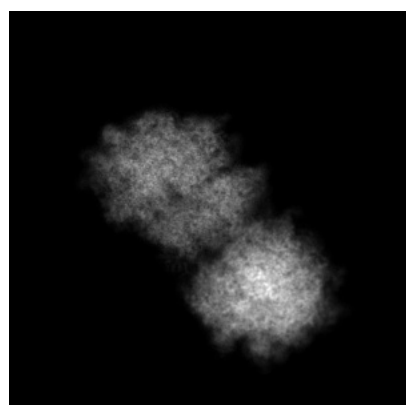
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44050. These allow visual inspection of the internal detail of the map and identification of artifacts.

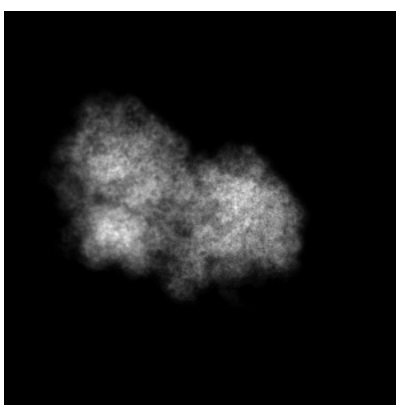
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

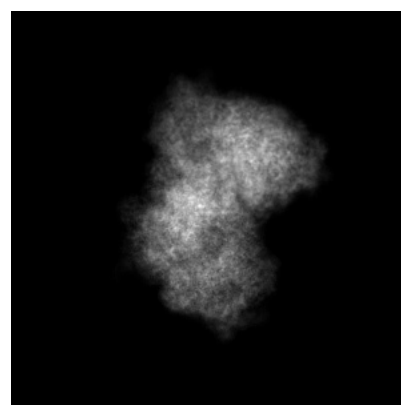
6.1.1 Primary map



X



Y

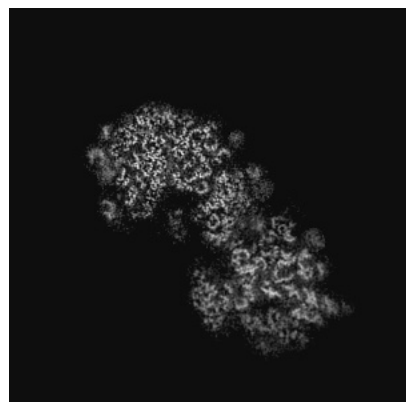


Z

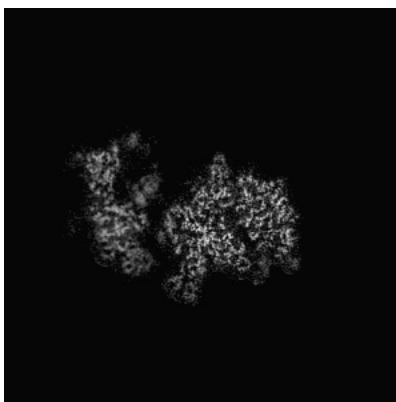
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

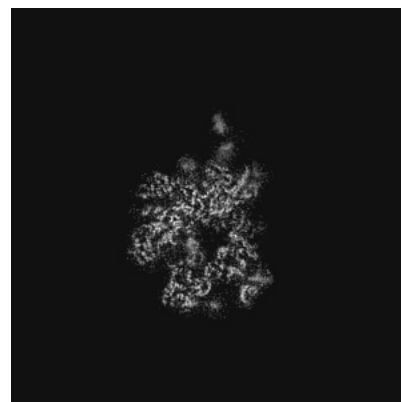
6.2.1 Primary map



X Index: 300



Y Index: 300

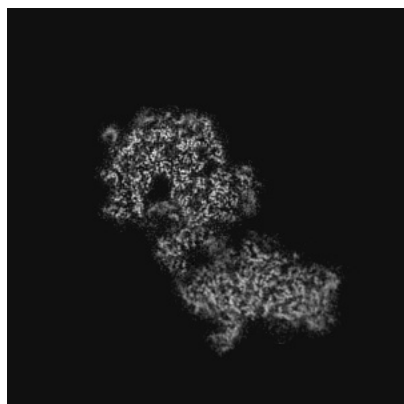


Z Index: 300

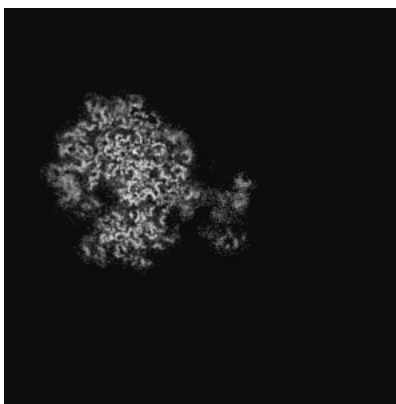
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

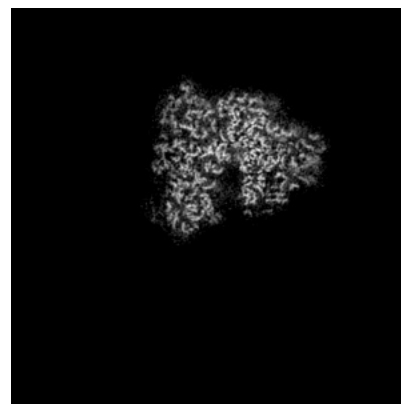
6.3.1 Primary map



X Index: 266



Y Index: 375

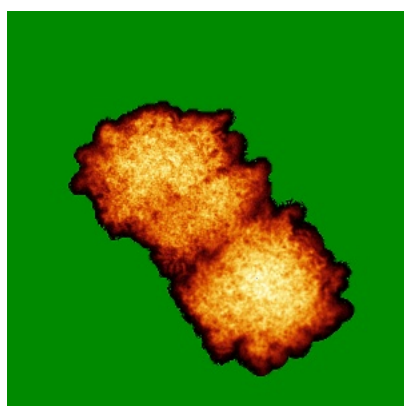


Z Index: 176

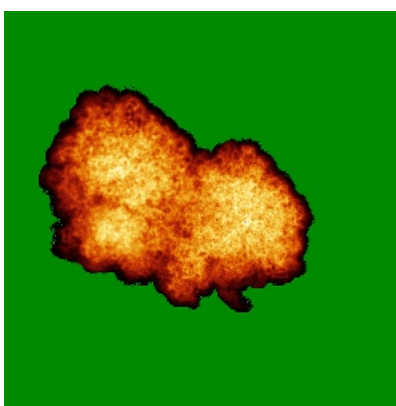
The images above show the largest variance slices of the map in three orthogonal directions.

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

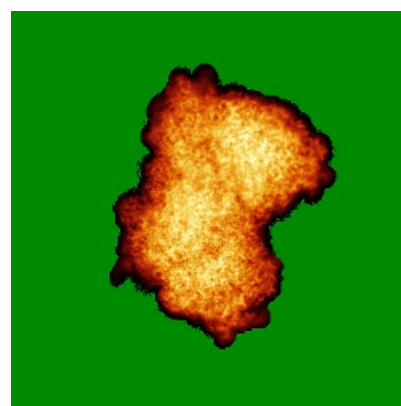
6.4.1 Primary map



X



Y

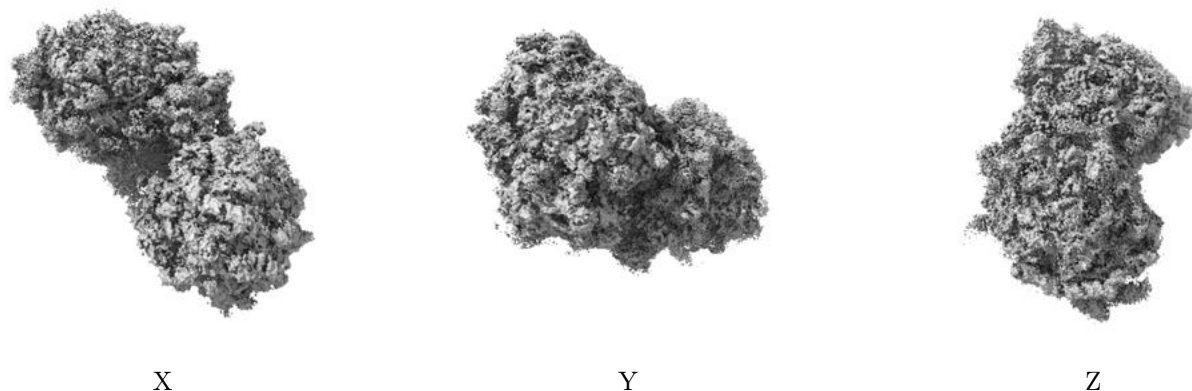


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.096. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

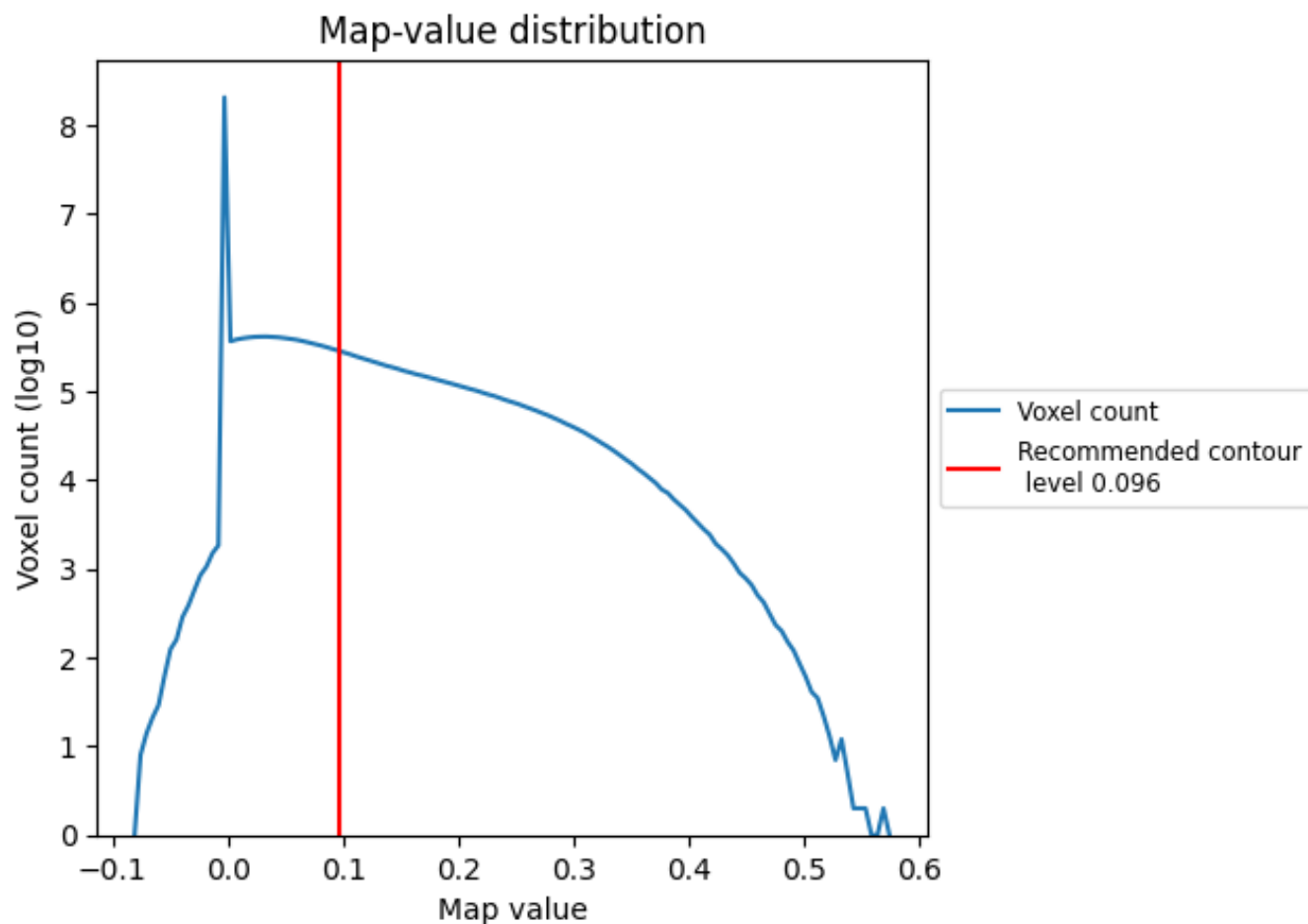
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

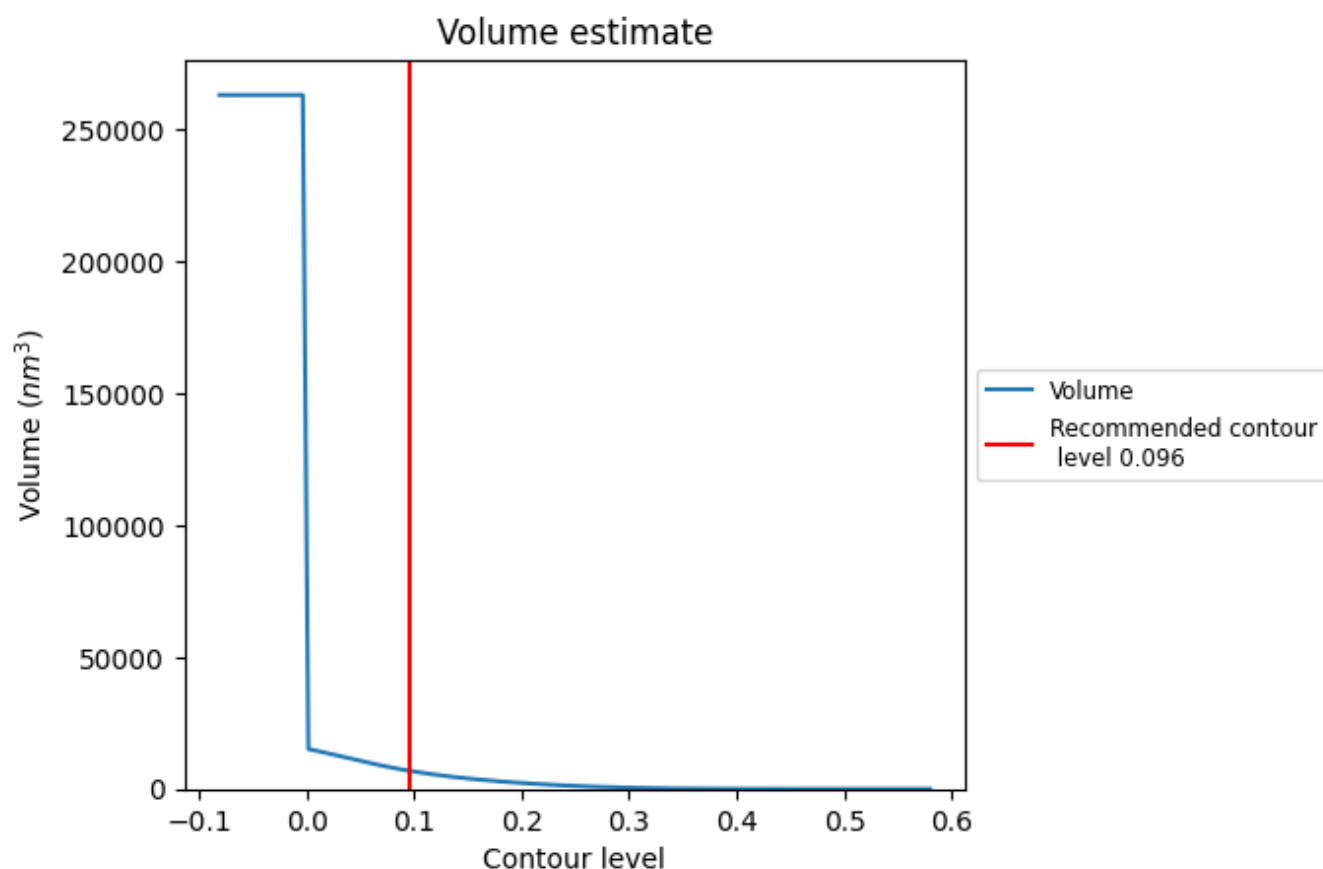
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

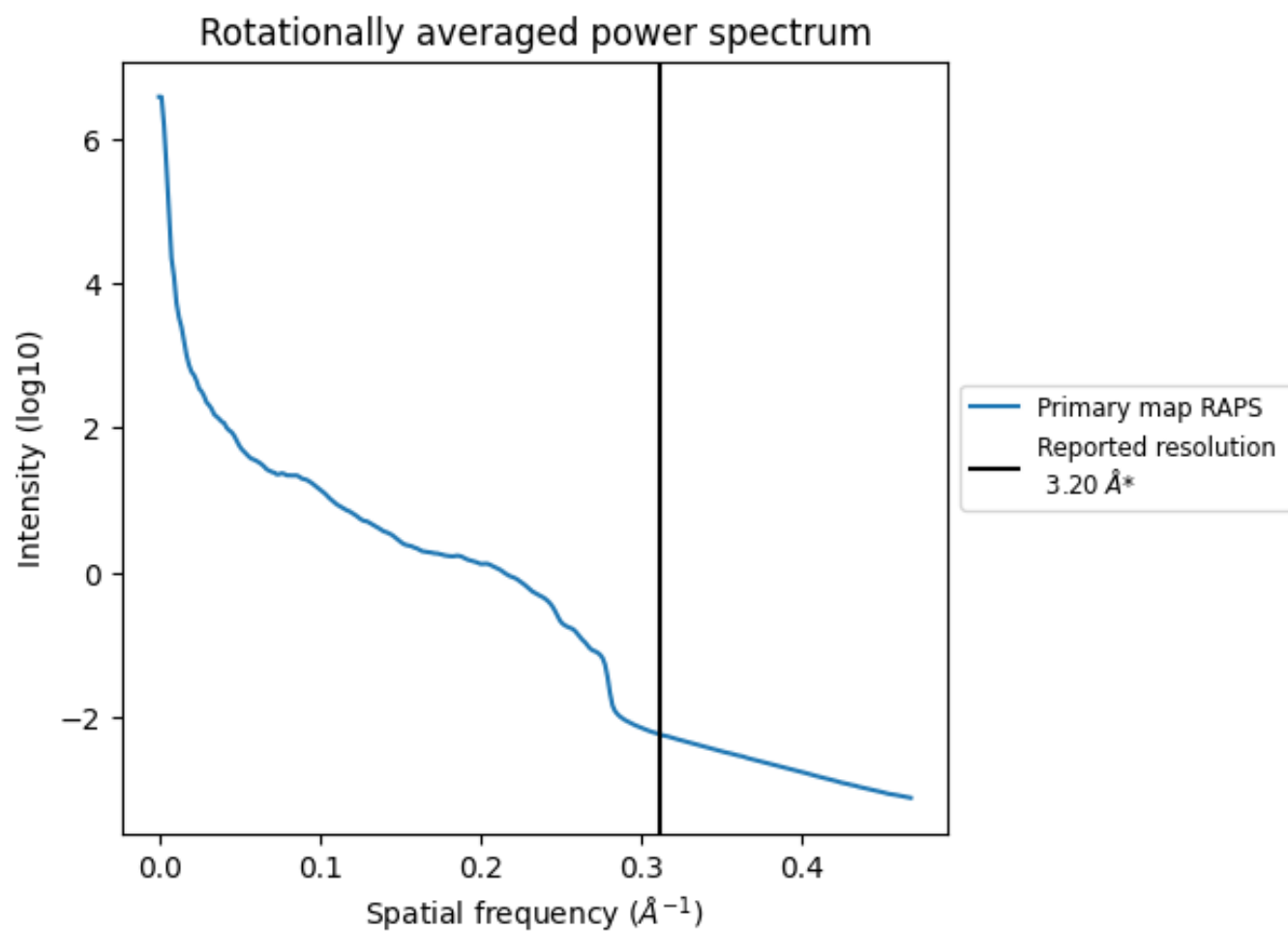
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6868 nm^3 ; this corresponds to an approximate mass of 6204 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

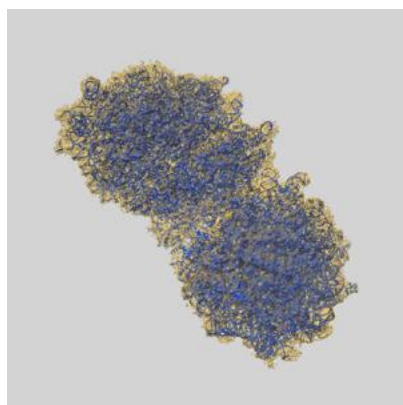
8 Fourier-Shell correlation

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

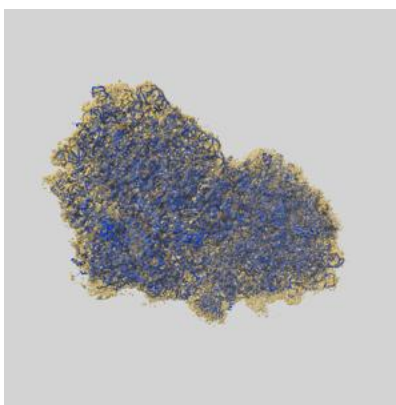
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-44050 and PDB model 9B0Q. Per-residue inclusion information can be found in [section 3](#) on [page 29](#).

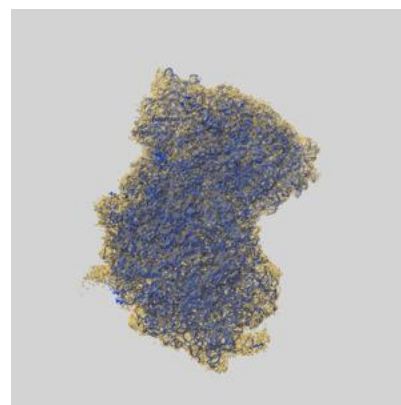
9.1 Map-model overlay [i](#)



X



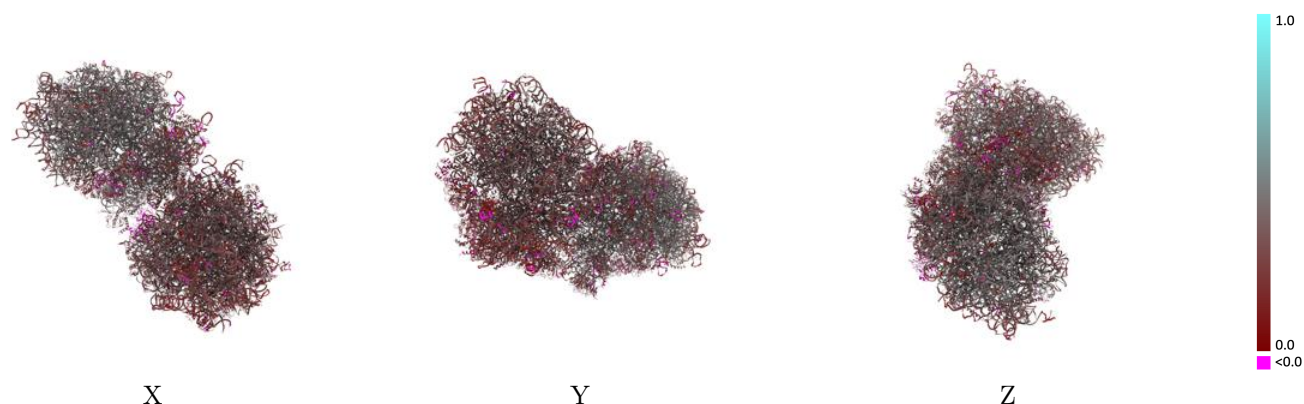
Y



Z

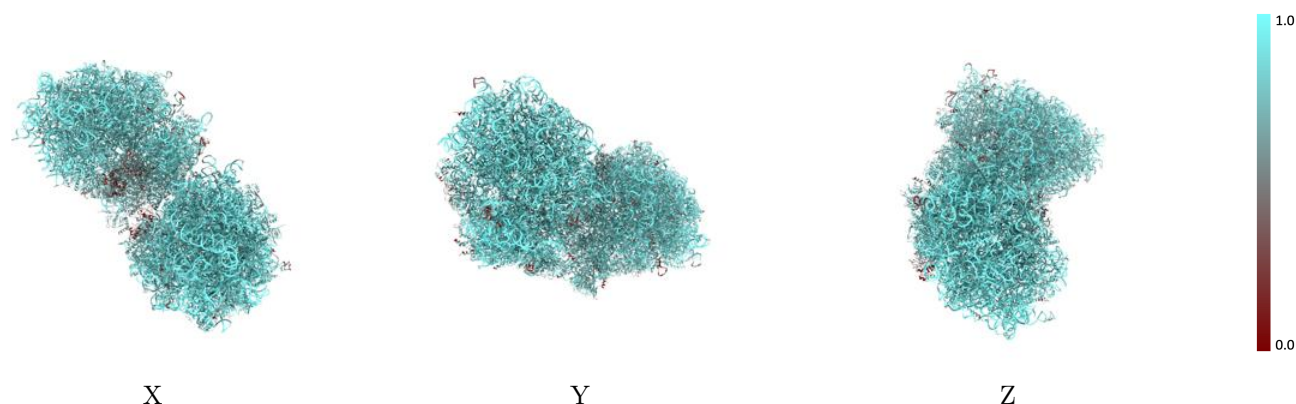
The images above show the 3D surface view of the map at the recommended contour level 0.096 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



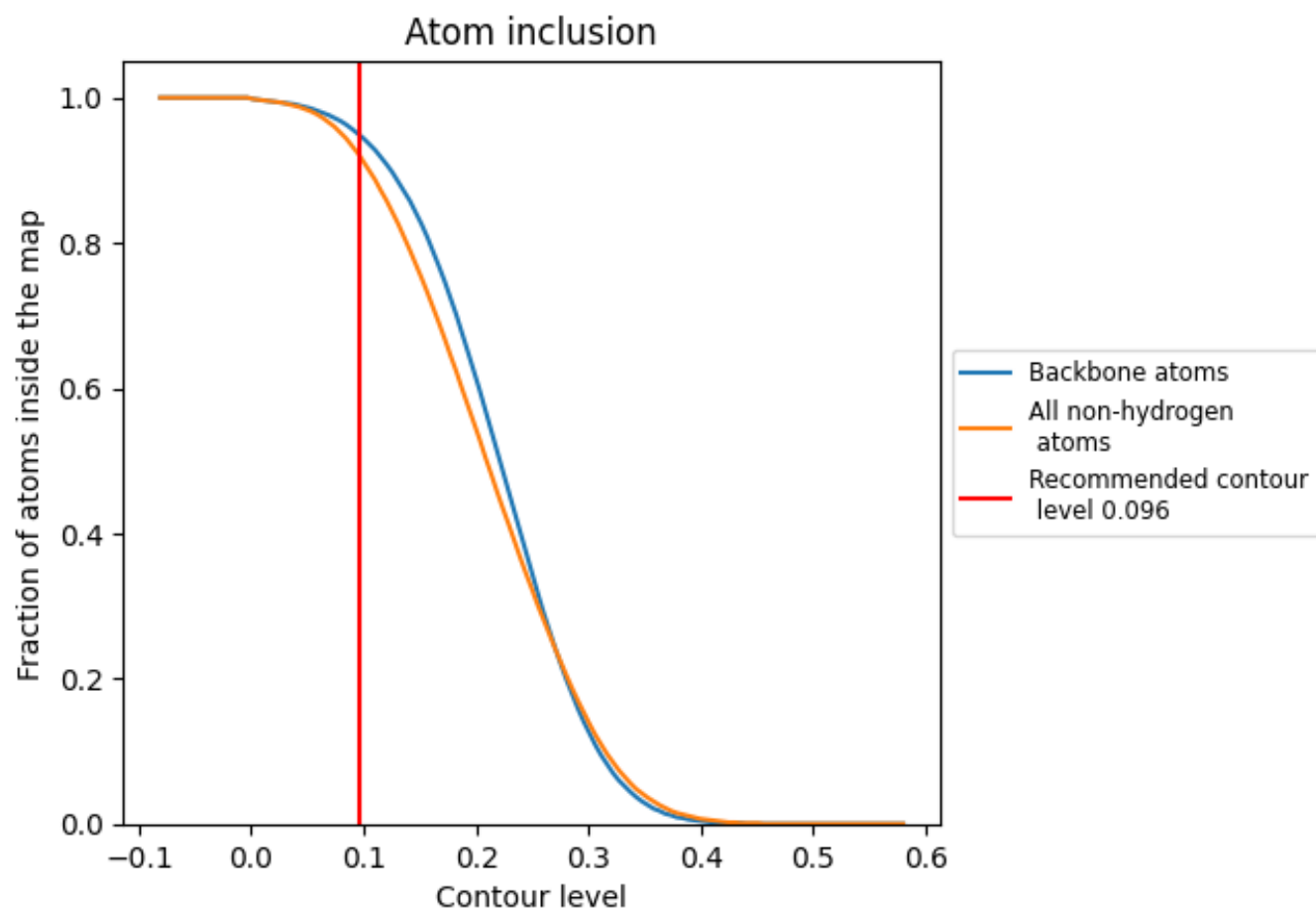
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.096).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 92% 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 (0.096) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9210	 0.3380
AP	 0.9890	 0.2490
CB	 0.7800	 0.2340
CH	 0.8100	 0.2630
L5	 0.9770	 0.3260
L7	 0.9940	 0.3480
L8	 0.9890	 0.3380
LA	 0.9430	 0.3620
LB	 0.9500	 0.3260
LC	 0.9170	 0.3350
LD	 0.8620	 0.3050
LE	 0.8910	 0.2770
LF	 0.9420	 0.3060
LG	 0.8550	 0.3020
LH	 0.9460	 0.2980
LI	 0.9600	 0.3440
LJ	 0.8400	 0.2860
LL	 0.8590	 0.3240
LM	 0.9390	 0.2950
LN	 0.9520	 0.3440
LO	 0.9490	 0.3060
LP	 0.9710	 0.3410
LQ	 0.9360	 0.3500
LR	 0.8780	 0.2920
LS	 0.9630	 0.3360
LT	 0.9420	 0.3450
LU	 0.8790	 0.2710
LV	 0.9800	 0.3660
LW	 0.8630	 0.2550
LX	 0.9060	 0.3360
LY	 0.9390	 0.3400
LZ	 0.8370	 0.3300
La	 0.9270	 0.3560
Lb	 0.8700	 0.3000
Lc	 0.8180	 0.3150



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Chain	Atom inclusion	Q-score
Ld	 0.9580	 0.3460
Le	 0.9750	 0.3560
Lf	 0.9830	 0.3420
Lg	 0.9210	 0.3380
Lh	 0.8980	 0.3140
Li	 0.8760	 0.3220
Lj	 0.9760	 0.3360
Lk	 0.8350	 0.3020
Ll	 0.9860	 0.3620
Lm	 0.9660	 0.3330
Ln	 1.0000	 0.3110
Lo	 0.9250	 0.3720
Lp	 0.9450	 0.3520
Lr	 0.9200	 0.3330
Ls	 0.6150	 0.1490
Lt	 0.6780	 0.1520
Lz	 0.2280	 0.0220
PE	 0.9750	 0.2490
S2	 0.9770	 0.3130
SA	 0.7830	 0.2940
SB	 0.8680	 0.3190
SC	 0.8790	 0.3120
SD	 0.8310	 0.2850
SE	 0.9030	 0.2810
SF	 0.8540	 0.2690
SG	 0.8750	 0.2410
SH	 0.7460	 0.2620
SI	 0.8770	 0.2800
SJ	 0.8770	 0.2650
SK	 0.8680	 0.2670
SL	 0.8780	 0.3170
SM	 0.6840	 0.2260
SN	 0.8540	 0.3050
SO	 0.8680	 0.3130
SP	 0.9020	 0.2970
SQ	 0.8740	 0.2650
SR	 0.7730	 0.2640
SS	 0.8410	 0.2900
ST	 0.8760	 0.2640
SU	 0.8450	 0.2660
SV	 0.8390	 0.2970
SW	 0.9210	 0.3140

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Chain	Atom inclusion	Q-score
SX	 0.9570	 0.3270
SY	 0.8950	 0.2280
SZ	 0.7920	 0.2820
Sa	 0.9240	 0.3510
Sb	 0.7920	 0.3030
Sc	 0.7690	 0.2130
Sd	 0.9910	 0.2900
Se	 0.9280	 0.2890
Sf	 0.7800	 0.2520
Sg	 0.7610	 0.2190
aP	 0.9410	 0.2670
cB	 0.4910	 0.2650
cH	 0.7590	 0.2850
l5	 0.9720	 0.3850
l7	 0.9900	 0.4140
l8	 0.9840	 0.3920
lA	 0.9490	 0.4410
lB	 0.9010	 0.4250
lC	 0.9370	 0.4300
lD	 0.9060	 0.3910
lE	 0.8760	 0.3780
lF	 0.9490	 0.4230
lG	 0.8750	 0.3660
lH	 0.8760	 0.4080
lI	 0.9190	 0.4380
lJ	 0.8060	 0.3410
lL	 0.9140	 0.4000
lM	 0.9010	 0.4050
lN	 0.9620	 0.4360
lO	 0.9270	 0.4220
lP	 0.9510	 0.4590
lQ	 0.9600	 0.4480
lR	 0.8850	 0.3770
lS	 0.9360	 0.4390
lT	 0.9530	 0.4330
lU	 0.8650	 0.3410
lV	 0.9000	 0.4350
lW	 0.8700	 0.3470
lX	 0.9200	 0.4110
lY	 0.9520	 0.4120
lZ	 0.8750	 0.3880
la	 0.9630	 0.4400

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Chain	Atom inclusion	Q-score
lb	 0.9070	 0.3700
lc	 0.8720	 0.3740
ld	 0.9290	 0.4230
le	 0.9600	 0.4530
lf	 0.9570	 0.4440
lg	 0.9400	 0.4310
lh	 0.9380	 0.3960
li	 0.9010	 0.3950
lj	 0.9910	 0.4490
lk	 0.8740	 0.3870
ll	 0.9740	 0.4330
lm	 0.9210	 0.4170
ln	 0.9670	 0.4230
lo	 0.9200	 0.4420
lp	 0.9300	 0.4150
lr	 0.9490	 0.4310
ls	 0.5370	 0.1750
lt	 0.4830	 0.1610
lz	 0.2500	 0.0520
pE	 0.9460	 0.2340
s2	 0.9720	 0.3540
sA	 0.8050	 0.3430
sB	 0.8870	 0.3690
sC	 0.8850	 0.3830
sD	 0.8530	 0.3680
sE	 0.9170	 0.3530
sF	 0.8590	 0.3310
sG	 0.8450	 0.2910
sH	 0.7730	 0.3100
sI	 0.8830	 0.3390
sJ	 0.8870	 0.3260
sK	 0.8550	 0.3460
sL	 0.8900	 0.3770
sM	 0.6750	 0.2310
sN	 0.9180	 0.3770
sO	 0.8750	 0.3800
sP	 0.8440	 0.3730
sQ	 0.8870	 0.3290
sR	 0.6810	 0.1450
sS	 0.8760	 0.3500
sT	 0.8650	 0.3330
sU	 0.8590	 0.3370

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Chain	Atom inclusion	Q-score
sV	 0.8180	 0.3410
sW	 0.9360	 0.4060
sX	 0.8980	 0.3890
sY	 0.8750	 0.2830
sZ	 0.8340	 0.3240
sa	 0.9020	 0.3880
sb	 0.8700	 0.3570
sc	 0.7570	 0.2720
sd	 0.9410	 0.3860
se	 0.7370	 0.2490
sf	 0.7320	 0.2540
sg	 0.7940	 0.2850