



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:08 PM GMT

PDB ID : 4V4G  
Title : Crystal structure of five 70s ribosomes from Escherichia Coli in complex with protein Y.  
Authors : Vila-Sanjurjo, A.; Schuwirth, B.S.; Hau, C.W.; Cate, J.H.  
Deposited on : 2004-10-06  
Resolution : 11.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

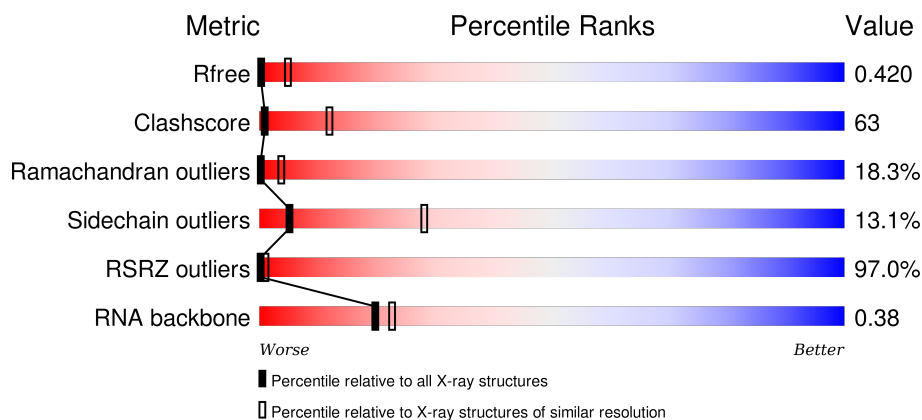
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 11.50 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	1015 (11.50-3.66)
Clashscore	102246	1065 (15.00-3.70)
Ramachandran outliers	100387	1036 (11.50-3.66)
Sidechain outliers	100360	1006 (11.50-3.66)
RSRZ outliers	91569	1014 (11.50-3.66)
RNA backbone	2183	1106 (11.50-2.80)

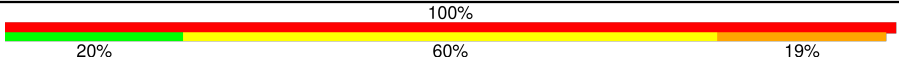
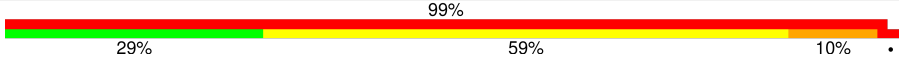
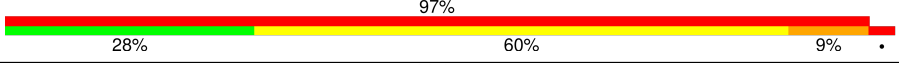
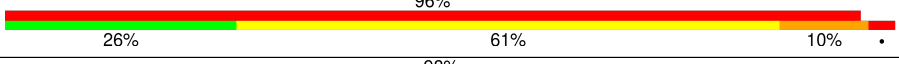
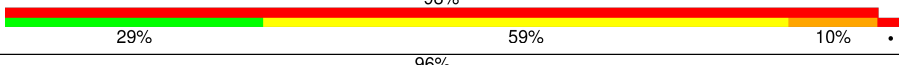
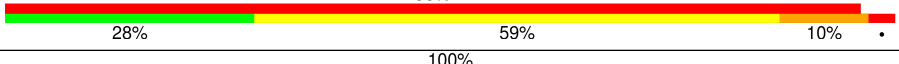
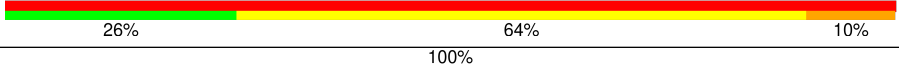


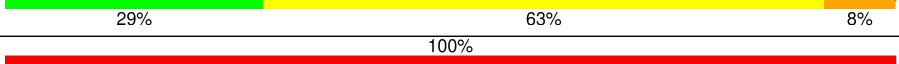

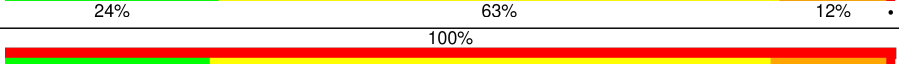
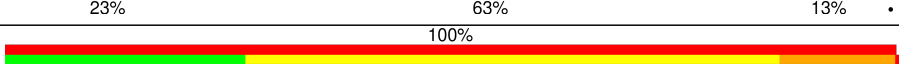
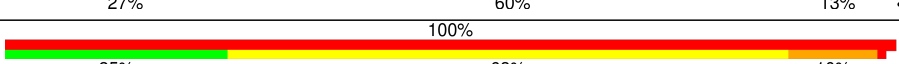
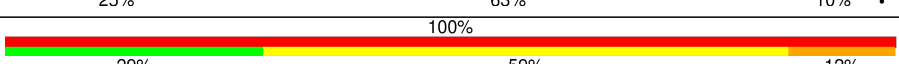
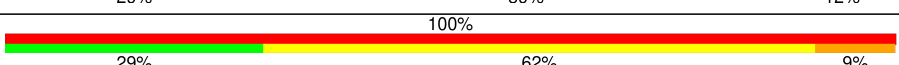
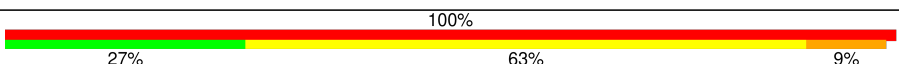
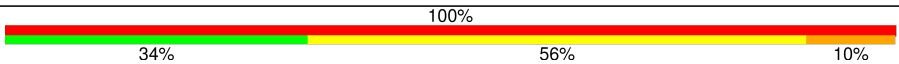



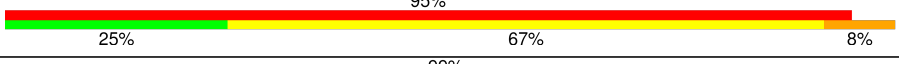
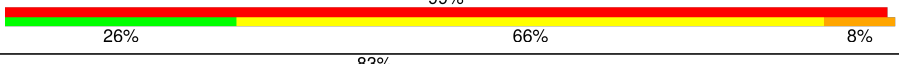


The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	1526	<div> <div>100%</div> <div> <div>20%</div> <div>61%</div> <div>19%</div> <div>.</div> </div> </div>
1	CA	1526	<div> <div>100%</div> <div> <div>20%</div> <div>60%</div> <div>19%</div> </div> </div>
1	EA	1526	<div> <div>100%</div> <div> <div>20%</div> <div>60%</div> <div>19%</div> </div> </div>
1	GA	1526	<div> <div>100%</div> <div> <div>20%</div> <div>61%</div> <div>19%</div> <div>.</div> </div> </div>

*Continued on next page...*



Continued from previous page...

Mol	Chain	Length	Quality of chain		
1	IA	1526			
2	AB	234			
2	CB	234			
2	EB	234			
2	GB	234			
2	IB	234			
3	AC	206			
3	CC	206			
3	EC	206			
3	GC	206			
3	IC	206			
4	AD	208			
4	CD	208			
4	ED	208			
4	GD	208			
4	ID	208			
5	AE	150			
5	CE	150			
5	EE	150			
5	GE	150			
5	IE	150			
6	AF	101			
6	CF	101			
6	EF	101			
6	GF	101			

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain		
6	IF	101	99%	27%	64% 9%
7	AG	155	100%	30%	61% 7%
7	CG	155	100%	29%	62% 8%
7	EG	155	100%	30%	61% 8%
7	GG	155	100%	26%	65% 8%
7	IG	155	100%	30%	61% 8%
8	AH	138	100%	30%	59% 9%
8	CH	138	100%	27%	62% 10%
8	EH	138	100%	25%	65% 9%
8	GH	138	100%	32%	59% 9%
8	IH	138	100%	26%	64% 9%
9	AI	127	100%	22%	61% 17%
9	CI	127	100%	23%	60% 17%
9	EI	127	100%	24%	60% 16%
9	GI	127	100%	23%	61% 16%
9	II	127	100%	21%	62% 17%
10	AJ	98	100%	16%	61% 20%
10	CJ	98	100%	18%	61% 18%
10	EJ	98	100%	17%	62% 18%
10	GJ	98	100%	14%	66% 17%
10	IJ	98	100%	17%	64% 16%
11	AK	119	99%	31%	55% 13%
11	CK	119	97%	30%	57% 13%
11	EK	119	92%	30%	57% 13%
11	GK	119	99%	29%	56% 14%

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
11	IK	119	
12	AL	124	
12	CL	124	
12	EL	124	
12	GL	124	
12	IL	124	
13	AM	125	
13	CM	125	
13	EM	125	
13	GM	125	
13	IM	125	
14	AN	60	
14	CN	60	
14	EN	60	
14	GN	60	
14	IN	60	
15	AO	88	
15	CO	88	
15	EO	88	
15	GO	88	
15	IO	88	
16	AP	83	
16	CP	83	
16	EP	83	
16	GP	83	

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
16	IP	83	
17	AQ	104	
17	CQ	104	
17	EQ	104	
17	GQ	104	
17	IQ	104	
18	AR	73	
18	CR	73	
18	ER	73	
18	GR	73	
18	IR	73	
19	AS	80	
19	CS	80	
19	ES	80	
19	GS	80	
19	IS	80	
20	AT	99	
20	CT	99	
20	ET	99	
20	GT	99	
20	IT	99	
21	Aa	90	
21	Ca	90	
21	Ea	90	
21	Ga	90	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain		
21	Ia	90	73%	79%	21%
22	BB	2825	100%	18%	22%
22	DB	2825	100%	19%	21%
22	FB	2825	100%	19%	22%
22	HB	2825	100%	18%	21%
22	JB	2825	100%	19%	21%
23	BA	119	99%	24%	18%
23	DA	119	99%	18%	20%
23	FA	119	99%	24%	22%
23	HA	119	99%	24%	18%
23	JA	119	99%	27%	22%
24	BD	270	93%	20%	30%
24	DD	270	98%	18%	28%
24	FD	270	100%	18%	30%
24	HD	270	92%	20%	28%
24	JD	270	100%	19%	30%
25	BE	205	89%	22%	23%
25	DE	205	86%	23%	24%
25	FE	205	83%	20%	23%
25	HE	205	91%	27%	21%
25	JE	205	87%	27%	23%
26	BF	198	99%	36%	19%
26	DF	198	99%	36%	18%
26	FF	198	94%	30%	19%
26	HF	198	99%	34%	18%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
26	JF	198	
27	BG	178	
27	DG	178	
27	FG	178	
27	HG	178	
27	JG	178	
28	BH	177	
28	DH	177	
28	FH	177	
28	HH	177	
28	JH	177	
29	BI	52	
29	DI	52	
29	FI	52	
29	HI	52	
29	JI	52	
30	BJ	143	
30	DJ	143	
30	FJ	143	
30	HJ	143	
30	JJ	143	
31	BK	143	
31	DK	143	
31	FK	143	
31	HK	143	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
31	JK	143	
32	BL	132	
32	DL	132	
32	FL	132	
32	HL	132	
32	JL	132	
33	BM	141	
33	DM	141	
33	FM	141	
33	HM	141	
33	JM	141	
34	BN	124	
34	DN	124	
34	FN	124	
34	HN	124	
34	JN	124	
35	BO	114	
35	DO	114	
35	FO	114	
35	HO	114	
35	JO	114	
36	BP	111	
36	DP	111	
36	FP	111	
36	HP	111	

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
36	JP	111	
37	BQ	125	
37	DQ	125	
37	FQ	125	
37	HQ	125	
37	JQ	125	
38	BR	117	
38	DR	117	
38	FR	117	
38	HR	117	
38	JR	117	
39	BS	100	
39	DS	100	
39	FS	100	
39	HS	100	
39	JS	100	
40	BT	130	
40	DT	130	
40	FT	130	
40	HT	130	
40	JT	130	
41	BU	93	
41	DU	93	
41	FU	93	
41	HU	93	

*Continued on next page...*



Continued from previous page...

Mol	Chain	Length	Quality of chain
41	JU	93	
42	BV	113	
42	DV	113	
42	FV	113	
42	HV	113	
42	JV	113	
43	BW	173	
43	DW	173	
43	FW	173	
43	HW	173	
43	JW	173	
44	BX	86	
44	DX	86	
44	FX	86	
44	HX	86	
44	JX	86	
45	BY	65	
45	DY	65	
45	FY	65	
45	HY	65	
45	JY	65	
46	BZ	55	
46	DZ	55	
46	FZ	55	
46	HZ	55	

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
46	JZ	55	
47	B1	73	
47	D1	73	
47	F1	73	
47	H1	73	
47	J1	73	
48	B2	58	
48	D2	58	
48	F2	58	
48	H2	58	
48	J2	58	
49	B3	53	
49	D3	53	
49	F3	53	
49	H3	53	
49	J3	53	
50	B4	46	
50	D4	46	
50	F4	46	
50	H4	46	
50	J4	46	
51	B5	63	
51	D5	63	
51	F5	63	
51	H5	63	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
51	J5	63	
52	B6	35	
52	D6	35	
52	F6	35	
52	H6	35	
52	J6	35	
53	B7	217	
53	D7	217	
53	F7	217	
53	H7	217	
53	J7	217	

## 2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 717805 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1526	Total	C	N	O	P	0	0	0
			32799	14601	6082	10590	1526			
1	CA	1526	Total	C	N	O	P	0	0	0
			32799	14601	6082	10590	1526			
1	EA	1526	Total	C	N	O	P	0	0	0
			32799	14601	6082	10590	1526			
1	GA	1526	Total	C	N	O	P	0	0	0
			32799	14601	6082	10590	1526			
1	IA	1526	Total	C	N	O	P	0	0	0
			32799	14601	6082	10590	1526			

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			
2	CB	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			
2	EB	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			
2	GB	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			
2	IB	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1613	1016	314	282	1			
3	CC	206	Total	C	N	O	S	0	0	0
			1613	1016	314	282	1			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	EC	206	Total	C	N	O	S	0	0	0
			1613	1016	314	282	1			
3	GC	206	Total	C	N	O	S	0	0	0
			1613	1016	314	282	1			
3	IC	206	Total	C	N	O	S	0	0	0
			1613	1016	314	282	1			

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			
4	CD	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			
4	ED	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			
4	GD	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			
4	ID	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	150	Total	C	N	O	S	0	0	0
			1147	724	217	202	4			
5	CE	150	Total	C	N	O	S	0	0	0
			1147	724	217	202	4			
5	EE	150	Total	C	N	O	S	0	0	0
			1147	724	217	202	4			
5	GE	150	Total	C	N	O	S	0	0	0
			1147	724	217	202	4			
5	IE	150	Total	C	N	O	S	0	0	0
			1147	724	217	202	4			

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			
6	CF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	EF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			
6	GF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			
6	IF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			
7	CG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			
7	EG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			
7	GG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			
7	IG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			
8	CH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			
8	EH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			
8	GH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			
8	IH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O	0	0	0
			1011	639	198	174			
9	CI	127	Total	C	N	O	0	0	0
			1011	639	198	174			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	EI	127	Total	C	N	O	0	0	0
			1011	639	198	174			
9	GI	127	Total	C	N	O	0	0	0
			1011	639	198	174			
9	II	127	Total	C	N	O	0	0	0
			1011	639	198	174			

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0	0
			795	499	156	139	1			
10	CJ	98	Total	C	N	O	S	0	0	0
			795	499	156	139	1			
10	EJ	98	Total	C	N	O	S	0	0	0
			795	499	156	139	1			
10	GJ	98	Total	C	N	O	S	0	0	0
			795	499	156	139	1			
10	IJ	98	Total	C	N	O	S	0	0	0
			795	499	156	139	1			

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			
11	CK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			
11	EK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			
11	GK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			
11	IK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AL	124	Total	C	N	O	S	0	0	0
			971	611	195	164	1			
12	CL	124	Total	C	N	O	S	0	0	0
			971	611	195	164	1			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	EL	124	Total	C	N	O	S	0	0	0
			971	611	195	164	1			
12	GL	124	Total	C	N	O	S	0	0	0
			971	611	195	164	1			
12	IL	124	Total	C	N	O	S	0	0	0
			971	611	195	164	1			

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AM	125	Total	C	N	O	S	0	0	0
			997	617	207	171	2			
13	CM	125	Total	C	N	O	S	0	0	0
			997	617	207	171	2			
13	EM	125	Total	C	N	O	S	0	0	0
			997	617	207	171	2			
13	GM	125	Total	C	N	O	S	0	0	0
			997	617	207	171	2			
13	IM	125	Total	C	N	O	S	0	0	0
			997	617	207	171	2			

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
14	CN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
14	EN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
14	GN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
14	IN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			
15	CO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	EO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			
15	GO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			
15	IO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AP	83	Total	C	N	O	S	0	0	0
			701	443	139	118	1			
16	CP	83	Total	C	N	O	S	0	0	0
			701	443	139	118	1			
16	EP	83	Total	C	N	O	S	0	0	0
			701	443	139	118	1			
16	GP	83	Total	C	N	O	S	0	0	0
			701	443	139	118	1			
16	IP	83	Total	C	N	O	S	0	0	0
			701	443	139	118	1			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	104	Total	C	N	O	S	0	0	0
			857	547	161	147	2			
17	CQ	104	Total	C	N	O	S	0	0	0
			857	547	161	147	2			
17	EQ	104	Total	C	N	O	S	0	0	0
			857	547	161	147	2			
17	GQ	104	Total	C	N	O	S	0	0	0
			857	547	161	147	2			
17	IQ	104	Total	C	N	O	S	0	0	0
			857	547	161	147	2			

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	AR	73	Total	C	N	O	0	0	0
			597	380	118	99			
18	CR	73	Total	C	N	O	0	0	0
			597	380	118	99			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	ER	73	Total	C	N	O	0	0	0
			597	380	118	99			
18	GR	73	Total	C	N	O	0	0	0
			597	380	118	99			
18	IR	73	Total	C	N	O	0	0	0
			597	380	118	99			

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	80	Total	C	N	O	S	0	0	0
			648	414	119	113	2			
19	CS	80	Total	C	N	O	S	0	0	0
			648	414	119	113	2			
19	ES	80	Total	C	N	O	S	0	0	0
			648	414	119	113	2			
19	GS	80	Total	C	N	O	S	0	0	0
			648	414	119	113	2			
19	IS	80	Total	C	N	O	S	0	0	0
			648	414	119	113	2			

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			
20	CT	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			
20	ET	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			
20	GT	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			
20	IT	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			

- Molecule 21 is a protein called protein Y.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	Aa	90	Total	C	N	O	S	0	0	0
			719	452	131	133	3			
21	Ca	90	Total	C	N	O	S	0	0	0
			719	452	131	133	3			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	Ea	90	Total	C	N	O	S	0	0	0
			719	452	131	133	3			
21	Ga	90	Total	C	N	O	S	0	0	0
			719	452	131	133	3			
21	Ia	90	Total	C	N	O	S	0	0	0
			719	452	131	133	3			

- Molecule 22 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	BB	2825	Total	C	N	O	P	0	0	0
			60635	27047	11190	19573	2825			
22	DB	2825	Total	C	N	O	P	0	0	0
			60635	27047	11190	19573	2825			
22	FB	2825	Total	C	N	O	P	0	0	0
			60635	27047	11190	19573	2825			
22	HB	2825	Total	C	N	O	P	0	0	0
			60635	27047	11190	19573	2825			
22	JB	2825	Total	C	N	O	P	0	0	0
			60635	27047	11190	19573	2825			

- Molecule 23 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	BA	118	Total	C	N	O	P	0	0	0
			2519	1124	464	813	118			
23	DA	118	Total	C	N	O	P	0	0	0
			2519	1124	464	813	118			
23	FA	118	Total	C	N	O	P	0	0	0
			2519	1124	464	813	118			
23	HA	118	Total	C	N	O	P	0	0	0
			2519	1124	464	813	118			
23	JA	118	Total	C	N	O	P	0	0	0
			2519	1124	464	813	118			

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	BD	270	Total	C	N	O	S	0	0	0
			2079	1294	417	365	3			
24	DD	270	Total	C	N	O	S	0	0	0
			2079	1294	417	365	3			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	FD	270	Total	C	N	O	S	0	0	0
			2079	1294	417	365	3			
24	HD	270	Total	C	N	O	S	0	0	0
			2079	1294	417	365	3			
24	JD	270	Total	C	N	O	S	0	0	0
			2079	1294	417	365	3			

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BE	205	Total	C	N	O	S	0	0	0
			1540	965	295	272	8			
25	DE	205	Total	C	N	O	S	0	0	0
			1540	965	295	272	8			
25	FE	205	Total	C	N	O	S	0	0	0
			1540	965	295	272	8			
25	HE	205	Total	C	N	O	S	0	0	0
			1540	965	295	272	8			
25	JE	205	Total	C	N	O	S	0	0	0
			1540	965	295	272	8			

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BF	197	Total	C	N	O	S	0	0	0
			1507	935	287	283	2			
26	DF	197	Total	C	N	O	S	0	0	0
			1507	935	287	283	2			
26	FF	197	Total	C	N	O	S	0	0	0
			1507	935	287	283	2			
26	HF	197	Total	C	N	O	S	0	0	0
			1507	935	287	283	2			
26	JF	197	Total	C	N	O	S	0	0	0
			1507	935	287	283	2			

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	BG	178	Total	C	N	O	S	0	0	0
			1410	897	249	257	7			
27	DG	178	Total	C	N	O	S	0	0	0
			1410	897	249	257	7			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	FG	178	Total	C	N	O	S	0	0	0
			1410	897	249	257	7			
27	HG	178	Total	C	N	O	S	0	0	0
			1410	897	249	257	7			
27	JG	178	Total	C	N	O	S	0	0	0
			1410	897	249	257	7			

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BH	177	Total	C	N	O	S	0	0	0
			1316	828	243	244	1			
28	DH	177	Total	C	N	O	S	0	0	0
			1316	828	243	244	1			
28	FH	177	Total	C	N	O	S	0	0	0
			1316	828	243	244	1			
28	HH	177	Total	C	N	O	S	0	0	0
			1316	828	243	244	1			
28	JH	177	Total	C	N	O	S	0	0	0
			1316	828	243	244	1			

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	BI	52	Total	C	N	O	S	0	0	0
			401	251	73	75	2			
29	DI	52	Total	C	N	O	S	0	0	0
			401	251	73	75	2			
29	FI	52	Total	C	N	O	S	0	0	0
			401	251	73	75	2			
29	HI	52	Total	C	N	O	S	0	0	0
			401	251	73	75	2			
29	JI	52	Total	C	N	O	S	0	0	0
			401	251	73	75	2			

- Molecule 30 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	BJ	143	Total	C	N	O	S	0	0	0
			1039	660	178	196	5			
30	DJ	143	Total	C	N	O	S	0	0	0
			1039	660	178	196	5			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	FJ	143	Total	C	N	O	S	0	0	0
			1039	660	178	196	5			
30	HJ	143	Total	C	N	O	S	0	0	0
			1039	660	178	196	5			
30	JJ	143	Total	C	N	O	S	0	0	0
			1039	660	178	196	5			

- Molecule 31 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	BK	143	Total	C	N	O	S	0	0	0
			1122	709	210	200	3			
31	DK	143	Total	C	N	O	S	0	0	0
			1122	709	210	200	3			
31	FK	143	Total	C	N	O	S	0	0	0
			1122	709	210	200	3			
31	HK	143	Total	C	N	O	S	0	0	0
			1122	709	210	200	3			
31	JK	143	Total	C	N	O	S	0	0	0
			1122	709	210	200	3			

- Molecule 32 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BL	132	Total	C	N	O	S	0	0	0
			981	603	196	178	4			
32	DL	132	Total	C	N	O	S	0	0	0
			981	603	196	178	4			
32	FL	132	Total	C	N	O	S	0	0	0
			981	603	196	178	4			
32	HL	132	Total	C	N	O	S	0	0	0
			981	603	196	178	4			
32	JL	132	Total	C	N	O	S	0	0	0
			981	603	196	178	4			

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
33	BM	141	Total	C	N	O	0	0	0
			1068	655	216	197			
33	DM	141	Total	C	N	O	0	0	0
			1068	655	216	197			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
33	FM	141	Total	C	N	O	0	0	0
			1068	655	216	197			
33	HM	141	Total	C	N	O	0	0	0
			1068	655	216	197			
33	JM	141	Total	C	N	O	0	0	0
			1068	655	216	197			

- Molecule 34 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BN	124	Total	C	N	O	S	0	0	0
			986	631	182	167	6			
34	DN	124	Total	C	N	O	S	0	0	0
			986	631	182	167	6			
34	FN	124	Total	C	N	O	S	0	0	0
			986	631	182	167	6			
34	HN	124	Total	C	N	O	S	0	0	0
			986	631	182	167	6			
34	JN	124	Total	C	N	O	S	0	0	0
			986	631	182	167	6			

- Molecule 35 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BO	114	Total	C	N	O	S	0	0	0
			886	546	179	159	2			
35	DO	114	Total	C	N	O	S	0	0	0
			886	546	179	159	2			
35	FO	114	Total	C	N	O	S	0	0	0
			886	546	179	159	2			
35	HO	114	Total	C	N	O	S	0	0	0
			886	546	179	159	2			
35	JO	114	Total	C	N	O	S	0	0	0
			886	546	179	159	2			

- Molecule 36 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
36	BP	111	Total	C	N	O	8	0	0
			834	512	168	154			
36	DP	111	Total	C	N	O	8	0	0
			834	512	168	154			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
36	FP	111	Total	C	N	O	8	0	0
			834	512	168	154			
36	HP	111	Total	C	N	O	8	0	0
			834	512	168	154			
36	JP	111	Total	C	N	O	8	0	0
			834	512	168	154			

- Molecule 37 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BQ	125	Total	C	N	O	S	0	0	0
			1008	625	204	178	1			
37	DQ	125	Total	C	N	O	S	0	0	0
			1008	625	204	178	1			
37	FQ	125	Total	C	N	O	S	0	0	0
			1008	625	204	178	1			
37	HQ	125	Total	C	N	O	S	0	0	0
			1008	625	204	178	1			
37	JQ	125	Total	C	N	O	S	0	0	0
			1008	625	204	178	1			

- Molecule 38 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BR	117	Total	C	N	O	S	16	0	0
			978	608	210	159	1			
38	DR	117	Total	C	N	O	S	16	0	0
			978	608	210	159	1			
38	FR	117	Total	C	N	O	S	16	0	0
			978	608	210	159	1			
38	HR	117	Total	C	N	O	S	16	0	0
			978	608	210	159	1			
38	JR	117	Total	C	N	O	S	16	0	0
			978	608	210	159	1			

- Molecule 39 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BS	100	Total	C	N	O	S	0	0	0
			787	495	146	145	1			
39	DS	100	Total	C	N	O	S	0	0	0
			787	495	146	145	1			

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	FS	100	Total	C	N	O	S	0	0	0
			787	495	146	145	1			
39	HS	100	Total	C	N	O	S	0	0	0
			787	495	146	145	1			
39	JS	100	Total	C	N	O	S	0	0	0
			787	495	146	145	1			

- Molecule 40 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BT	130	Total	C	N	O	S	0	0	0
			1039	653	203	181	2			
40	DT	130	Total	C	N	O	S	0	0	0
			1039	653	203	181	2			
40	FT	130	Total	C	N	O	S	0	0	0
			1039	653	203	181	2			
40	HT	130	Total	C	N	O	S	0	0	0
			1039	653	203	181	2			
40	JT	130	Total	C	N	O	S	0	0	0
			1039	653	203	181	2			

- Molecule 41 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BU	93	Total	C	N	O	S	0	0	0
			727	458	136	131	2			
41	DU	93	Total	C	N	O	S	0	0	0
			727	458	136	131	2			
41	FU	93	Total	C	N	O	S	0	0	0
			727	458	136	131	2			
41	HU	93	Total	C	N	O	S	0	0	0
			727	458	136	131	2			
41	JU	93	Total	C	N	O	S	0	0	0
			727	458	136	131	2			

- Molecule 42 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BV	113	Total	C	N	O	S	0	0	0
			852	530	166	155	1			
42	DV	113	Total	C	N	O	S	0	0	0
			852	530	166	155	1			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	FV	113	Total	C	N	O	S	0	0	0
			852	530	166	155	1			
42	HV	113	Total	C	N	O	S	0	0	0
			852	530	166	155	1			
42	JV	113	Total	C	N	O	S	0	0	0
			852	530	166	155	1			

- Molecule 43 is a protein called general stress protein Ctc.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BW	173	Total	C	N	O	S	0	0	0
			1328	838	231	253	6			
43	DW	173	Total	C	N	O	S	0	0	0
			1328	838	231	253	6			
43	FW	173	Total	C	N	O	S	0	0	0
			1328	838	231	253	6			
43	HW	173	Total	C	N	O	S	0	0	0
			1328	838	231	253	6			
43	JW	173	Total	C	N	O	S	0	0	0
			1328	838	231	253	6			

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	BX	86	Total	C	N	O	S	0	0	0
			642	402	124	115	1			
44	DX	86	Total	C	N	O	S	0	0	0
			642	402	124	115	1			
44	FX	86	Total	C	N	O	S	0	0	0
			642	402	124	115	1			
44	HX	86	Total	C	N	O	S	0	0	0
			642	402	124	115	1			
44	JX	86	Total	C	N	O	S	0	0	0
			642	402	124	115	1			

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BY	65	Total	C	N	O	S	0	0	0
			526	322	106	96	2			
45	DY	65	Total	C	N	O	S	0	0	0
			526	322	106	96	2			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	FY	65	Total	C	N	O	S	0	0	0
			526	322	106	96	2			
45	HY	65	Total	C	N	O	S	0	0	0
			526	322	106	96	2			
45	JY	65	Total	C	N	O	S	0	0	0
			526	322	106	96	2			

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	BZ	55	Total	C	N	O	S	4	0	0
			424	264	82	76	2			
46	DZ	55	Total	C	N	O	S	4	0	0
			424	264	82	76	2			
46	FZ	55	Total	C	N	O	S	4	0	0
			424	264	82	76	2			
46	HZ	55	Total	C	N	O	S	4	0	0
			424	264	82	76	2			
46	JZ	55	Total	C	N	O	S	4	0	0
			424	264	82	76	2			

- Molecule 47 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	B1	73	Total	C	N	O	S	0	0	0
			604	382	110	108	4			
47	D1	73	Total	C	N	O	S	0	0	0
			604	382	110	108	4			
47	F1	73	Total	C	N	O	S	0	0	0
			604	382	110	108	4			
47	H1	73	Total	C	N	O	S	0	0	0
			604	382	110	108	4			
47	J1	73	Total	C	N	O	S	0	0	0
			604	382	110	108	4			

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	B2	58	Total	C	N	O	S	0	0	0
			458	281	94	78	5			
48	D2	58	Total	C	N	O	S	0	0	0
			458	281	94	78	5			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	F2	58	Total	C	N	O	S	0	0	0
			458	281	94	78	5			
48	H2	58	Total	C	N	O	S	0	0	0
			458	281	94	78	5			
48	J2	58	Total	C	N	O	S	0	0	0
			458	281	94	78	5			

- Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	B3	53	Total	C	N	O	S	0	0	0
			432	274	80	77	1			
49	D3	53	Total	C	N	O	S	0	0	0
			432	274	80	77	1			
49	F3	53	Total	C	N	O	S	0	0	0
			432	274	80	77	1			
49	H3	53	Total	C	N	O	S	0	0	0
			432	274	80	77	1			
49	J3	53	Total	C	N	O	S	0	0	0
			432	274	80	77	1			

- Molecule 50 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B4	46	Total	C	N	O	S	0	0	0
			384	230	91	61	2			
50	D4	46	Total	C	N	O	S	0	0	0
			384	230	91	61	2			
50	F4	46	Total	C	N	O	S	0	0	0
			384	230	91	61	2			
50	H4	46	Total	C	N	O	S	0	0	0
			384	230	91	61	2			
50	J4	46	Total	C	N	O	S	0	0	0
			384	230	91	61	2			

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B5	63	Total	C	N	O	S	0	0	0
			496	312	101	78	5			
51	D5	63	Total	C	N	O	S	0	0	0
			496	312	101	78	5			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	F5	63	Total 496	C 312	N 101	O 78	S 5	0	0	0
51	H5	63	Total 496	C 312	N 101	O 78	S 5	0	0	0
51	J5	63	Total 496	C 312	N 101	O 78	S 5	0	0	0

- Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	B6	35	Total 285	C 172	N 64	O 45	S 4	0	0	0
52	D6	35	Total 285	C 172	N 64	O 45	S 4	0	0	0
52	F6	35	Total 285	C 172	N 64	O 45	S 4	0	0	0
52	H6	35	Total 285	C 172	N 64	O 45	S 4	0	0	0
52	J6	35	Total 285	C 172	N 64	O 45	S 4	0	0	0

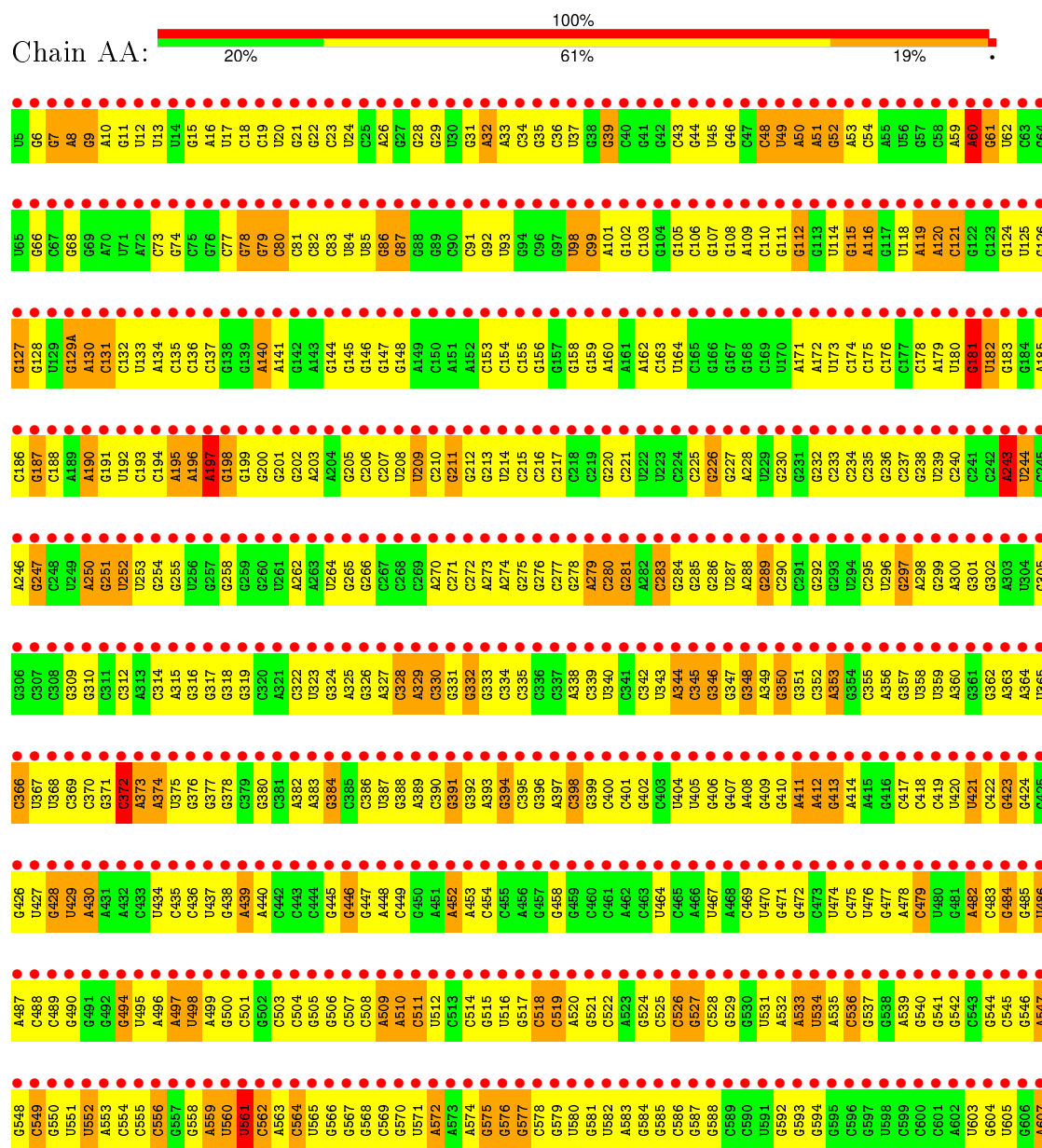
- Molecule 53 is a protein called 50S ribosomal protein L1P.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
53	B7	217	Total 1720	C 1098	N 304	O 313	S 1	Se 4	0	0	0
53	D7	217	Total 1720	C 1098	N 304	O 313	S 1	Se 4	0	0	0
53	F7	217	Total 1720	C 1098	N 304	O 313	S 1	Se 4	0	0	0
53	H7	217	Total 1720	C 1098	N 304	O 313	S 1	Se 4	0	0	0
53	J7	217	Total 1720	C 1098	N 304	O 313	S 1	Se 4	0	0	0

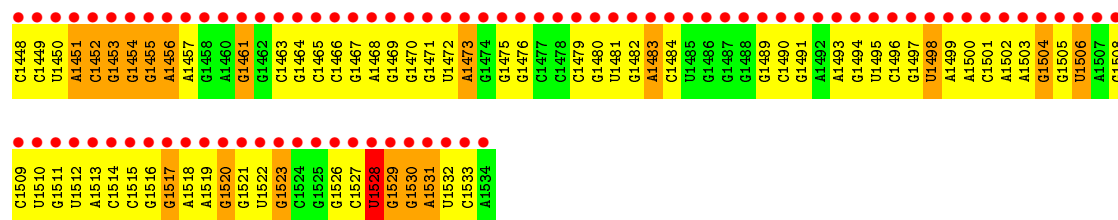
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). 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.

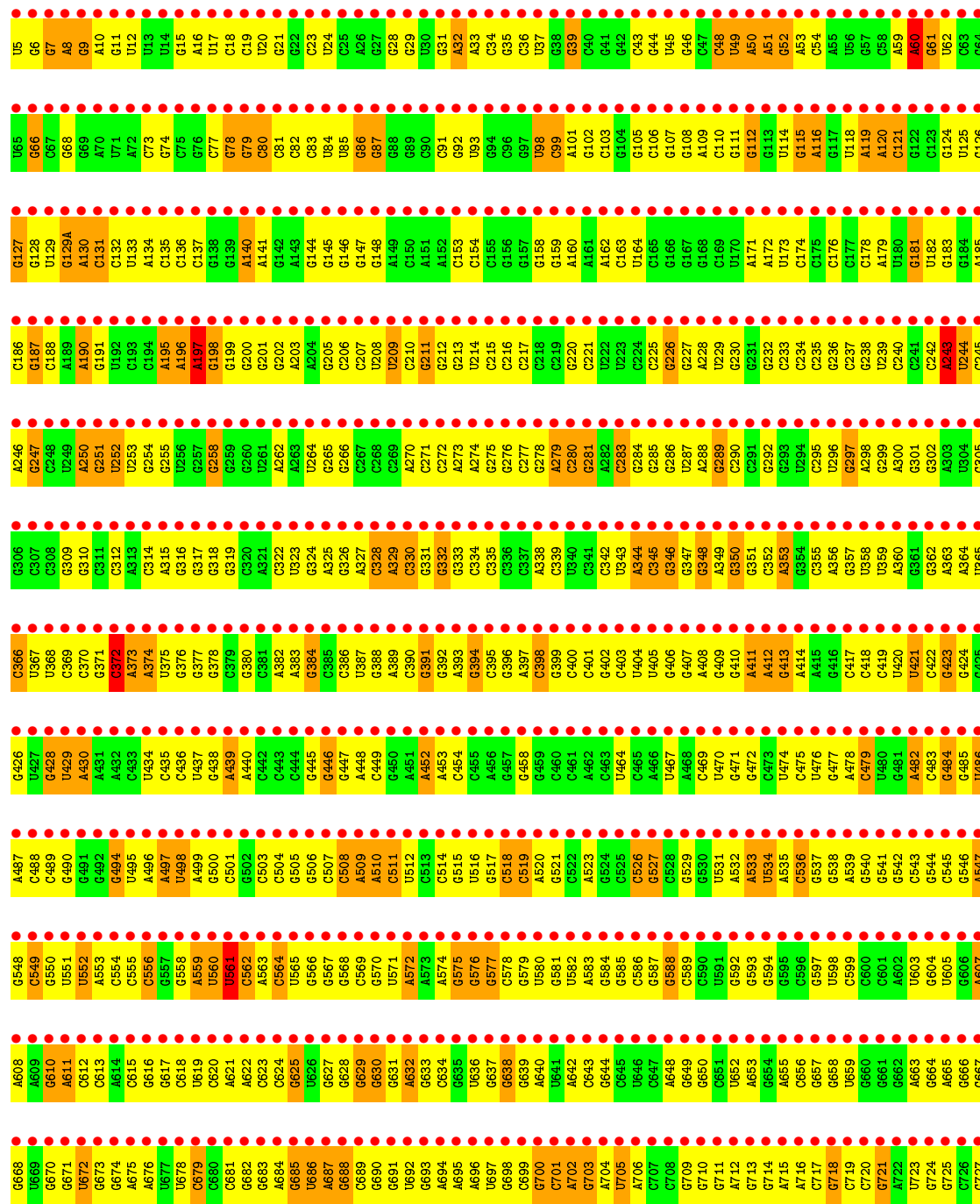
#### • Molecule 1: 16S ribosomal RNA







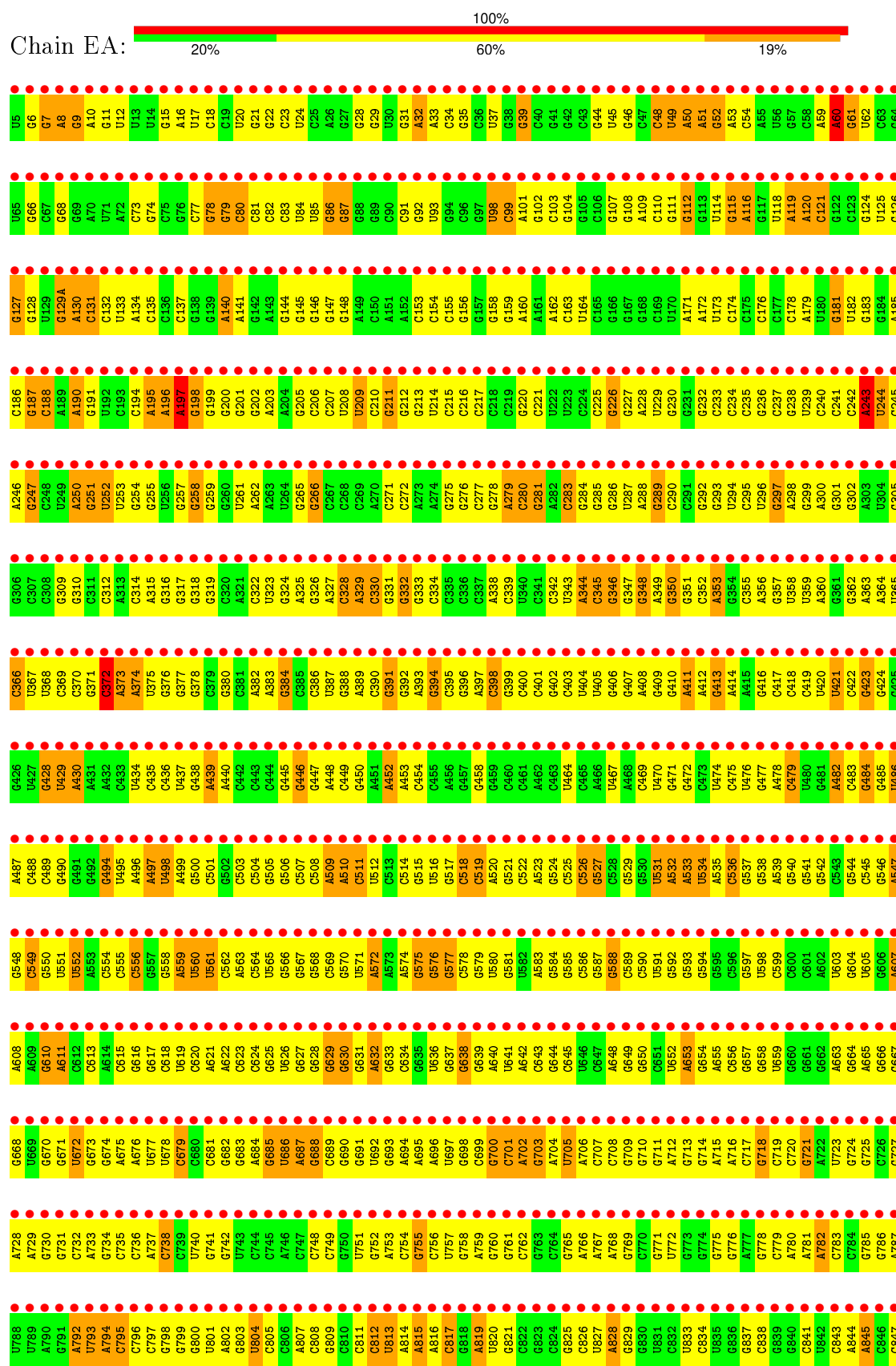
● Molecule 1: 16S ribosomal RNA





C1509	C1448	C1387	C1328	A1268	C1208	C1147	G1087	C1027	A968	A908	G848	U768	A728
U1510	C1449	C1388	A1329	A1269	C1209	U1448	G1088	C1028	A969	A909	C849	U769	A729
G1511	C1450	C1389	U1330	C1270	U1210	U1449	U1089	U1029	C970	A910	U850	A790	G730
U1512	A1451	U1390	G1331	U1271	U1211	U1450	U1090	U1030	C971	U911	G851	G791	G731
C1513	C1452	U1391	A1332	G1272	A1212	A1451	U1091	C1031	C972	C912	G852	A792	A732
C1514	G1453	C1392	A1333	G1273	A1213	A1452	A1092	G1032	G973	A913	G853	U793	A733
C1515	C1454	U1393	G1334	G1274	C1214	C1453	A1093	G1033	A974	A914	G854	A794	G734
C1516	A1455	C1394	C1335	A1275	G1215	C1454	U1094	G1034	A975	A915	G855	C795	C735
G1517	A1456	C1395	C1336	G1276	G1216	G1455	U1095	A1035	C976	G916	C856	C796	C736
A1518	A1457	A1396	G1337	C1277	C1217	G1456	U1096	C1036	A977	A917	C857	C797	A737
A1519	G1458	C1397	G1338	U1278	C1218	A1457	C1097	C1037	A978	A918	G858	G798	C738
G1520	A1460	A1398	A1339	A1279	U1219	G1458	U1098	C1038	C979	A919	A859	G799	C739
G1521	G1461	C1399	A1340	A1280	G1220	U1459	U1099	C1039	C980	U920	A860	G800	U740
U1522	G1462	C1400	U1341	U1281	G1221	G1460	C1100	U1040	U881	U921	G861	U801	G741
G1523	G1463	G1401	C1342	C1282	G1222	A1461	A1101	A1041	U882	G922	C862	A802	G742
C1524	G1464	C1402	G1343	G1283	C1223	C1462	A1102	G1042	A883	A923	U863	G803	U743
G1525	C1465	C1403	C1344	A1284	G1224	C1463	C1103	C1043	C984	C924	A864	U804	C744
G1526	C1466	C1404	A1345	A1285	A1225	G1464	G1104	A1044	C985	G925	A865	C745	C745
C1527	G1467	G1405	A1346	A1286	C1226	C1465	A1105	C1045	A886	G926	C866	C906	A746
U1528	A1468	G1406	G1347	A1287	A1227	G1466	C1106	A1046	G887	G927	G867	A807	C747
G1529	C1469	C1407	U1348	A1288	C1228	A1467	C1107	U1047	C988	G928	C868	C808	C748
G1530	A1470	A1408	A1349	A1289	A1229	A1468	G1108	U1048	C989	G929	G869	G809	C749
A1531	C1471	C1409	A1350	A1290	C1230	A1469	U1109	U1049	C990	C930	U870	C810	G750
U1532	U1472	G1410	U1351	G1291	G1231	G1470	A1110	G1050	U991	C931	U871	C811	U751
C1533	A1473	C1411	C1352	U1292	U1232	C1471	C1051	C1051	U992	C932	A872	C812	G752
A1534	G1474	C1412	G1353	G1293	G1233	G1472	U1052	U1052	G993	G933	A873	U813	A753
	G1475	A1413	C1354	G1294	C1234	G1473	C1113	G1053	A994	C934	G874	A814	C754
	G1476	U1414	G1355	G1295	U1235	G1474	C1114	C1054	C995	A935	C875	A815	G755
	G1477	G1415	C1356	C1296	A1236	A1475	C1115	A1055	A996	C936	G876	A816	C756
	C1478	G1416	C1357	C1297	C1237	G1476	U1056	U1056	U997	A937	C877	C817	U757
	G1479	U1417	U1358	C1298	A1238	G1477	G1117	G1057	C998	A938	G878	G818	G758
	C1480	A1418	C1359	A1299	A1239	A1478	C1118	G1058	C999	G939	C879	A819	A759
	U1481	G1419	A1360	G1300	U1240	A1479	C1119	C1059	U1000	G940	C880	U820	G760
	G1482	C1420	G1361	U1301	G1241	G1480	G1120	G1060	A1001	G941	G881	G821	G761
	A1483	G1421	C2361	U1302	C1242	G1481	U1121	G1061	G1002	G942	C882	C822	C762
	C1484	G1422	C1362	C1303	C1243	A1482	U1122	U1062	C1003	G943	C883	C823	G763
	U1485	G1423	A1363	G1304	C1244	G1483	U1123	G1063	G2003	G944	U884	C824	C764
	G1486	C1424	U1364	G1305	A1245	G1484	G1124	G1064	A1004	G945	G885	G825	G765
	G1487	U1425	G1365	A1306	C1246	G1485	U1125	U1065	A1005	A946	G886	C826	A766
	G1488	C1426	C1366	U1307	U1247	G1486	G1126	C1066	C1006	G947	G887	U827	A767
	U1489	U1427	C1367	U1308	A1248	G1487	G1127	A1067	C1007	C948	G888	A828	A768
	C1490	A1428	G1368	G1309	C1249	A1488	U1128	G1068	G1008	A949	A889	G829	G769
	G1491	C1429	C1369	G1310	A1250	G1489	C1129	C1069	U1009	U950	G890	G830	C770
	A1492	C1430	G1370	G1311	A1251	A1490	U1130	G1070	G1010	G951	U891	U831	G771
	A1493	C1431	G1371	G1312	A1252	C1491	G1131	C1071	G1011	U952	A892	C832	U772
	G1494	A1432	U1372	C1313	G1253	G1492	C1132	U1072	U1012	G953	C893	U833	G773
	U1495	C1433	G1373	C1314	C1254	U1493	U1073	G1073	G894	C854	G894	C834	G774
	C1496	A1434	U1374	U1315	G1255	C1494	G1074	A1014	G895	U956	G895	U835	G775
	G1497	G1435	A1375	G1316	A1256	U1495	C1075	A1015	C896	U957	C896	G836	G776
	U1498	U1436	U1376	G1317	U1257	G1496	U1136	A1016	C897	U957	C897	G837	A777
	A1499	C1437	A1377	A1318	G1258	G1497	C1137	G1077	G898	A958	G898	C838	G778
	U1500	G1438	C1378	A1319	C1259	U1498	U1138	U1078	C899	A959	G899	G839	C779
	C1501	A1439	G1379	C1320	U1260	G1499	G1139	G1079	A900	U960	G900	G840	A780
	A1502	C1440	U1380	C1321	A1261	A1501	C1140	A1080	U1020	U961	A901	C841	A781
	G1503	G1441	U1381	C1322	C1262	G1502	G1141	G1081	G1021	C962	G902	U842	C782
	C1504	G1442	C1382	G1323	C1263	C1503	C1142	G1082	G1022	G963	G903	C843	C783
	G1505	C1443	C1383	A1324	C1264	A1504	G1143	U1083	G1023	A964	C904	A844	C784
	U1506	A1444	C1384	C1325	G1265	U1505	G1144	U1084	U1024	A965	U905	A845	G785
	G1507	A1445	C1385	C1326	G1266	G1506	G1145	U1085	U1025	G966	G906	G846	G786
	A1508	A1447	G1386	C1327	C1267	G1507	A1146	U1086	G1026	C967	A907	C847	A787

● Molecule 1: 16S ribosomal RNA



G509	G1387	G1328	A1268	C1208	G1147	G1087	C1027	A968	A908	G948
U510	C1388	A1329	A1269	C1209	U1148	G1088	C1028	A969	A909	C949
U511	C1389	U1330	G1270	U1210	U1149	G1089	U1029	A970	C910	U950
U512	A1451	G1331	G1271	U1211	U1150	G1090	U1030	G971	U911	G951
A1513	U1391	A1332	G1272	U1212	A1151	U1091	G1031	C972	C912	G952
C1514	G1392	A1333	G1273	A1213	A1152	A1092	G1032	G973	A913	G953
C1515	U1393	G1334	G1274	C1214	C1153	A1093	G1033	A974	A914	G954
G1516	A1394	C1335	A1275	G1215	G1094	U1095	G1034	A975	A915	G955
G1517	C1395	C1336	G1276	G1216	G1155	U1096	A1035	A976	G916	C956
U1518	A1396	G1337	C1277	C1217	G1156	C1097	G1036	A977	G917	C957
A1519	G1397	G1338	U1278	C1218	A1157	C1097	G1037	A978	A918	G958
G1520	A1398	A1339	A1279	A1219	C1158	C1098	C1038	C979	A919	A959
U1521	A1460	A1340	A1280	G1220	U1159	C1099	C1039	C980	U920	A960
U1522	G1462	U1341	U1281	G1221	G1160	C1100	U1040	U981	U921	G961
G1523	G1401	C1342	C1282	G1222	C1161	A1101	A1041	U982	G922	C962
C1524	A1402	G1343	G1283	C1223	A1102	A1102	G1042	A983	A923	U963
G1525	C1403	C1344	C1284	G1224	C1163	C1103	A1043	C984	C924	A964
G1526	C1404	U1345	A1285	A1225	G1164	G1104	A1044	C985	G925	A965
C1527	G1405	A1346	A1286	C1226	C1165	A1105	C1045	A986	G926	C966
U1528	U1406	G1347	A1287	A1227	G1166	C1106	A1046	G987	G927	G967
C1529	C1407	U1348	A1288	C1228	A1167	C1107	G1047	G988	G928	C968
A1530	A1408	A1349	A1289	A1229	A1168	G1108	U1048	C989	G929	G969
G1531	C1409	A1350	G1290	C1230	A1169	C1109	U1049	C990	C930	U970
U1532	U1472	U1351	G1291	G1231	G1171	A1110	G1050	U991	G931	U971
C1533	G1473	C1352	U1292	U1232	C1172	A1111	C1051	U992	C932	A972
A1534	C1411	G1353	G1293	G1233	G1173	C1112	U1052	G993	G933	A973
	A1412	C1354	G1294	U1234	G1174	C1113	C1053	A994	A934	G974
	A1413	G1355	G1295	U1235	G1175	C1114	C1054	C995	A935	C975
	U1414	C1356	G1296	A1236	A1176	C1115	U1055	A996	G936	G976
	G1415	A1357	C1297	C1237	G1177	C1116	U1056	U997	A937	C977
	G1416	A1358	C1298	A1238	G1178	C1117	G1057	G998	A938	G978
	G1417	U1359	A1299	C1239	A1179	C1118	G1058	C999	G939	C979
	A1418	A1360	G1300	U1240	A1180	C1119	C1059	U1000	C940	C980
	U1419	C1361	U1301	G1241	G1181	G1120	C1060	G1001	G941	G981
	G1420	C2361	U1302	C1242	G1182	U1121	G1061	G1002	G942	C982
	G1421	C1362	G1303	C1243	A1183	U1122	U1062	G1003	U943	C983
	G1422	G1363	G1304	G1244	G1184	A1123	C1063	G2003	G944	U984
	G1423	U1364	G1305	A1245	G1185	G1124	G1064	A1004	G945	G985
	C1424	C1365	A1306	C1246	G1186	U1125	U1065	A1005	A946	G986
	U1425	C1366	U1307	U1247	G1187	U1126	C1066	C1006	G947	G987
	G1426	G1367	U1308	A1248	A1188	C1127	C1067	C1007	C948	G988
	G1427	G1368	G1309	C1249	C1189	G1128	G1068	G1008	A949	A989
	A1428	G1369	G1310	A1250	G1190	C1129	C1069	G1009	U950	G990
	C1429	G1370	G1311	A1251	A1191	A1130	U1070	G1010	G951	U991
	C1430	G1371	G1312	A1252	C1192	G1131	C1071	G1011	U952	A992
	G1431	U1372	U1313	G1253	G1193	C1132	G1072	U1012	G953	C993
	G1432	G1373	C1314	C1254	U1194	G1133	U1073	G1013	G954	G994
	A1433	A1374	U1315	G1255	C1195	G1134	G1074	A1014	U955	G995
	C1434	A1375	G1316	A1256	U1196	U1135	C1075	A1015	U956	C996
	G1435	U1376	C1317	U1257	G1197	U1136	C1076	A1016	U957	C997
	U1436	A1377	A1318	G1258	G1198	C1137	G1077	G1017	A958	G998
	C1437	C1378	A1319	C1259	U1199	G1138	U1078	C1018	C999	G999
	G1438	G1379	C1320	G1260	U1200	G1139	G1079	C1019	U960	A900
	C1439	U1380	C1321	A1261	A1201	C1140	A1080	U1020	U961	A901
	C1440	U1381	C1322	C1262	G1202	C1141	G1081	G1021	G962	G902
	G1441	C1382	G1323	C1263	C1203	G1142	U1082	G1022	G963	G903
	G1442	C1383	A1324	C1264	A1204	G1143	U1083	G1023	A964	C904
	G1443	C1384	C1325	G1265	U1205	G1144	U1084	G1024	A965	U905
	U1444	G1385	C1326	G1266	C1206	G1145	U1085	U1025	G966	G906
	A1445	C1386	C1327	C1267	G1207	A1146	U1086	G1026	C967	A907

• Molecule 1: 16S ribosomal RNA

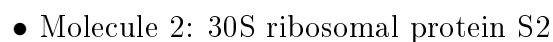
Chain GA: 

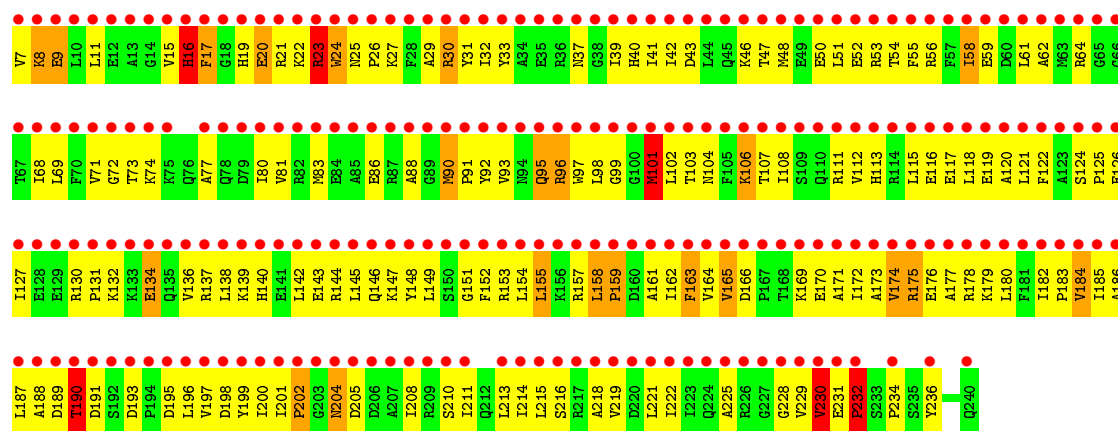
U5	G48
G6	U49
G7	A50
A8	A51
G9	G52
A10	C45
C1514	G46
C1515	G47
G1516	C48
G1517	A49
U1518	A50
A1519	G51
G1520	C58
U1521	A52
U1522	A53
G1523	C54
C1524	A55
G1525	G57
G1526	C59
C1527	A59
U1528	A60
C1529	G61
A1530	U62
G1531	C63
U1532	G64
C1533	
A1534	

A908	G848	U788	A728	G668	A608	G548	A487	G426	C366	G306	A246	C186	G127	U685
A909	C849	U789	A729	U669	A609	C549	C488	U427	U367	C307	G247	G187	G128	G66
C910	U850	A790	G730	G670	G610	C550	C489	U428	U368	C308	C248	C188	U129	C67
U911	G851	G791	G731	G671	A611	U551	C490	U429	U369	G309	U249	A189	G129A	G68
C912	G852	A792	C732	U672	G612	U552	G491	A430	C370	A250	G310	A190	A130	G69
A913	G853	U793	C733	G673	G613	A553	G492	A431	G371	G311	G251	G191	C131	A70
A914	G854	A794	G734	G674	A614	C554	G494	A432	G372	C312	U252	U192	C132	U71
G915	G855	C795	C735	A675	G615	C555	U495	C433	A373	A313	U253	C193	U133	A72
G916	C856	C796	C736	A676	G616	C556	A496	U434	A374	C314	G254	C194	A134	C73
G917	C857	U797	A737	U677	G617	C557	A497	C435	U375	A315	G255	A195	C135	G74
A918	G858	U798	C738	G678	G618	G558	U498	C436	G376	G316	U256	A196	C136	C75
A919	A859	G799	C739	G679	U619	A559	A499	U437	G377	G317	G257	A197	G137	A76
A920	G860	C800	U740	C680	G620	U560	G500	C438	G378	G318	G258	G198	G138	C77
U921	G861	U801	G741	C681	A621	U561	C501	A439	C379	G319	G259	G199	G139	G78
G922	C862	A802	G742	G682	A622	C562	G502	A440	C380	C320	G260	G200	A140	G79
A923	U863	G803	U743	G683	G623	A563	C503	C442	C381	G321	U261	G201	A141	C80
C924	A864	U804	C744	A684	C624	C564	C504	C443	A382	C322	A262	G202	G142	C81
G925	A865	C805	C745	G685	G625	U565	G505	C444	A383	C323	A263	G203	A143	C82
G926	C866	C806	A746	U686	U626	G566	G506	G445	C384	G324	U264	A204	G144	C83
G927	G867	A807	A747	A687	G627	G567	C507	G446	C385	A325	G265	G205	G145	U84
G928	C868	C808	C748	G688	G628	G568	C508	A447	C386	G326	G266	C206	G146	U85
G929	G869	G809	C749	G689	G629	C569	A509	A448	U387	A327	C267	C207	G147	G86
C930	U870	U810	G750	G690	G630	C570	A510	C449	G388	C328	C268	U208	G148	G87
C931	U871	C811	U751	G691	G631	U571	C511	G450	A389	A329	C269	U209	A149	G88
A932	A872	G812	G752	U692	A632	A572	U512	A451	C390	C330	A270	C210	C150	G89
G933	C873	U813	A753	G693	G633	A573	C513	A452	G391	G331	C271	G211	A151	C90
C934	C874	A814	C754	A694	G634	A574	C514	A453	G392	G332	C272	G212	A152	C91
A935	G875	A815	G755	A695	G635	G575	G515	C454	A393	G333	C273	G213	C153	G92
C936	G876	G816	C756	A696	G636	G576	U516	C455	G394	C334	A274	U214	C154	U93
A937	C877	U817	U757	G697	G637	G577	G517	A456	C395	G335	G275	C215	G155	G94
G938	G878	G818	G758	G698	G638	C578	C518	G457	G396	C336	G276	C216	G156	C96
C939	C879	A819	A759	G699	G639	G579	C519	G458	A397	C337	C277	C217	G157	G97
C940	C880	U820	G760	G700	A640	U580	A520	G459	C398	A338	G278	C218	G158	U98
G941	G881	G821	C761	A701	U641	U581	G521	C460	G399	C339	A279	C219	G159	C99
C942	C882	A822	G762	A702	A642	U582	C522	C461	C400	U340	G280	G220	A160	A101
U943	G883	G823	G763	G703	C643	A583	A523	A462	C401	G341	G281	C221	A161	G102
G944	C884	C824	C764	A704	G644	G584	G524	C463	G402	C342	A282	U222	C162	G103
G945	G885	G825	G765	U705	G645	G585	C525	U464	C403	U343	C283	U223	C163	G104
A946	G886	C826	A766	A706	U646	C586	C526	C465	U404	A344	G284	C224	U164	G105
G947	C887	U827	A767	C707	C647	G587	G527	A466	U405	C345	G285	C225	C165	C106
C948	G888	A828	A768	G708	A648	G588	C528	U467	G406	G346	G286	G226	G166	G107
A949	A889	G829	G769	A709	G649	C589	G529	A468	U407	G347	U287	G227	G167	G108
U950	G890	C830	C770	G710	G650	C590	G530	C469	A408	G348	A288	A228	G168	A109
G951	U891	U831	G771	U711	G651	U591	U531	U470	G409	A349	G289	U229	C169	C110
C952	A892	G832	U772	A712	U652	G592	A532	G471	G410	G350	C290	G230	U170	G111
G953	C893	U833	G773	G713	A653	G593	A533	C472	A411	G351	C291	G231	A171	G112
C954	G894	C834	G774	G714	G654	G594	U534	C473	A412	C352	G292	G232	A172	G113
U955	G895	U835	G775	A715	A655	C595	A535	U474	G413	A353	G293	C233	U173	U114
G956	C896	G836	G776	A716	C556	G596	G536	C475	A414	G354	U294	C234	G174	G115
U957	C897	G837	A777	C717	G657	G597	G537	U476	A415	C355	C295	C235	C175	A116
A958	G898	C838	G778	G718	G658	U598	G538	G477	G416	A356	U296	G236	C176	G117
C959	C899	U839	C779	A719	U659	C599	A539	A478	C417	G357	G297	C237	G177	U118
U960	A900	G840	G780	C720	G660	C600	G540	C479	C418	A298	G298	G238	A178	A119
U961	U901	A841	A781	U801	G661	C601	G541	U480	C419	U359	G299	U239	A179	A120
G962	G902	U842	A782	A602	G662	A602	G542	G481	A620	A360	U300	C240	U180	C121
G963	G903	C843	C783	A603	A663	U603	C543	A482	U421	G361	G301	C241	G181	G122
A964	C904	A844	G784	G604	G664	G604	G544	C483	C422	G362	G302	C242	U182	C123
U965	U905	G845	G785	C545	A665	U605	C545	C484	G423	A363	A303	A243	G183	G124
G966	G906	C846	G786	G546	G666	G606	G546	G485	G424	A364	U304	U244	G184	U125
C967	A907	G847	A787	G547	G667	A607	A547	U486	G425	U365	G305	C245	A185	G126

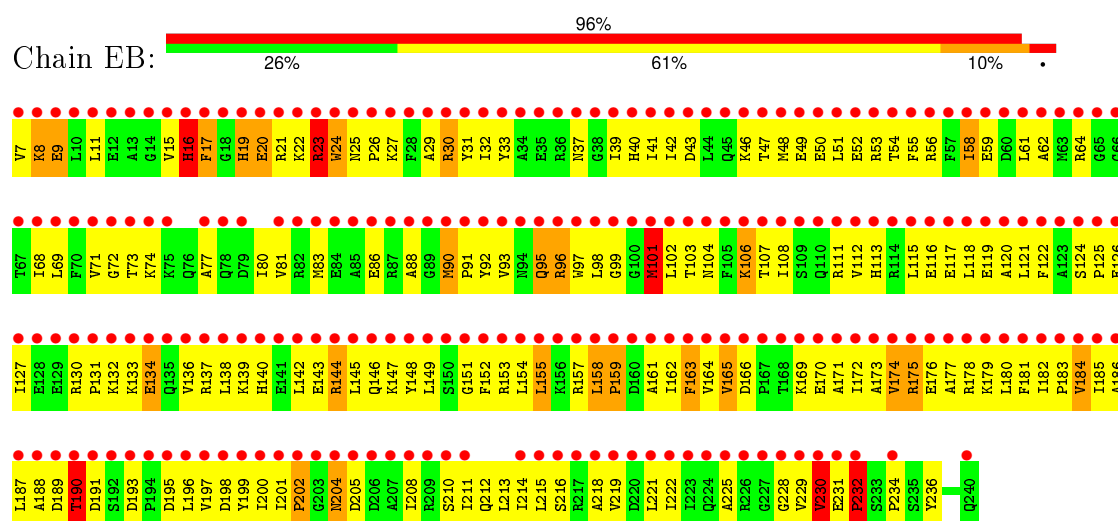


G1027	A968	G848	G788	A608	G548	A487	G426	C366	G306	A246	C186
C1028	A969	C849	U789	A609	C549	C488	U427	U367	C307	G247	G187
U1029	G970	U850	G790	G610	C550	C489	G428	U368	C308	C248	C188
U1030	G971	G851	U791	A611	U551	G490	U429	C369	G309	U249	A189
C1031	C972	C852	A792	G612	U552	G491	A430	C370	G310	A250	A190
G1032	G973	G853	U793	C613	A553	G492	A431	G371	C311	G251	G191
G1033	A974	G854	A794	A614	C554	G494	A432	C372	C312	U252	U192
A975	A975	G855	C795	G615	C555	G495	A433	C373	A313	U253	C193
A1035	G976	G856	G796	G616	C556	G496	U434	A374	C314	G254	C194
G1036	A977	C857	U797	G617	G557	G497	C435	U375	A315	G255	A195
G1037	A978	C858	G798	C618	G558	U498	C436	G376	G316	U256	A196
C1038	A979	A859	G799	U619	A559	A499	U437	G377	G317	G257	A197
C1039	C980	A860	G800	C620	U560	G500	U438	G378	G318	G258	G198
U1040	U981	G861	U801	A621	U561	C501	A439	C379	G319	G259	G199
A1041	U982	C862	A802	G622	C562	G502	A440	C380	C320	G260	G200
A983	A983	U863	G803	C623	A563	C503	U442	C381	C321	U261	G201
C1043	C984	A864	U804	G624	C564	C504	U443	A382	C322	A262	G202
A1044	G985	A865	C805	C625	G565	G505	C444	A383	U323	A263	A203
C1045	A986	C866	C806	U626	G566	G506	U445	G384	G324	U264	A204
A1046	G987	G867	A807	G627	G567	C507	U446	C385	A325	G265	G205
G1047	G988	C868	C808	G628	G568	C508	U447	G386	G326	G266	G206
G1048	G989	G869	G809	G629	C569	A509	U448	U387	A327	C267	C207
U1049	C990	U870	C810	G630	G570	A510	C449	G388	C328	C268	U208
G1050	U991	U871	C811	G631	U571	C511	U450	A389	C329	C269	U209
C1051	U992	A872	G812	A632	A572	U512	A451	C390	C330	A270	C210
U1052	G993	A873	U813	G633	A573	C513	A452	G391	G331	C271	G211
A994	A994	C874	A814	C634	G574	C514	A453	G392	G332	C272	G212
C1054	C995	G875	A815	G635	A575	G515	C454	A393	G333	A273	G213
A1055	A996	G876	A816	U636	G576	U516	U455	G394	C334	A274	U214
U1056	U997	C877	C817	G637	G577	G517	U456	C395	G335	G275	G215
G1057	G998	G878	G818	G638	G578	C518	U457	G396	C336	G276	C216
C1058	C999	C879	A819	G639	G579	C519	U458	A397	C337	C277	C217
U1059	U1000	C880	U820	A640	U580	A520	U459	C398	A338	C278	C218
C1060	A1001	G881	G821	U641	G581	G521	C460	G399	C339	A279	C219
G1061	G1002	C882	C822	A642	U582	C522	U461	C400	U340	C280	G220
U1062	U1003	G883	G823	C643	A583	A523	A462	C401	C341	G281	C221
G1063	G1004	U884	C824	G644	G584	G524	C463	G402	C342	A282	U222
A1064	G1005	G885	G825	G645	G585	C525	U464	C403	U343	G283	U223
U1065	A1006	G886	C826	U646	C586	C526	U465	U404	A344	G284	C224
C1066	G1006	U887	U827	G647	G587	G527	A466	U405	C345	G285	C225
A1067	C1007	G888	A828	A648	G588	C528	U467	G406	G346	G286	G226
G1068	A948	A889	G829	G649	C589	G529	U468	G407	G347	U287	G227
U1069	U950	G890	G830	G650	C590	G530	C469	A408	A348	A288	A228
C1070	G951	U891	U831	G651	U591	U531	U470	G409	A349	G289	U229
G1071	U952	A892	C832	U652	G592	A532	C471	G410	G350	C290	G230
U1072	G953	C893	U833	A653	G593	A533	U472	A411	G351	G291	G231
G1073	G954	G894	C834	G654	G594	U534	C473	A412	C352	G292	G232
U1074	U955	C895	U835	A655	G595	A535	U474	G413	A353	G293	C233
C1075	U956	C896	G836	G656	C596	C536	U475	A414	G354	U294	C234
G1076	U957	C897	G837	G657	G597	G537	U476	A415	C355	G295	C235
U1077	A958	G898	C838	G658	U598	G538	U477	G416	A356	U296	G236
U1078	A959	C899	G839	U659	C599	A539	U478	C417	G357	G297	G237
G1079	U960	A900	C840	G660	G600	A540	C479	A418	A298	A298	G238
A1080	U1020	A901	G841	G661	C601	G541	U480	C419	U359	G299	U239
G1081	C962	G902	U842	G662	A602	G542	U481	G420	A360	A300	C240
U1082	G963	G903	U843	A663	U603	C543	A482	U421	G361	G301	C241
U1083	A964	C904	C844	G664	G604	G544	C483	C422	G362	G302	C242
G1084	G965	U905	A845	A665	U605	C545	G484	G423	A363	A303	A243
U1085	U1025	G906	C846	G666	G606	G546	U485	G424	A364	U304	U244
U1086	G1026	A907	C847	G667	A607	A547	U486	G425	U365	G305	C245

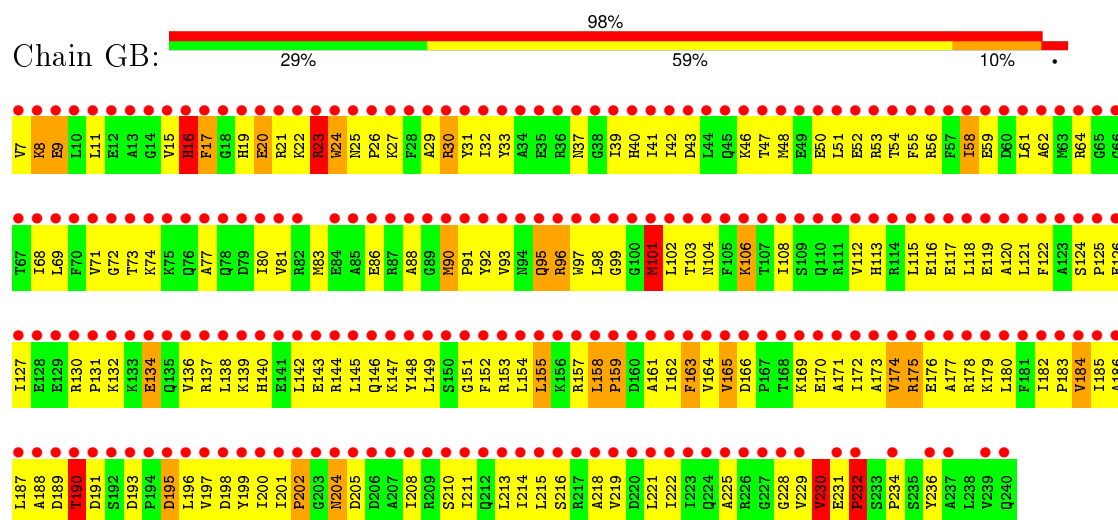




• Molecule 2: 30S ribosomal protein S2



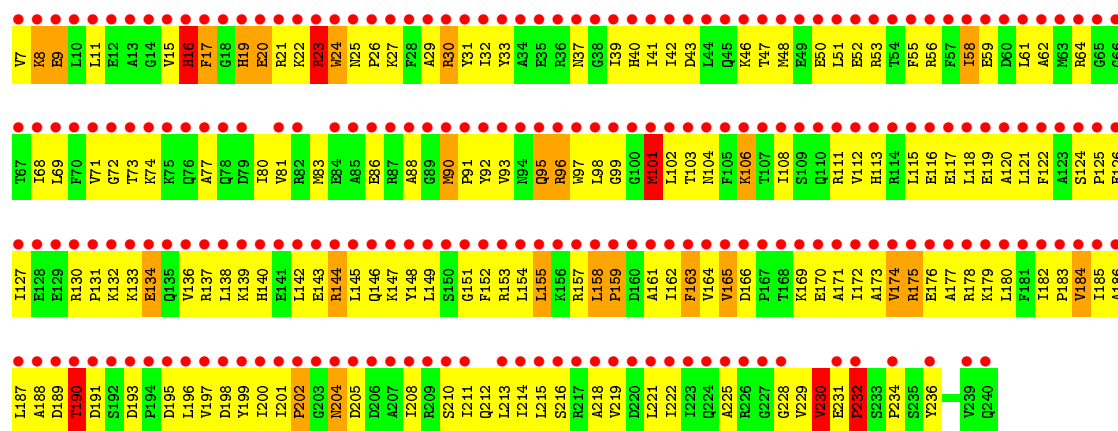
• Molecule 2: 30S ribosomal protein S2



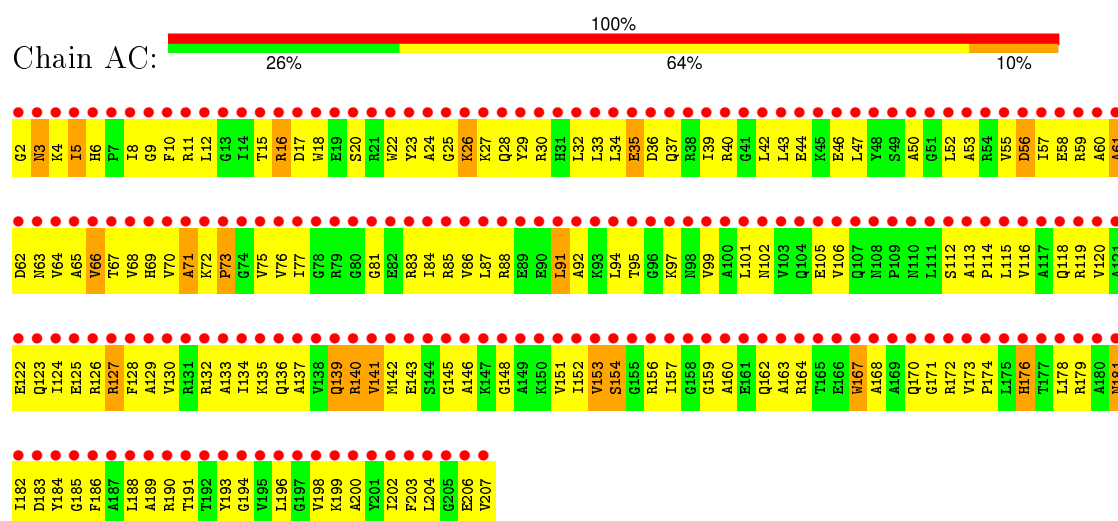
• Molecule 2: 30S ribosomal protein S2



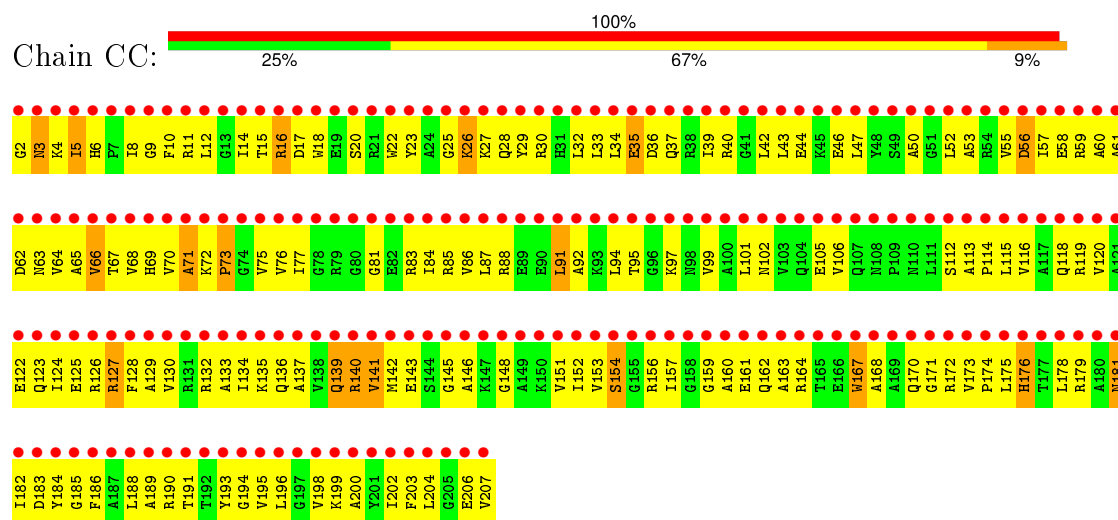




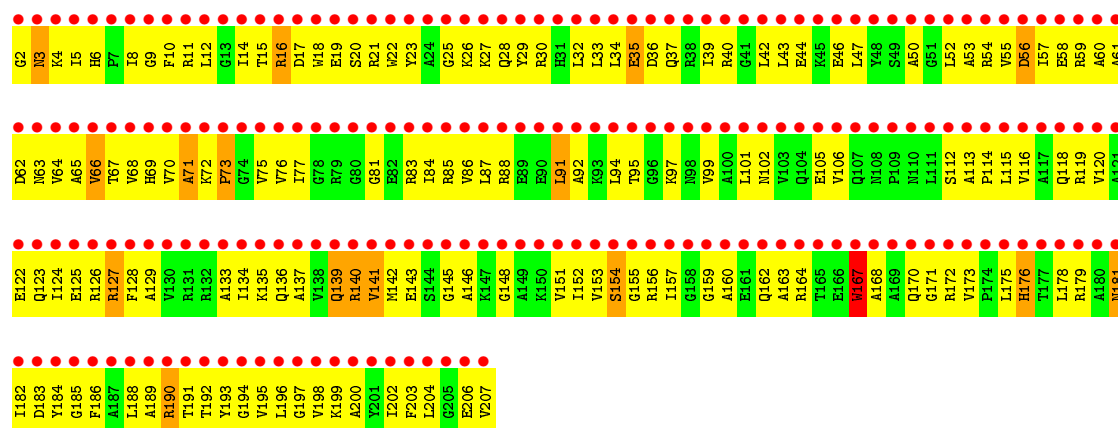
• Molecule 3: 30S ribosomal protein S3



• Molecule 3: 30S ribosomal protein S3



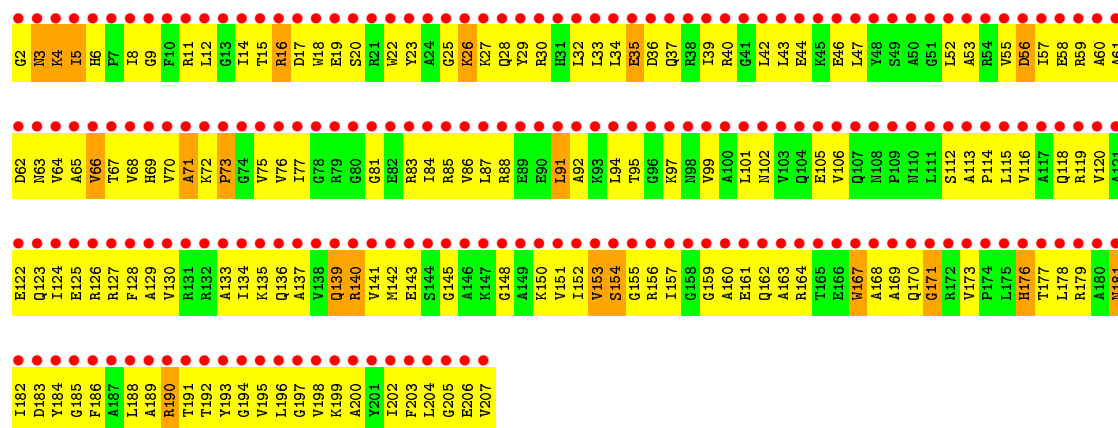
• Molecule 3: 30S ribosomal protein S3



• Molecule 3: 30S ribosomal protein S3

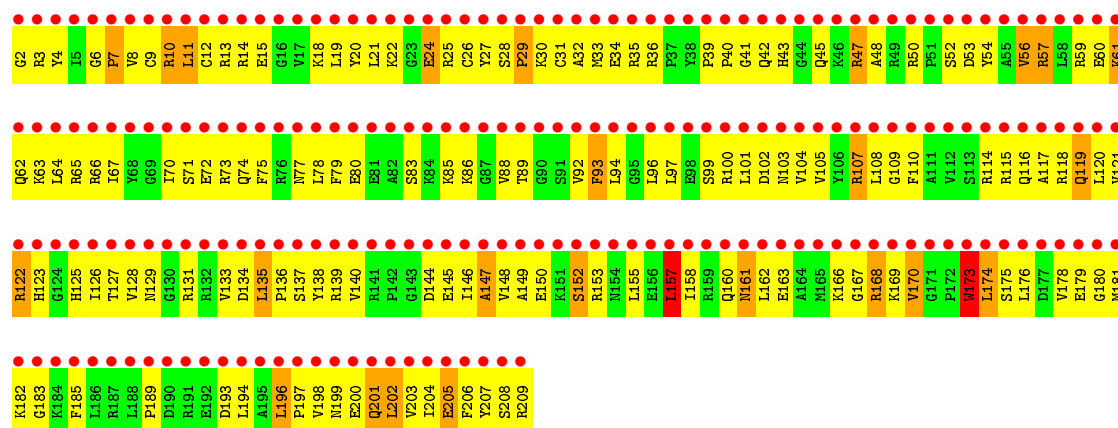


• Molecule 3: 30S ribosomal protein S3

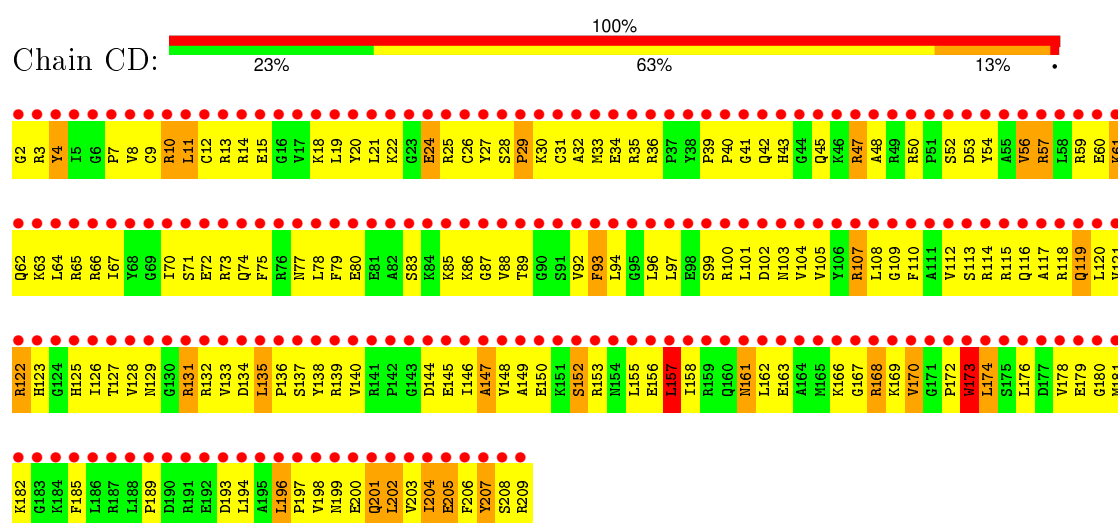


• Molecule 4: 30S ribosomal protein S4

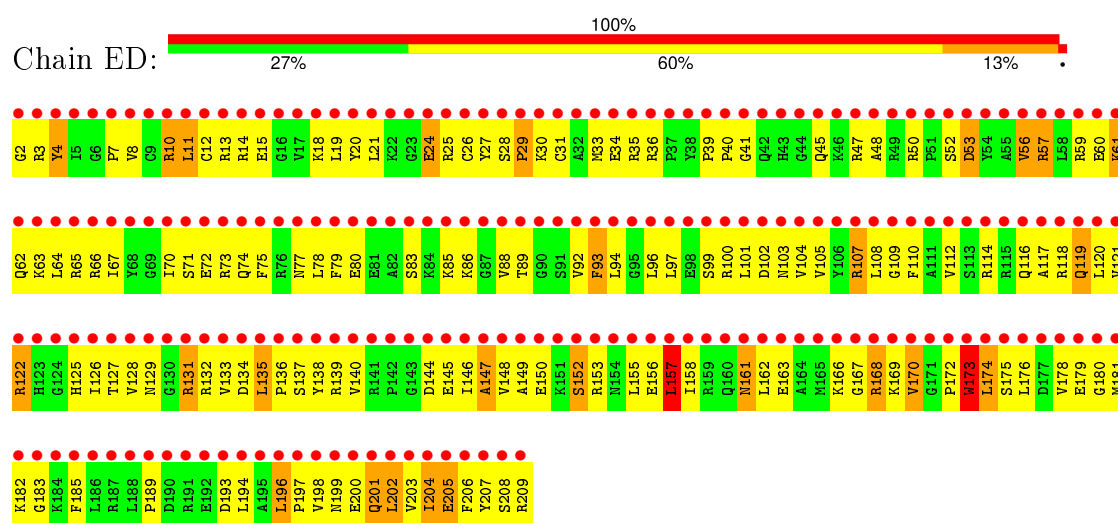




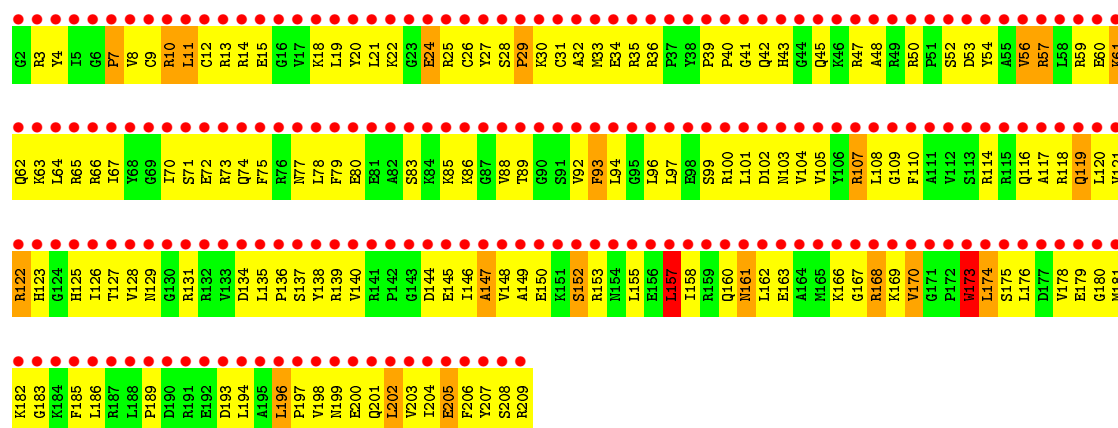
• Molecule 4: 30S ribosomal protein S4



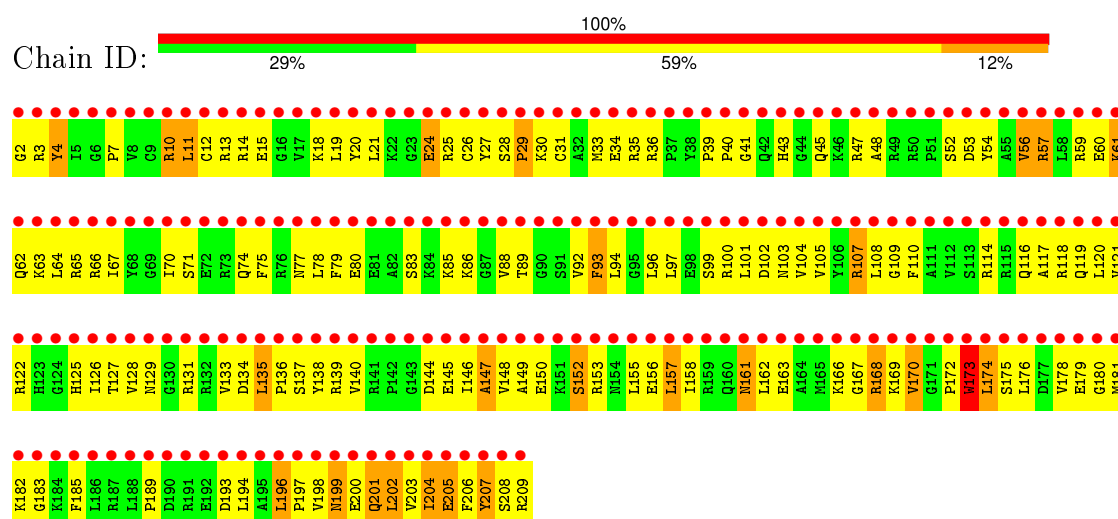
• Molecule 4: 30S ribosomal protein S4



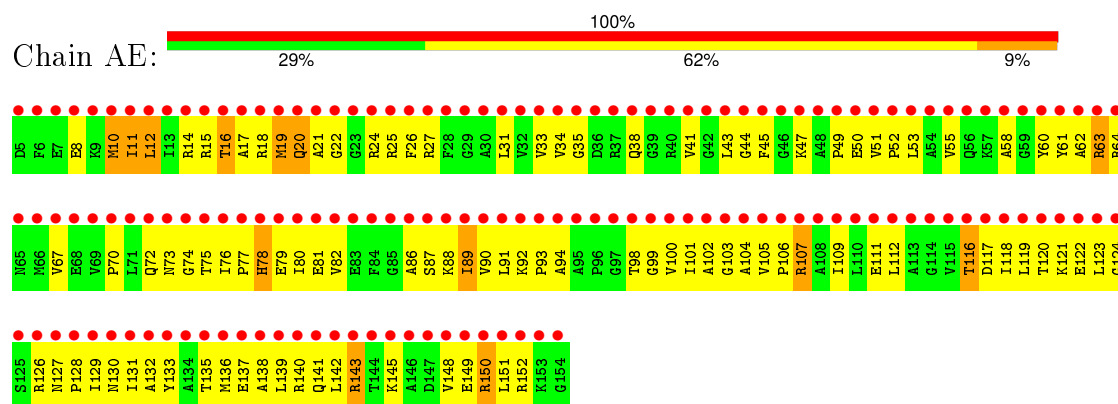
• Molecule 4: 30S ribosomal protein S4



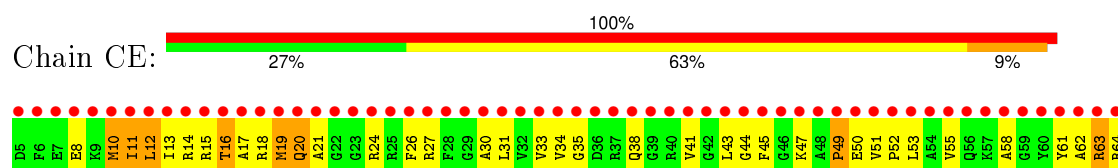
### • Molecule 4: 30S ribosomal protein S4

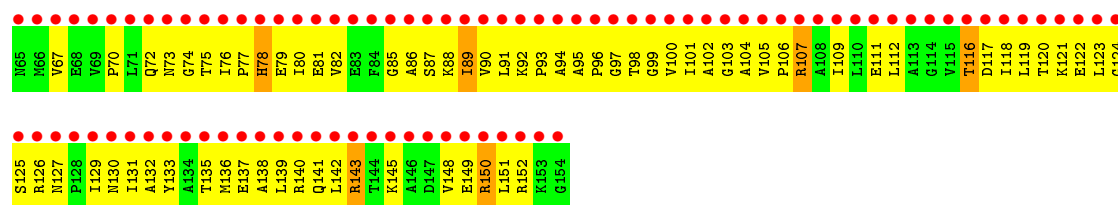


### • Molecule 5: 30S ribosomal protein S5

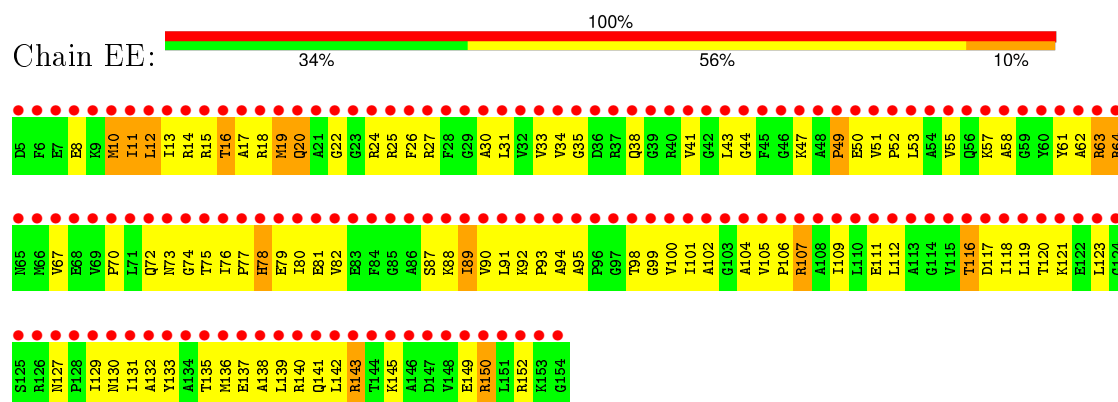


### • Molecule 5: 30S ribosomal protein S5

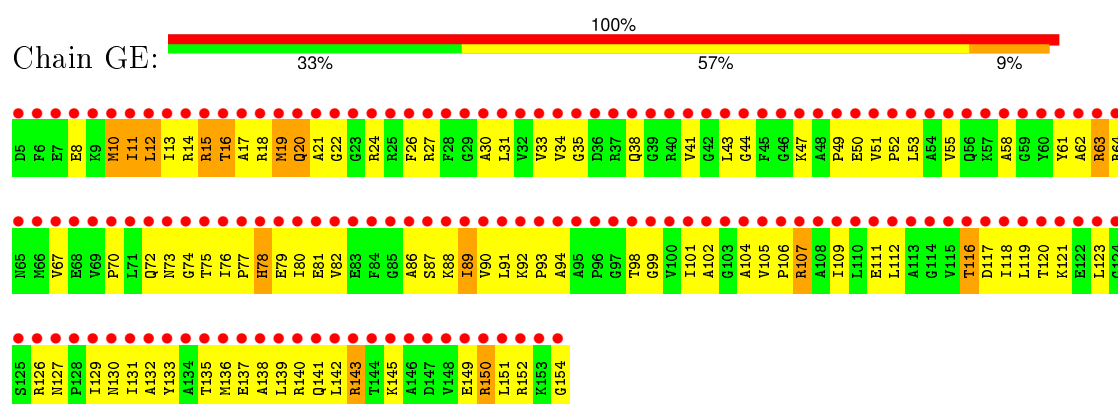




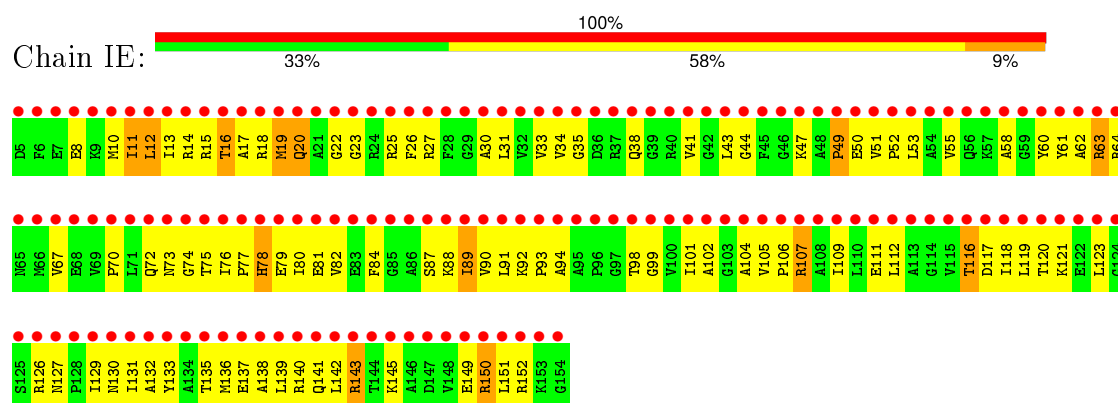
• Molecule 5: 30S ribosomal protein S5



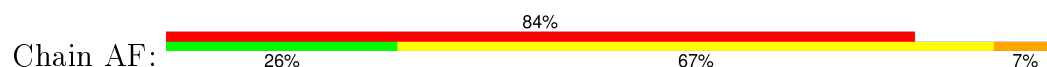
• Molecule 5: 30S ribosomal protein S5

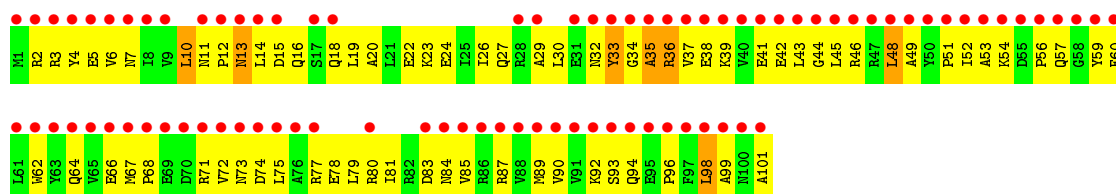


• Molecule 5: 30S ribosomal protein S5

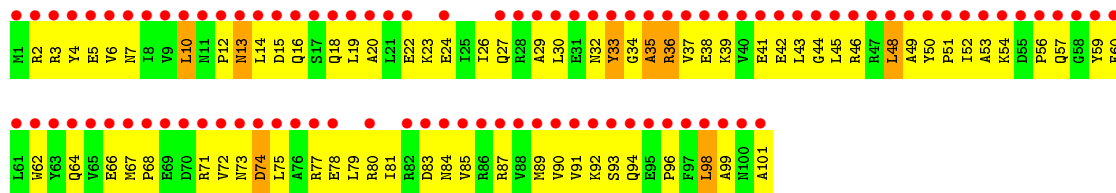


• Molecule 6: 30S ribosomal protein S6

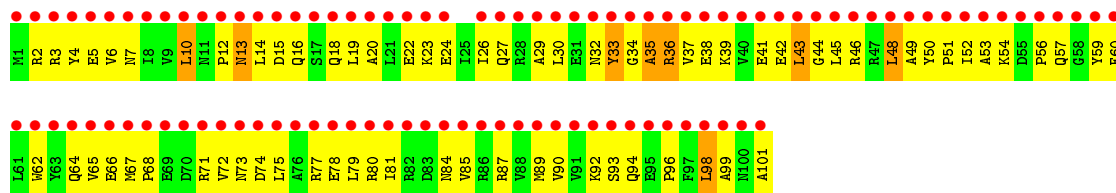




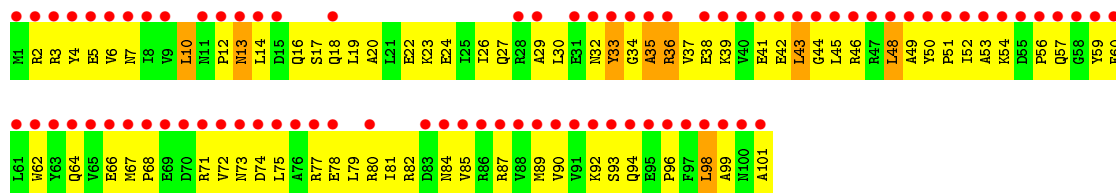
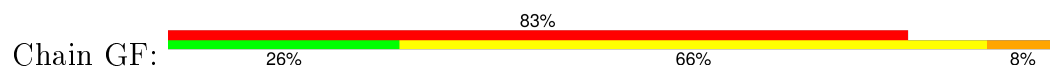
• Molecule 6: 30S ribosomal protein S6



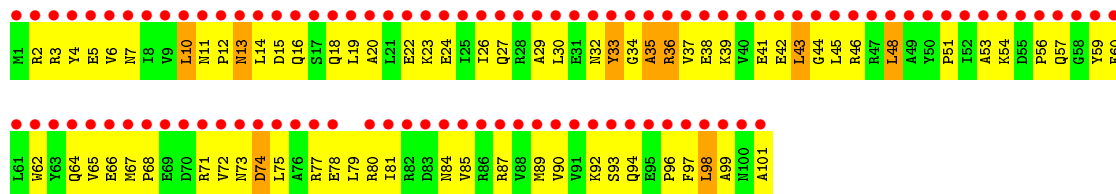
• Molecule 6: 30S ribosomal protein S6



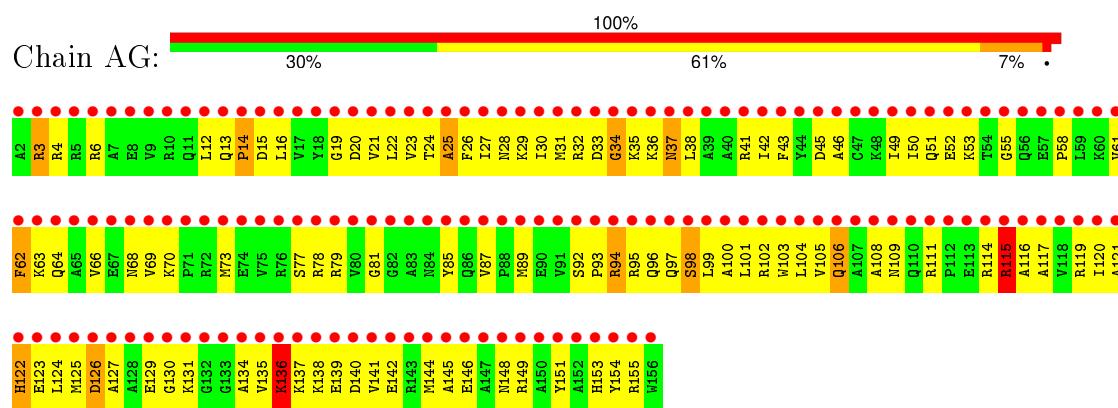
• Molecule 6: 30S ribosomal protein S6



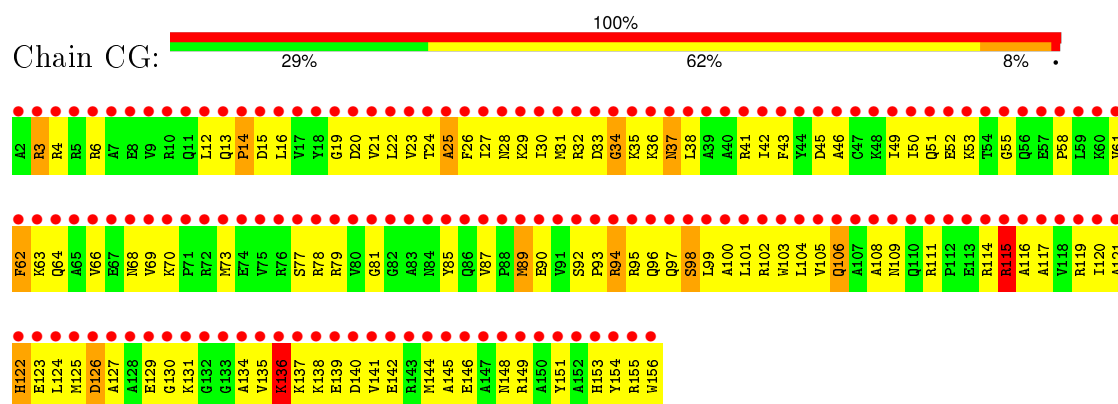
• Molecule 6: 30S ribosomal protein S6



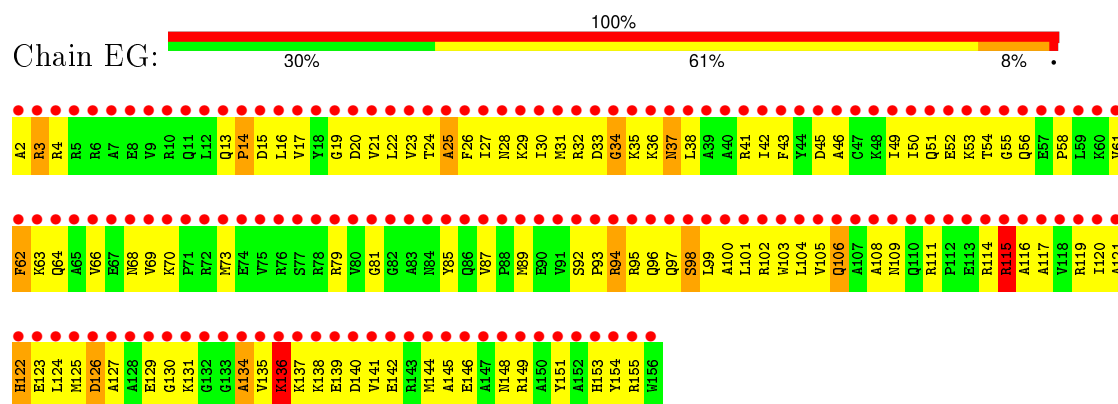
• Molecule 7: 30S ribosomal protein S7



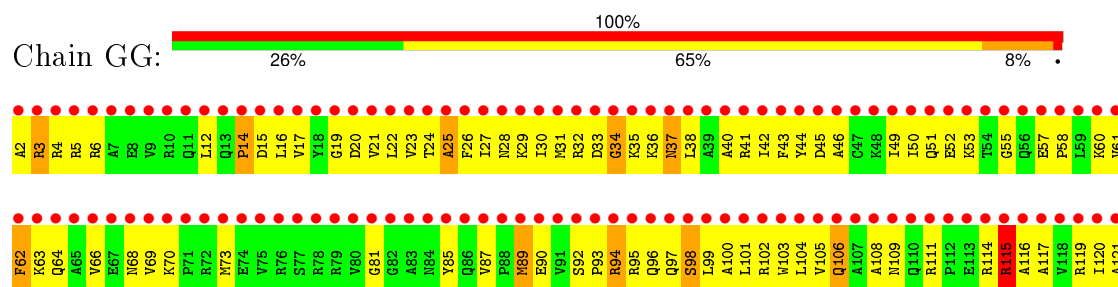
- Molecule 7: 30S ribosomal protein S7



- Molecule 7: 30S ribosomal protein S7

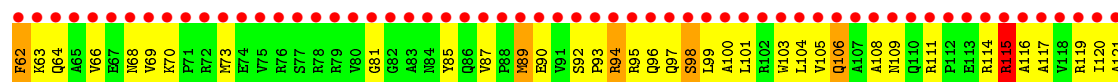
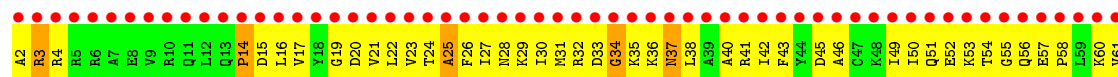


- Molecule 7: 30S ribosomal protein S7

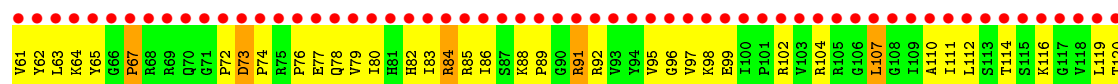
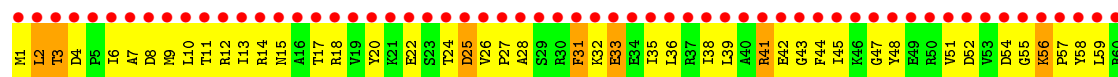




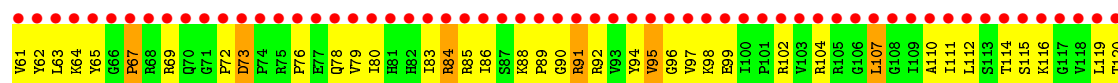
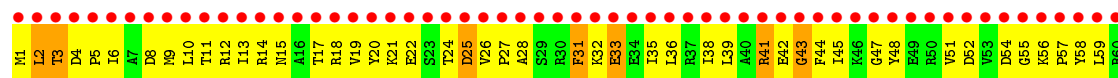
• Molecule 7: 30S ribosomal protein S7



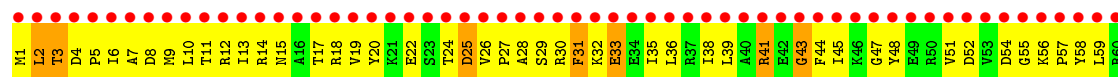
• Molecule 8: 30S ribosomal protein S8



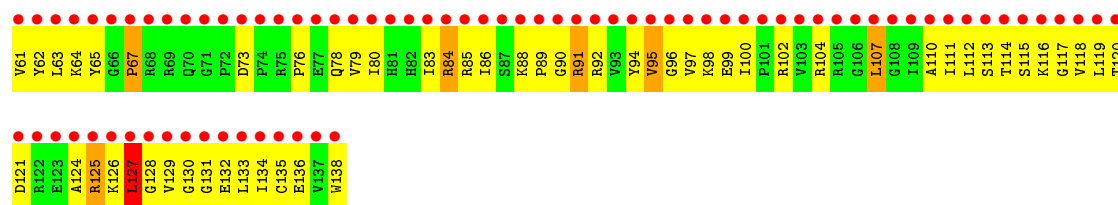
• Molecule 8: 30S ribosomal protein S8



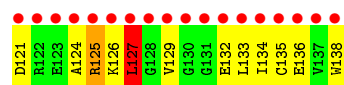
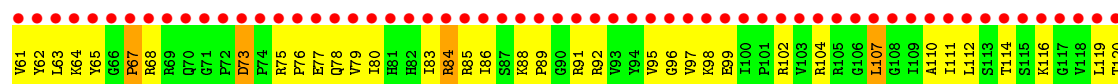
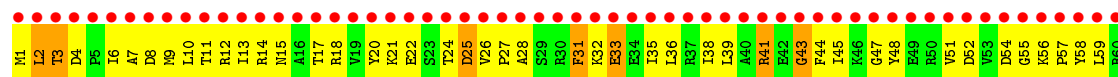
• Molecule 8: 30S ribosomal protein S8



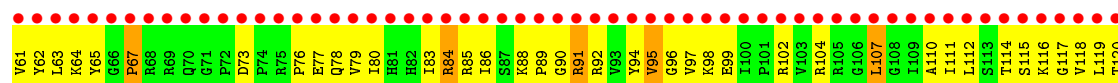
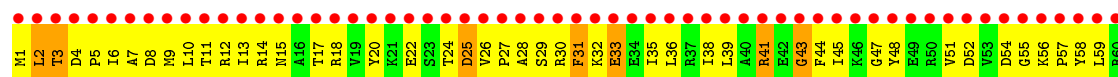




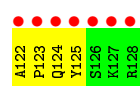
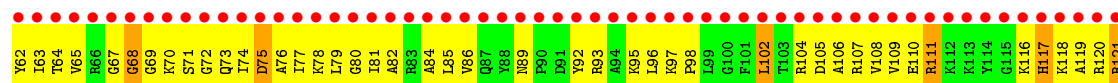
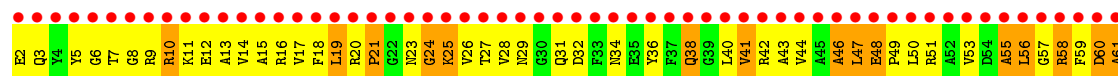
• Molecule 8: 30S ribosomal protein S8



• Molecule 8: 30S ribosomal protein S8

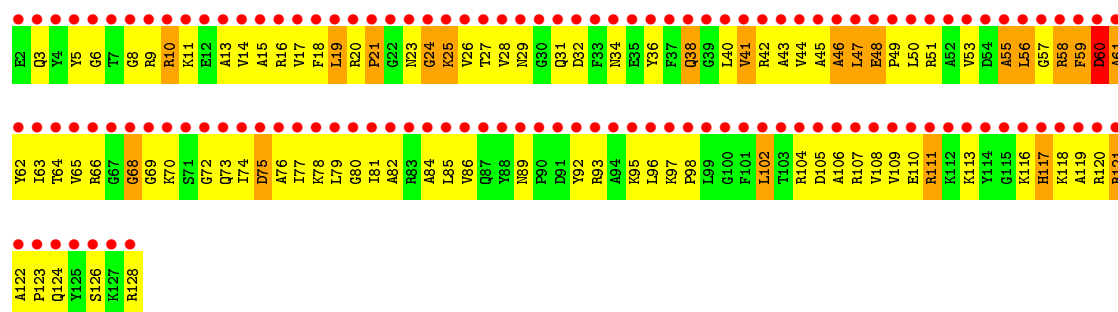


• Molecule 9: 30S ribosomal protein S9

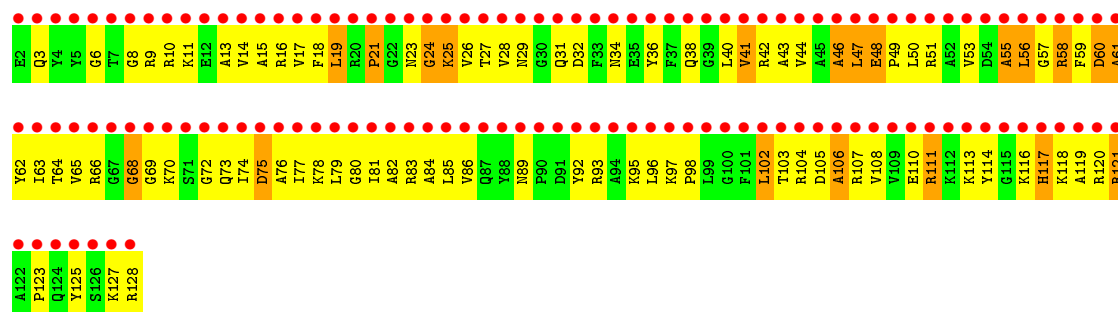


• Molecule 9: 30S ribosomal protein S9

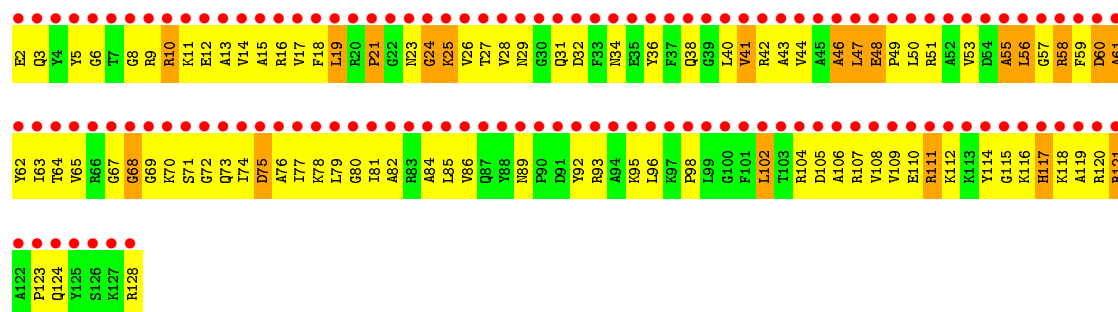




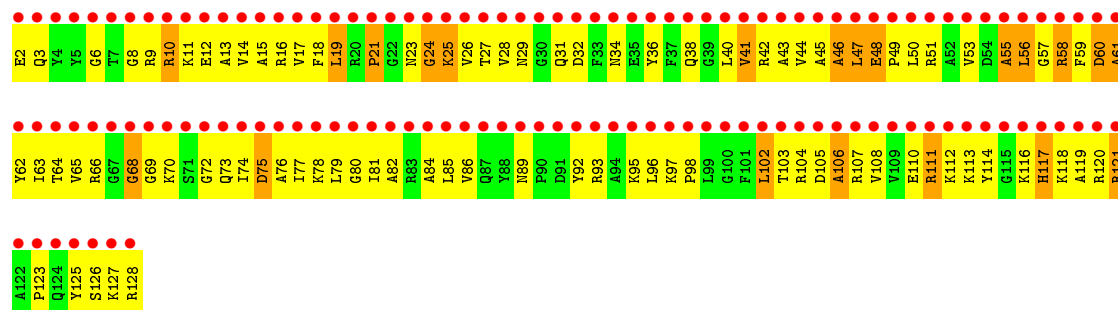
• Molecule 9: 30S ribosomal protein S9



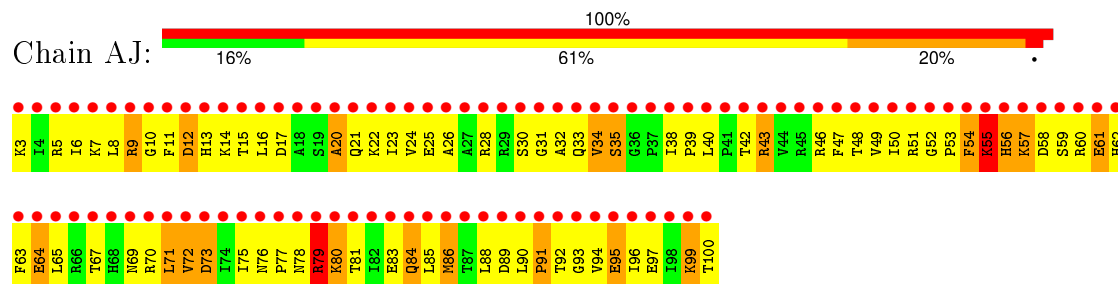
• Molecule 9: 30S ribosomal protein S9



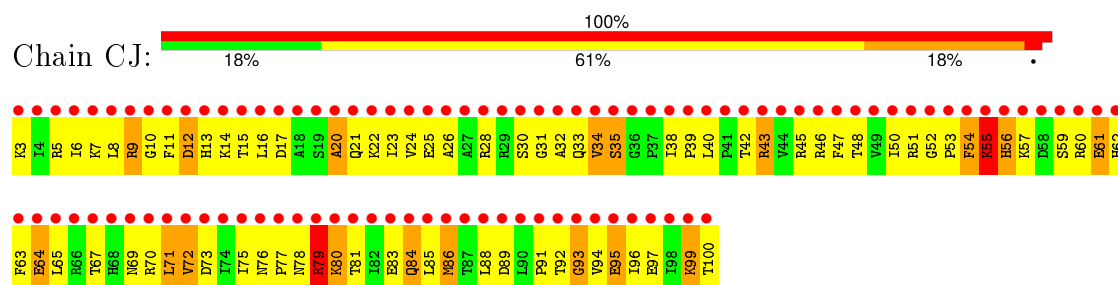
• Molecule 9: 30S ribosomal protein S9



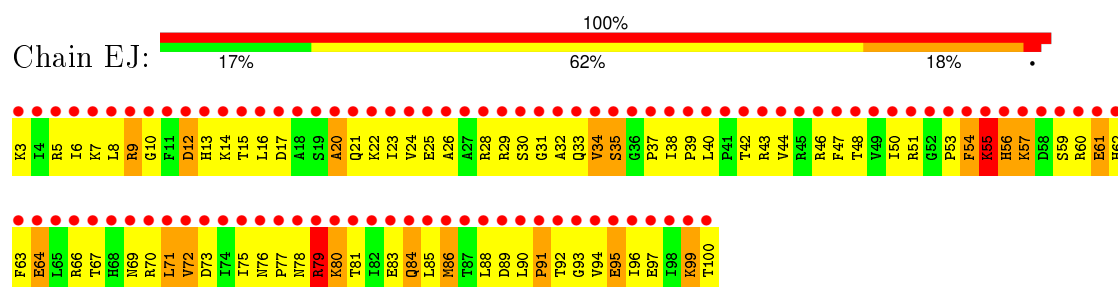
- Molecule 10: 30S ribosomal protein S10



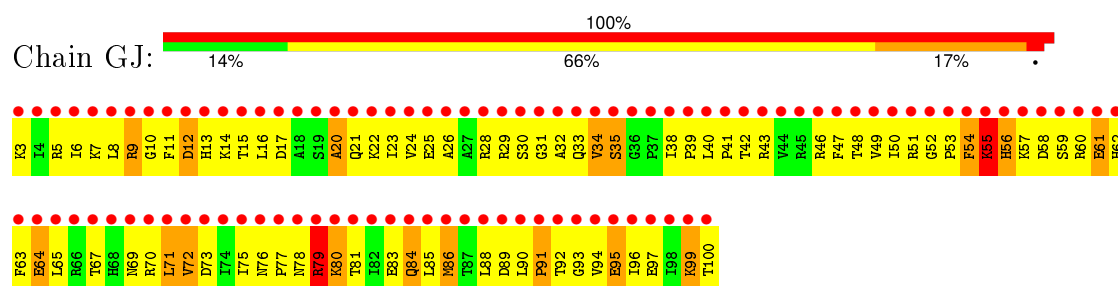
- Molecule 10: 30S ribosomal protein S10



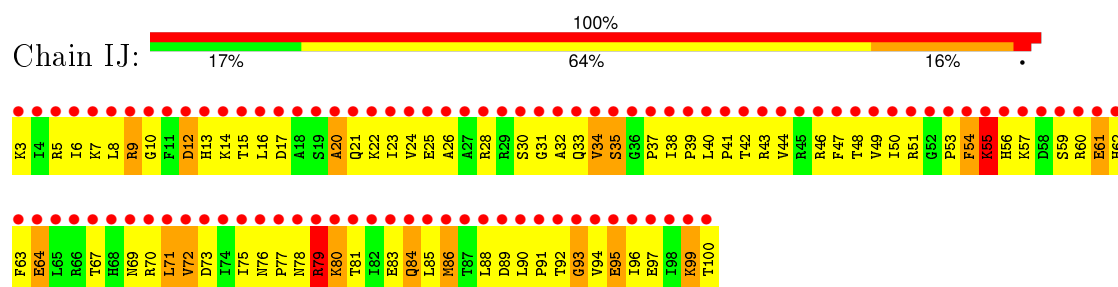
- Molecule 10: 30S ribosomal protein S10



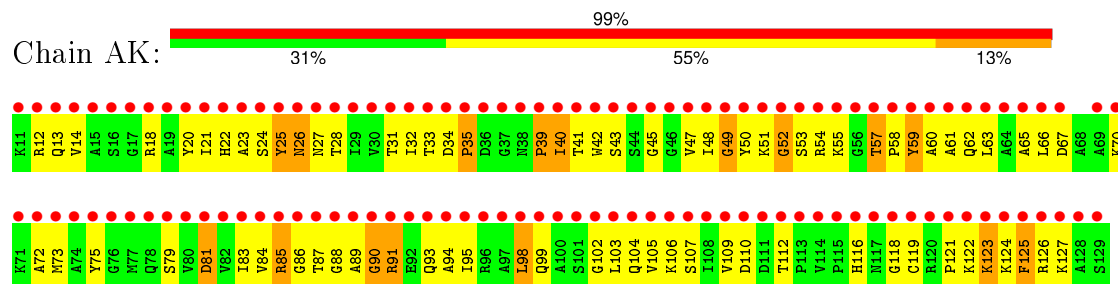
- Molecule 10: 30S ribosomal protein S10



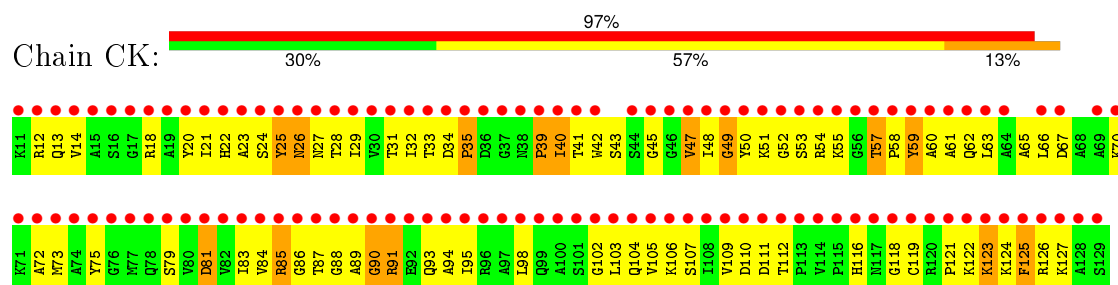
- Molecule 10: 30S ribosomal protein S10



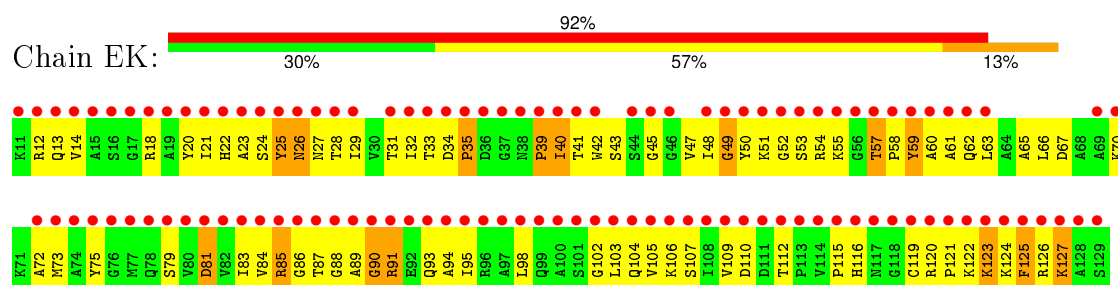
- Molecule 11: 30S ribosomal protein S11



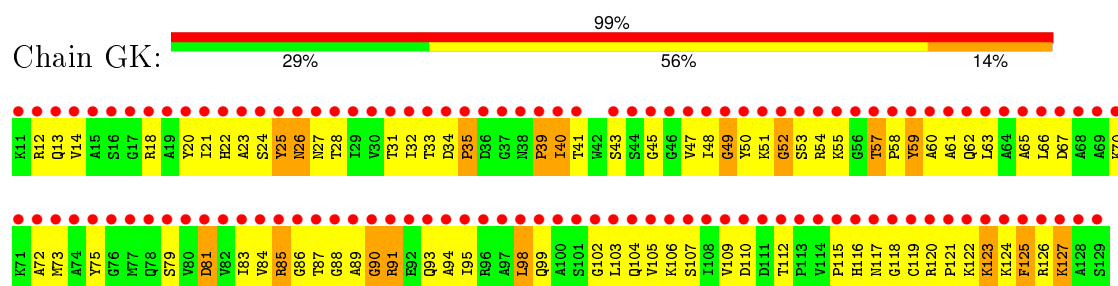
- Molecule 11: 30S ribosomal protein S11



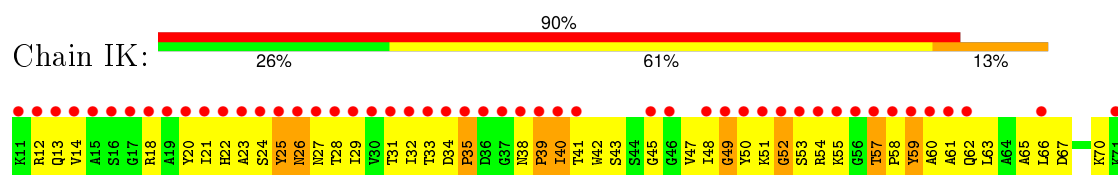
- Molecule 11: 30S ribosomal protein S11

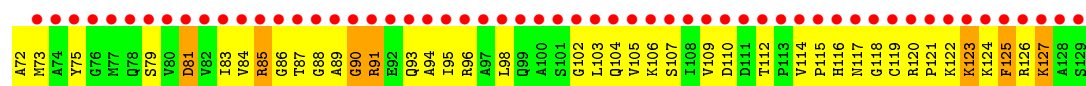


- Molecule 11: 30S ribosomal protein S11

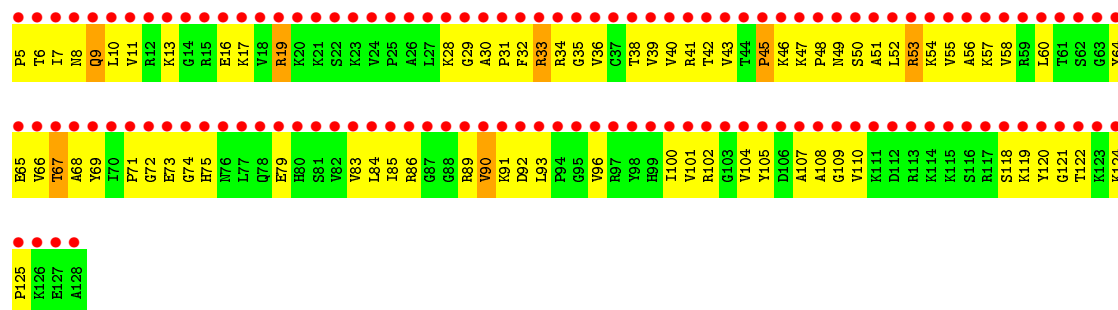


- Molecule 11: 30S ribosomal protein S11

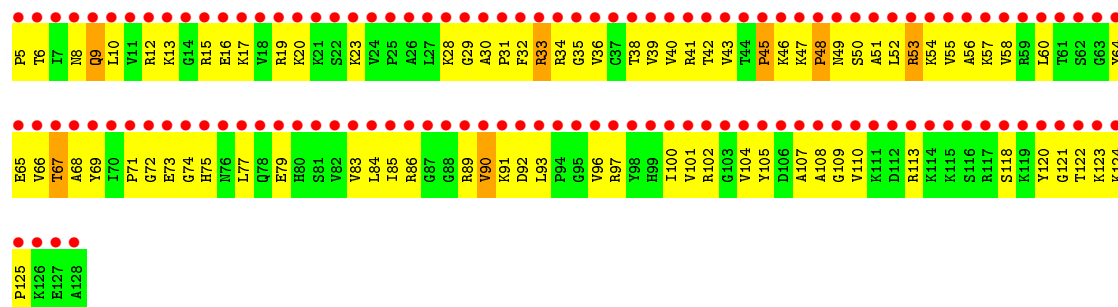




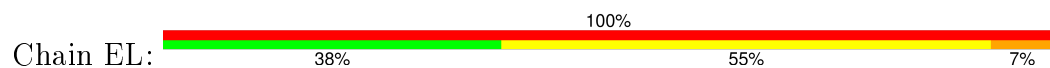
• Molecule 12: 30S ribosomal protein S12



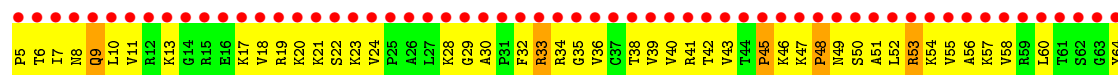
• Molecule 12: 30S ribosomal protein S12

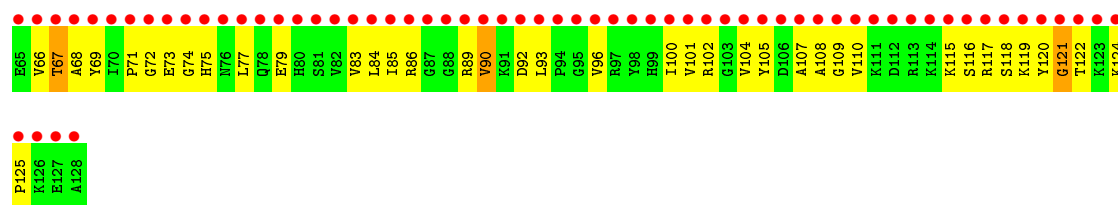


• Molecule 12: 30S ribosomal protein S12

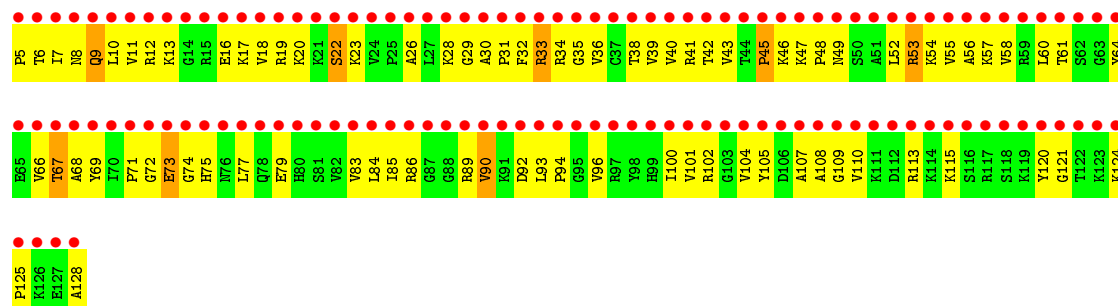


• Molecule 12: 30S ribosomal protein S12

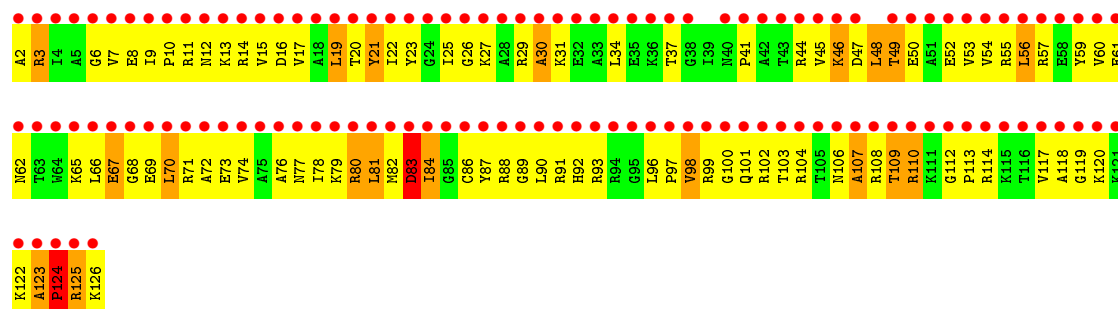




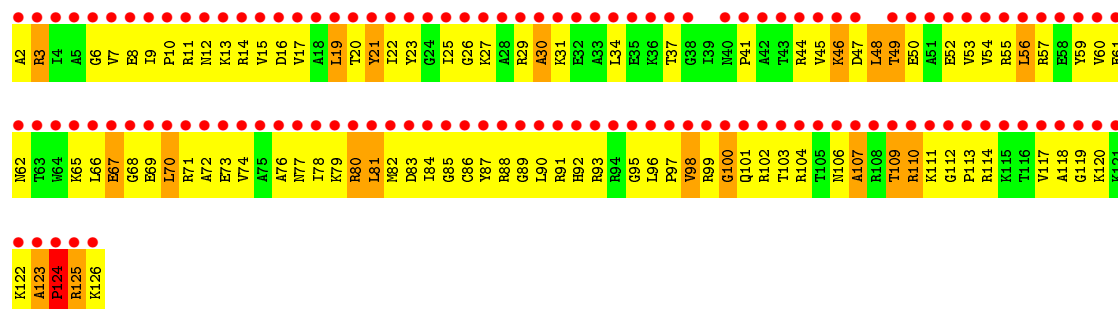
• Molecule 12: 30S ribosomal protein S12



• Molecule 13: 30S ribosomal protein S13

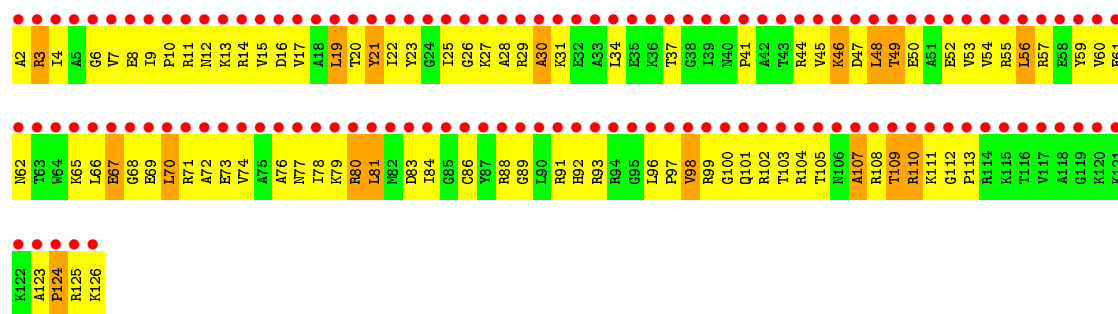


• Molecule 13: 30S ribosomal protein S13

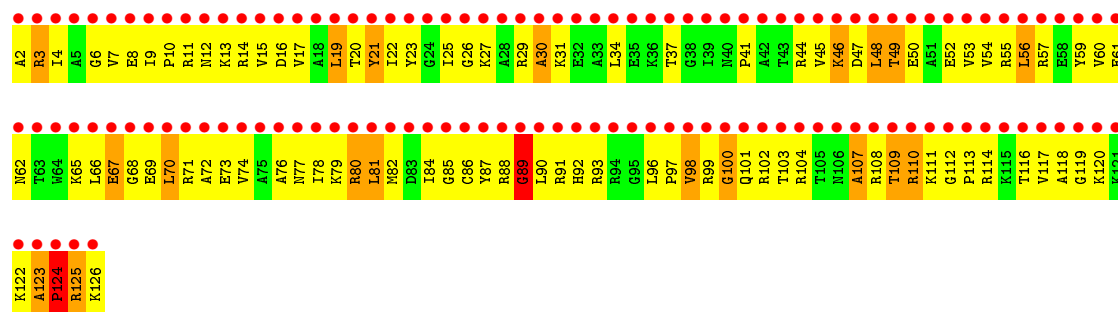


• Molecule 13: 30S ribosomal protein S13

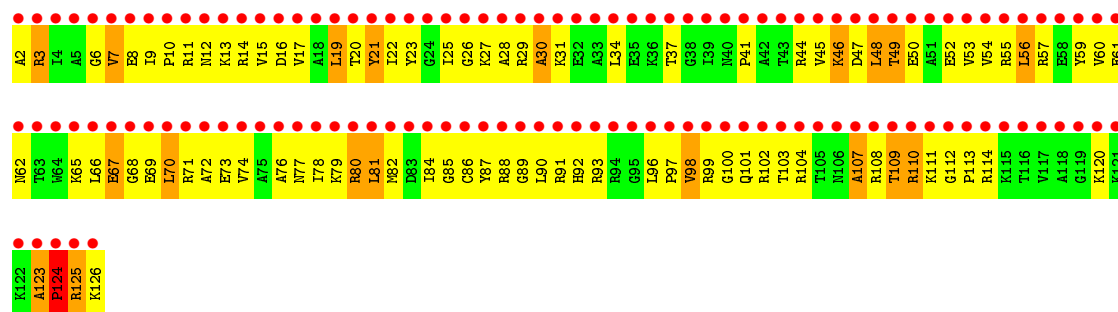




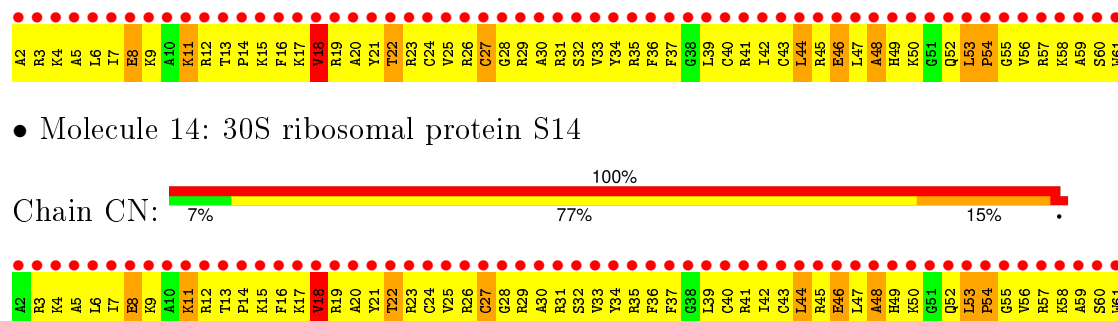
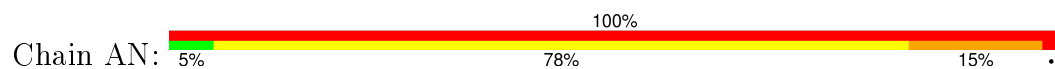
• Molecule 13: 30S ribosomal protein S13



• Molecule 13: 30S ribosomal protein S13



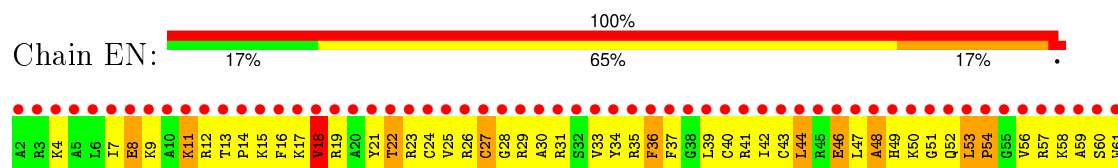
• Molecule 14: 30S ribosomal protein S14



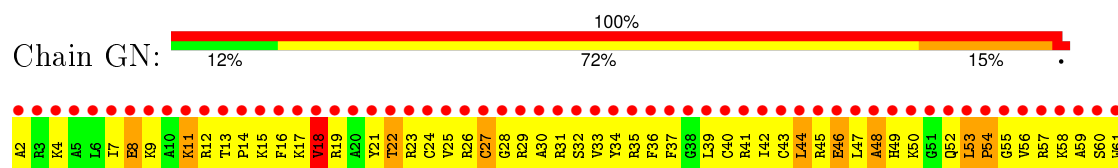
• Molecule 14: 30S ribosomal protein S14



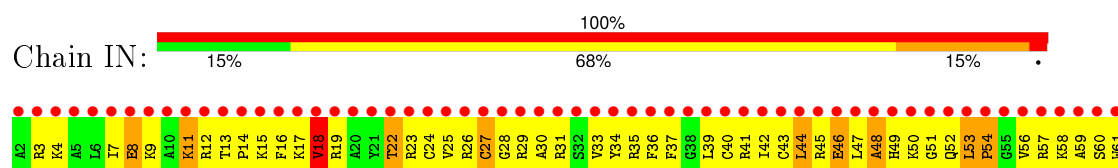
- Molecule 14: 30S ribosomal protein S14



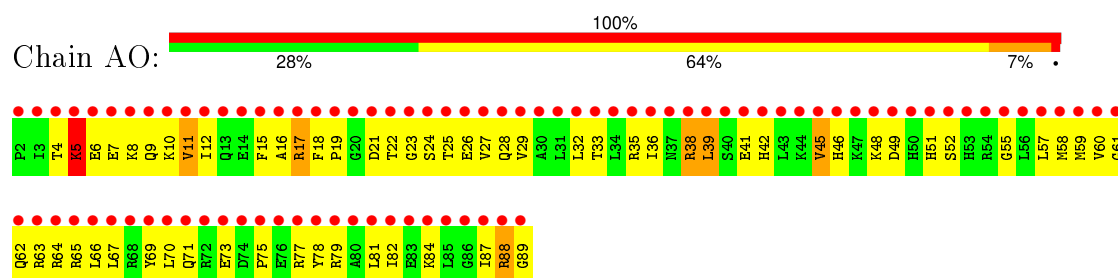
- Molecule 14: 30S ribosomal protein S14



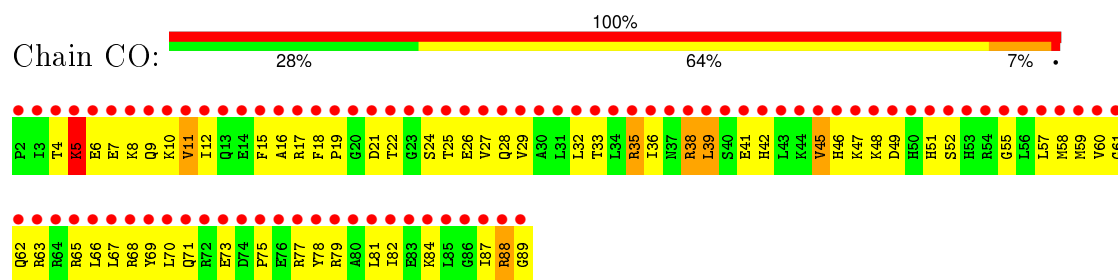
- Molecule 14: 30S ribosomal protein S14



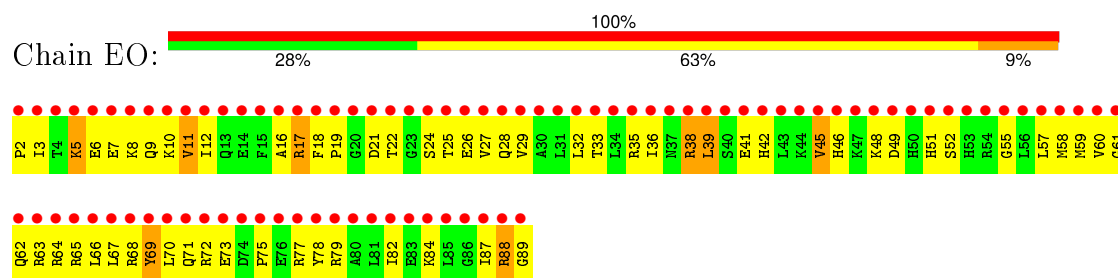
- Molecule 15: 30S ribosomal protein S15



- Molecule 15: 30S ribosomal protein S15

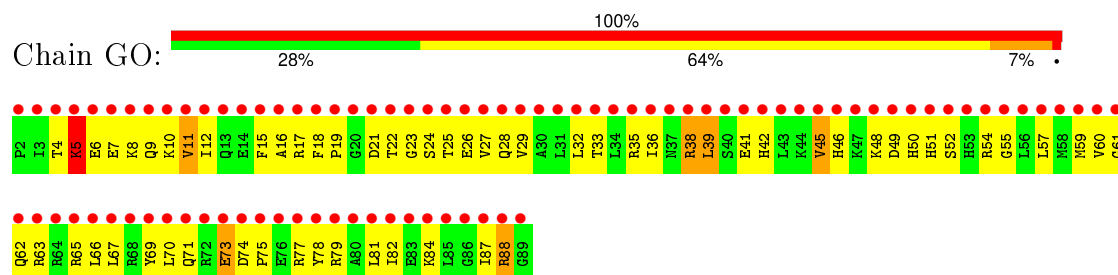


- Molecule 15: 30S ribosomal protein S15

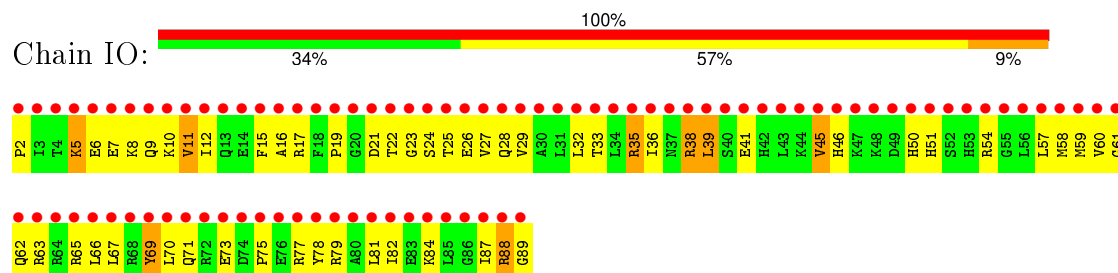




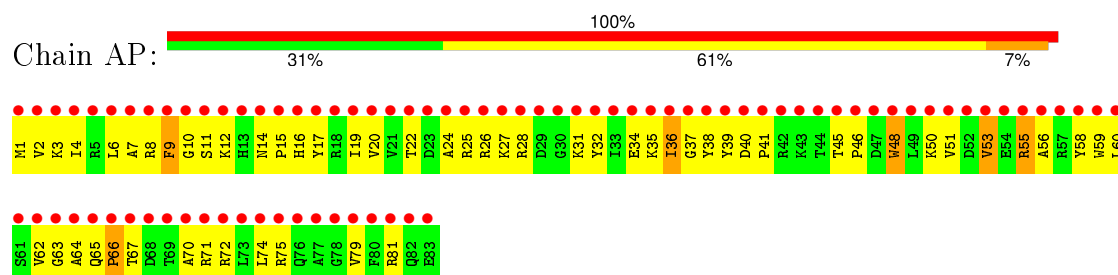
- Molecule 15: 30S ribosomal protein S15



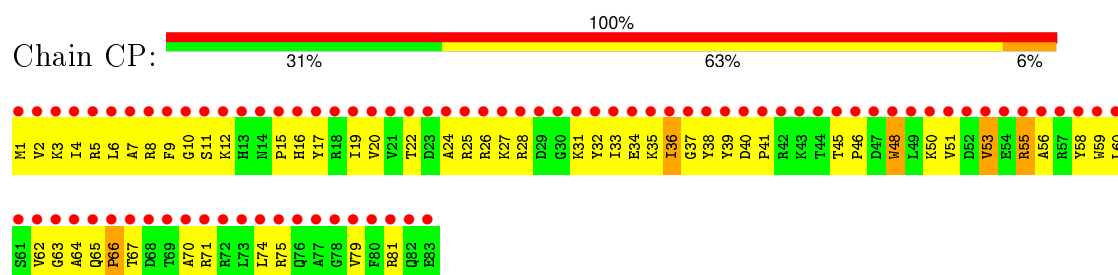
- Molecule 15: 30S ribosomal protein S15



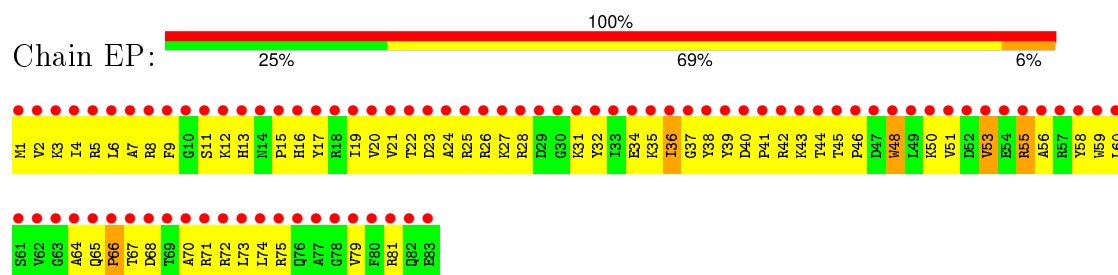
- Molecule 16: 30S ribosomal protein S16



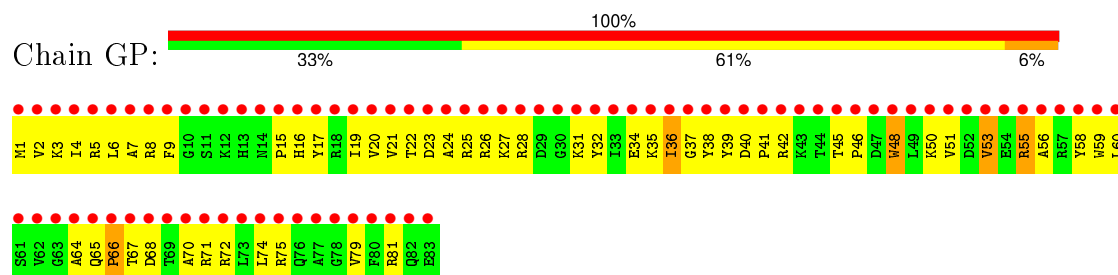
- Molecule 16: 30S ribosomal protein S16



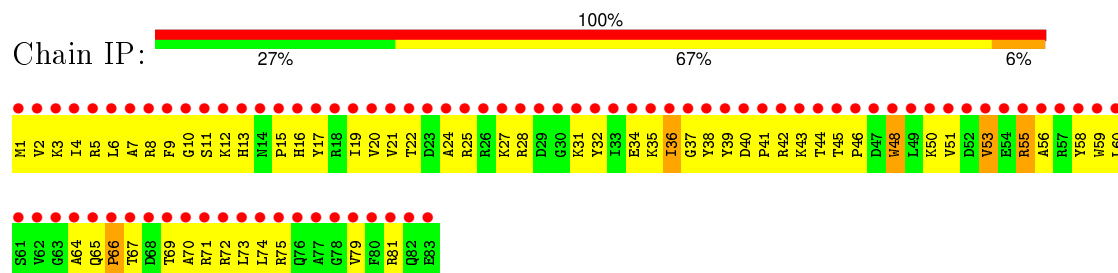
- Molecule 16: 30S ribosomal protein S16



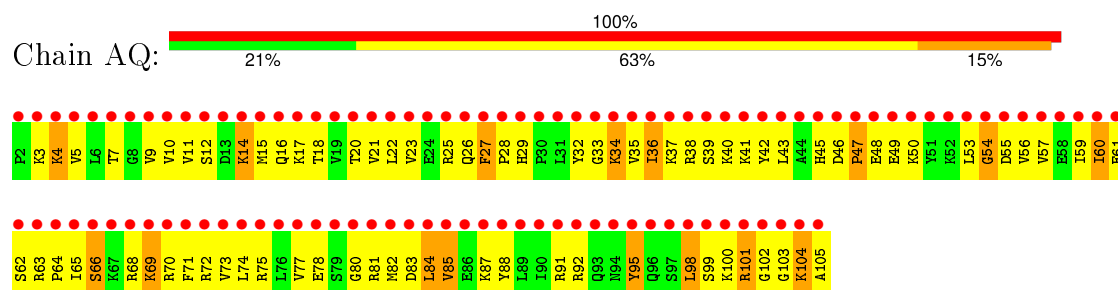
- Molecule 16: 30S ribosomal protein S16



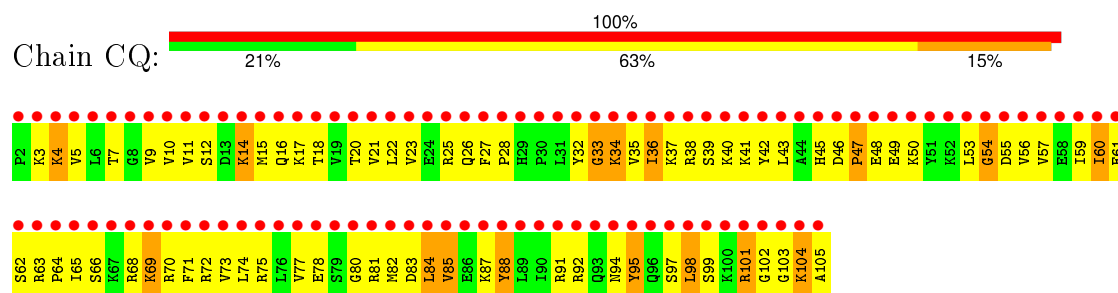
- Molecule 16: 30S ribosomal protein S16



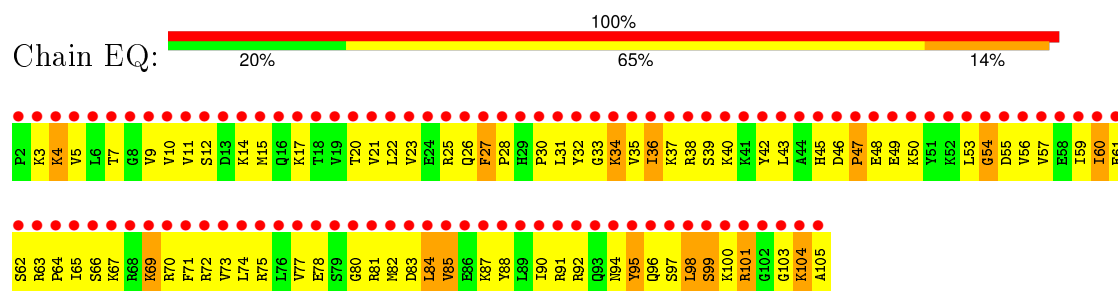
- Molecule 17: 30S ribosomal protein S17



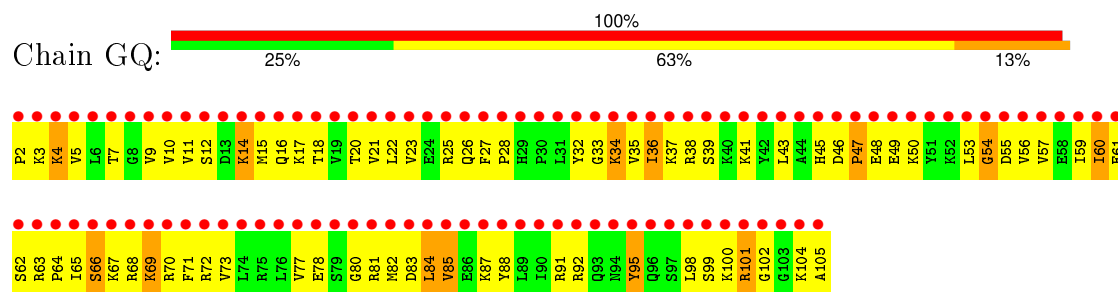
- Molecule 17: 30S ribosomal protein S17



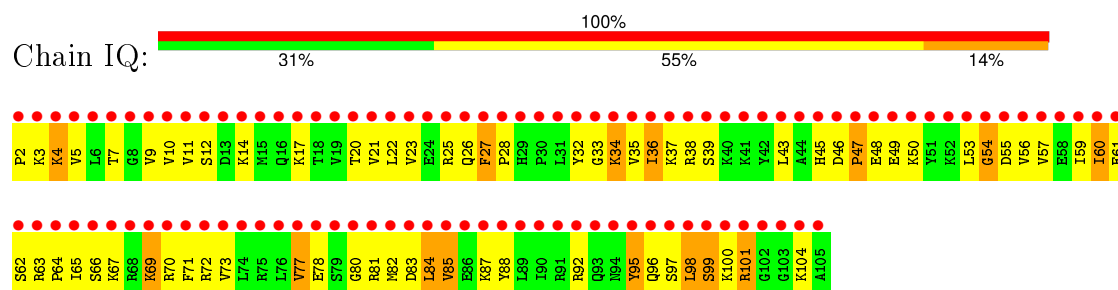
- Molecule 17: 30S ribosomal protein S17



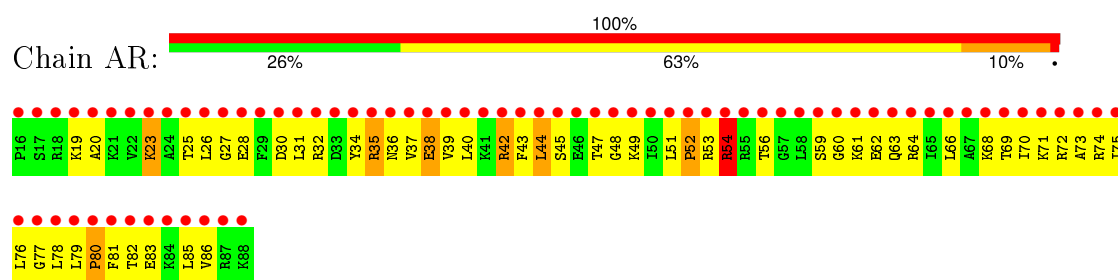
- Molecule 17: 30S ribosomal protein S17



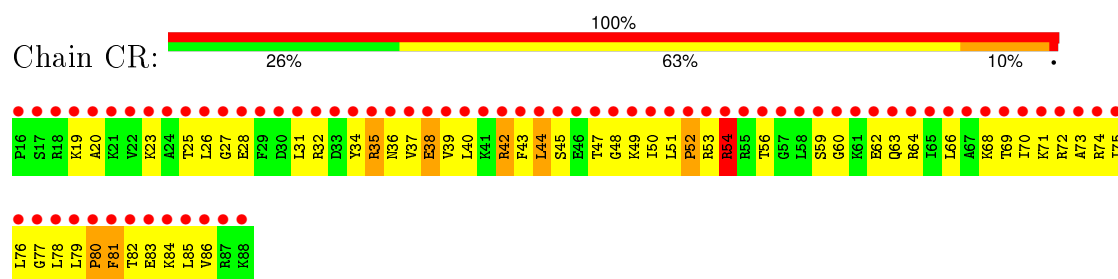
- Molecule 17: 30S ribosomal protein S17



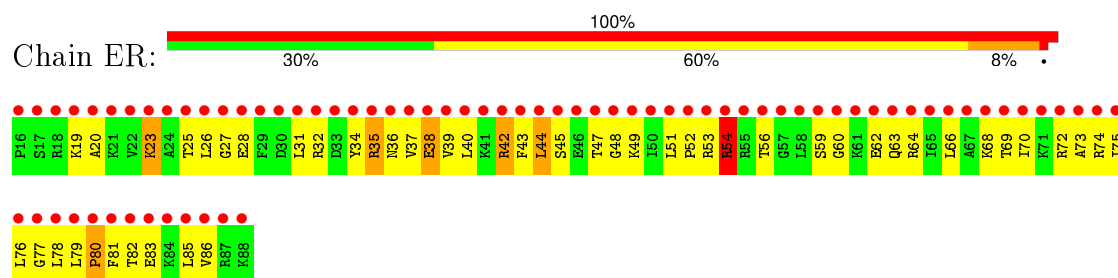
- Molecule 18: 30S ribosomal protein S18



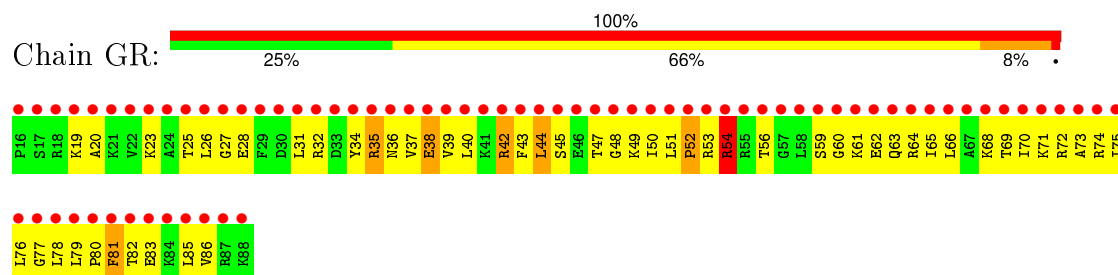
- Molecule 18: 30S ribosomal protein S18



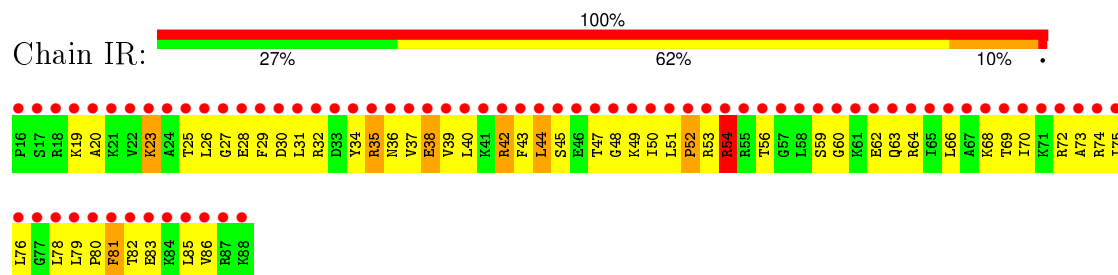
- Molecule 18: 30S ribosomal protein S18



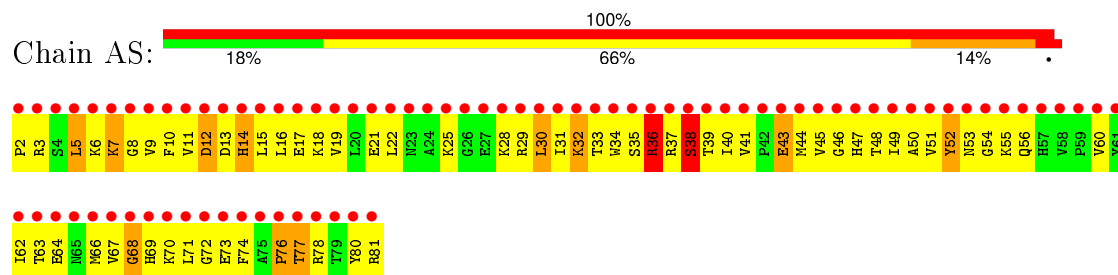
- Molecule 18: 30S ribosomal protein S18



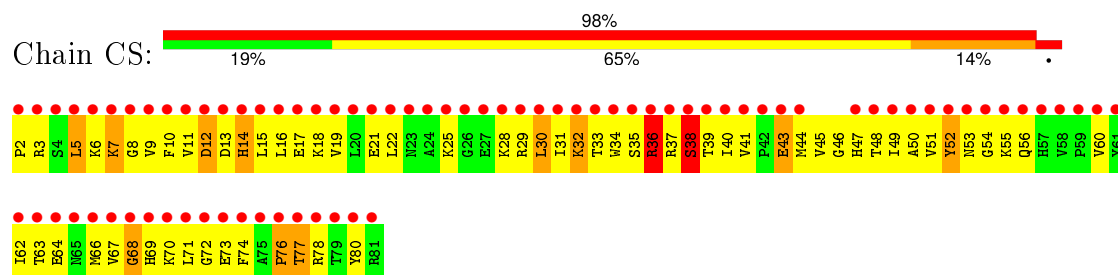
- Molecule 18: 30S ribosomal protein S18



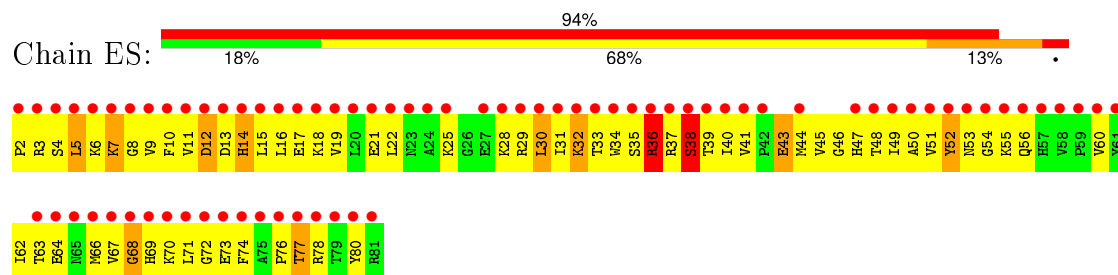
- Molecule 19: 30S ribosomal protein S19



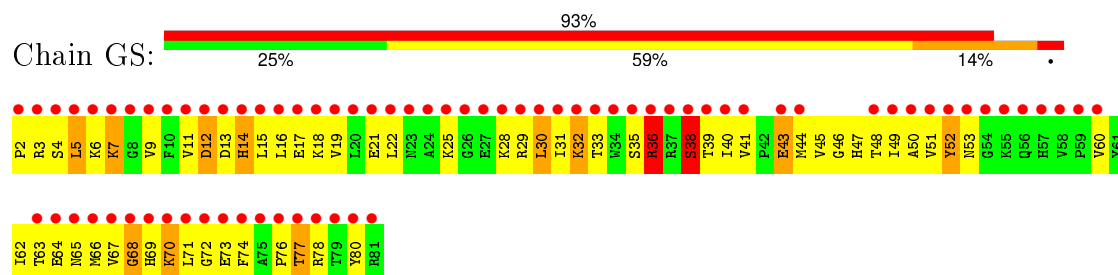
- Molecule 19: 30S ribosomal protein S19



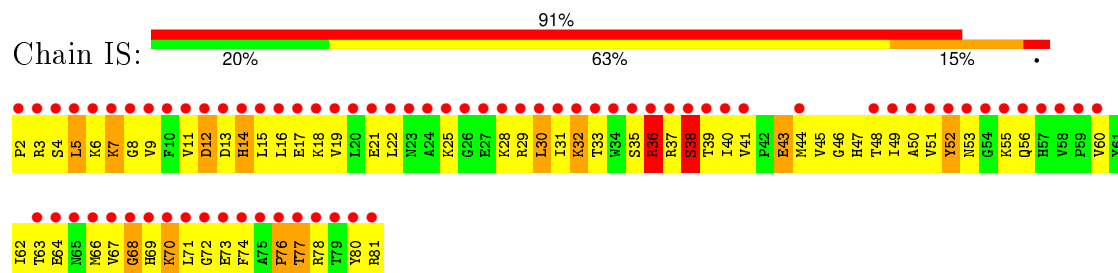
- Molecule 19: 30S ribosomal protein S19



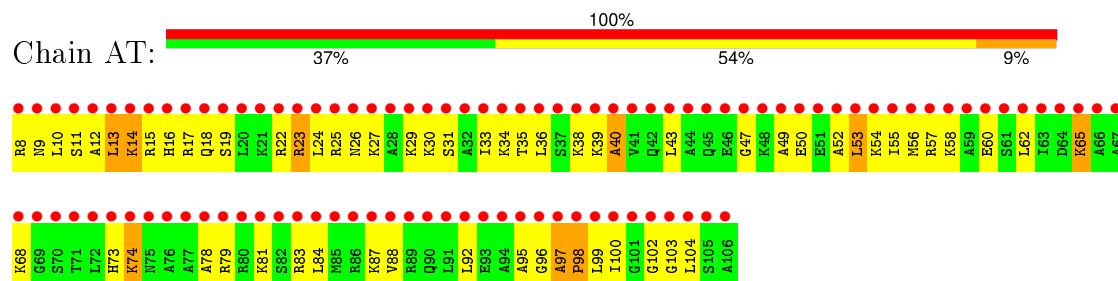
## • Molecule 19: 30S ribosomal protein S19



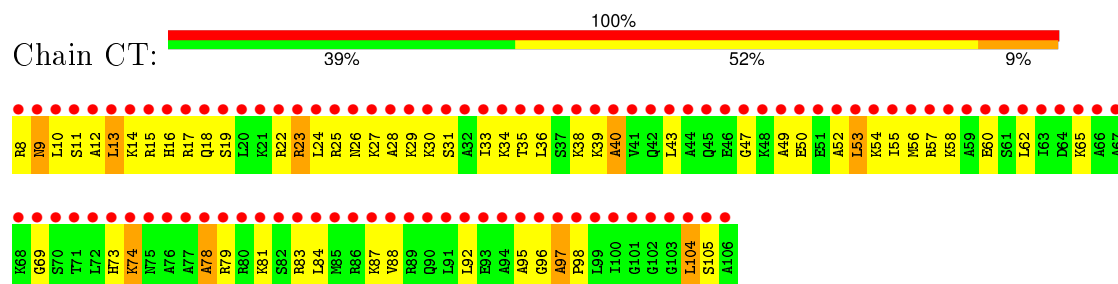
## • Molecule 19: 30S ribosomal protein S19



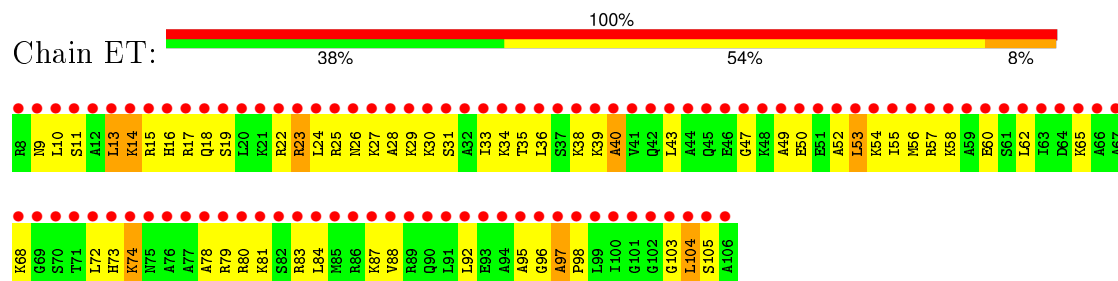
## • Molecule 20: 30S ribosomal protein S20



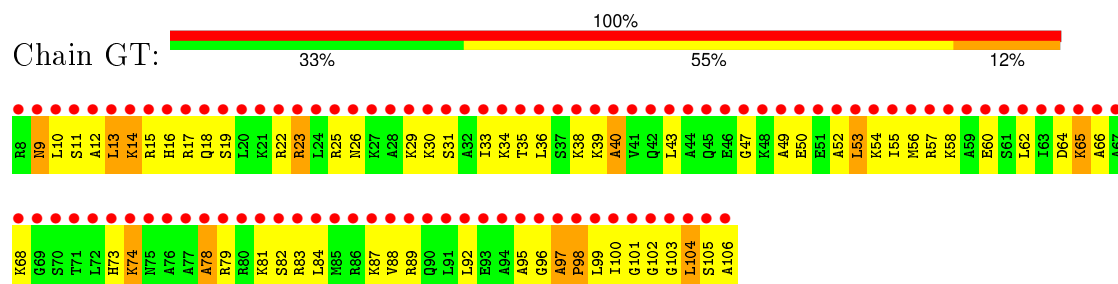
## • Molecule 20: 30S ribosomal protein S20



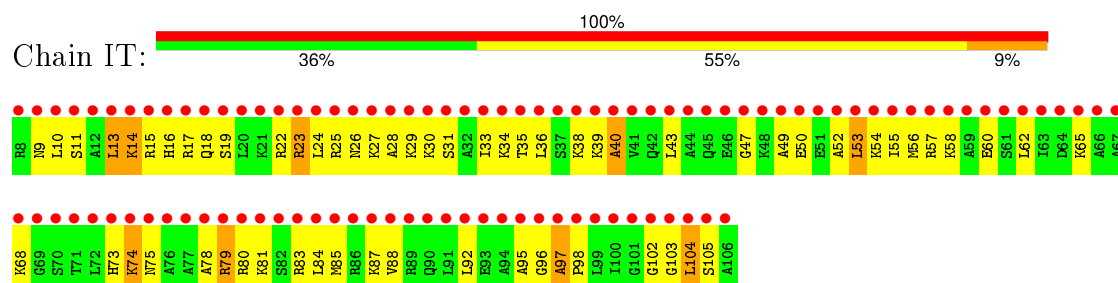
## • Molecule 20: 30S ribosomal protein S20



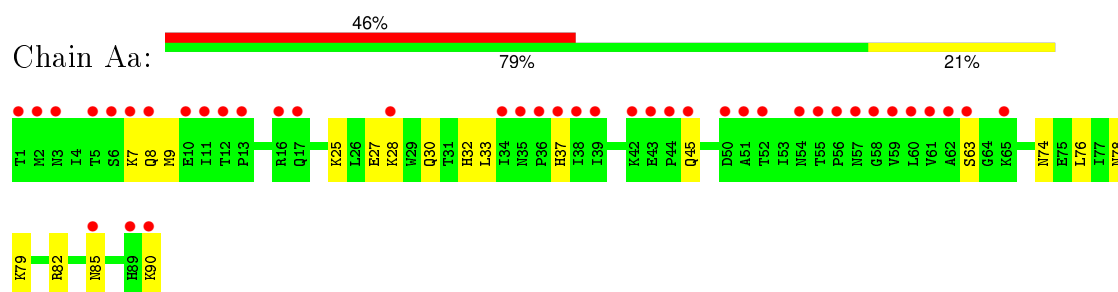
- Molecule 20: 30S ribosomal protein S20



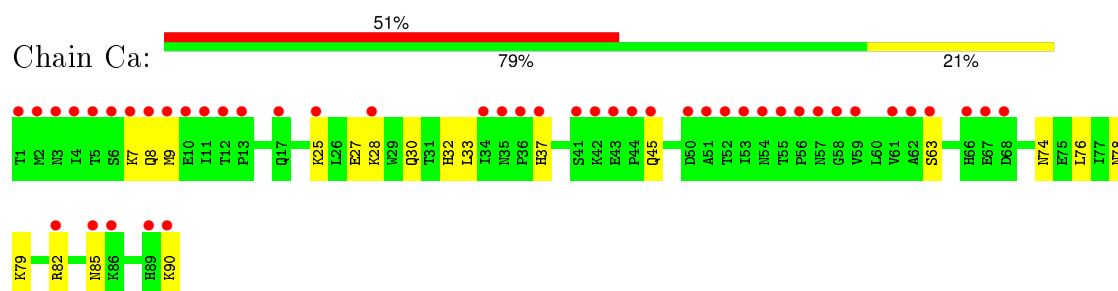
- Molecule 20: 30S ribosomal protein S20



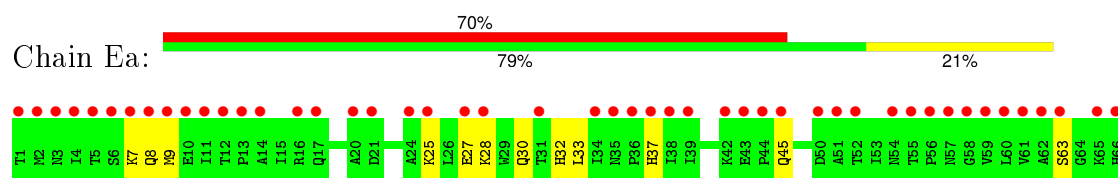
- Molecule 21: protein Y

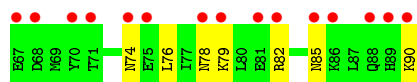


- Molecule 21: protein Y

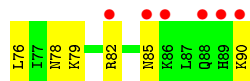
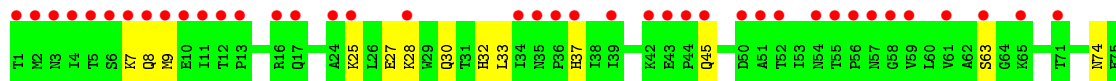
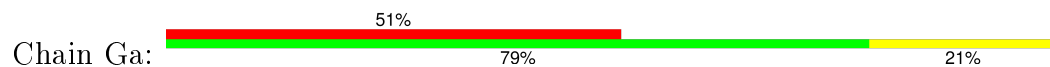


- Molecule 21: protein Y

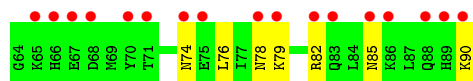
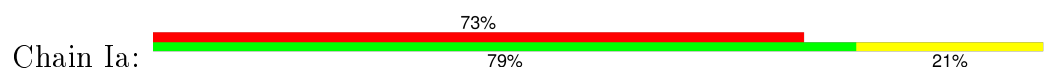




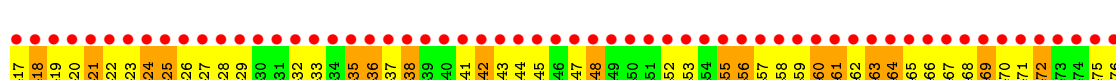
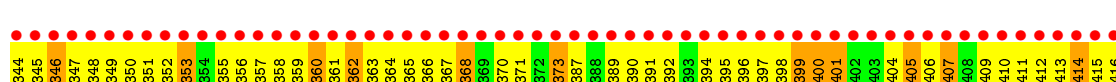
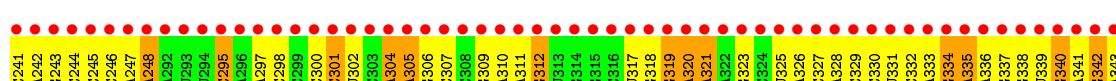
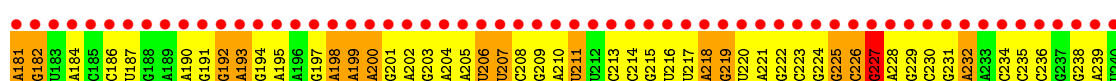
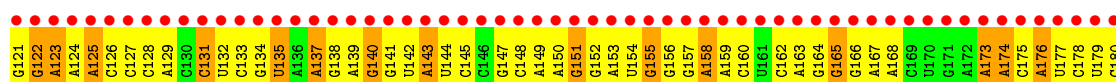
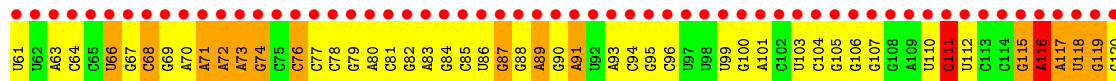
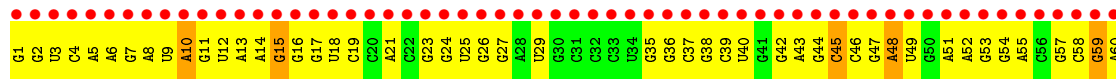
• Molecule 21: protein Y



• Molecule 21: protein Y



• Molecule 22: 23S RIBOSOMAL RNA



U1257	U1197	A1137	U1077	G1017	G957	A897	U837	A777	G717	A857	U597	C537	A477
G1258	C1198	A1138	A1078	C1018	G958	C998	A838	G778	A718	G658	U598	A538	G478
A1259	U1199	A1139	G1079	U1019	C959	G899	U839	U779	A719	G659	U599	A539	G479
A1260	A1200	A1140	A1080	U1020	U960	U900	U840	U780	A720	G660	G600	G540	G480
G1261	G1201	A1141	A1081	A1021	G961	A901A	G841	G781	C721	C661	A601	C541	A481
U1262	U1202	G1142	G1082	U1022	G962	A901	A842	U782	C722	G662	C602	A542	A482
G1263	A1203	A1143	G1083	U1023	G963	U902	G843	G783	C723	G663	G603	C543	A483
G1264	G1204	U1144	A1084	A1024	A964	U903	G844	U784	C724	G664	U604	U544	G484
G1265	G1205	C1145	G1085	A1025	G965	U904	U845	U785	C725	A665	G605	C545	G485
A1266	G1206	G1146	G1086	U1026	A966	G905	A846	U786	G726	U666	A606	A546	U486
G1267	G1207	G1147	C1087	U1027	G967	U906	C847	U787	U727	U667	C607	U547	G487
U1268	A1208	A1148	A1088	G1028	G968	U907	A848	G788	G728	A668	G608	G548	A488
G1269	G1209	G1149	C1089	C1029	U969	C909	G849	G789	A729	G669	U609	G549	A489
C1270	C1210	C1150	C1090	U1030	A970	U910	C850	A790	C730	G670	G610	C550	A490
G1271	G1211	A1151	C1091	A1031	A971	A911	C851	G791	A731	A671	C611	A551	G491
G1272	U1212	C1152	U1092	A1032	C972	A912	U852	U792	C732	C672	G612	C552	G492
G1273	U1213	A1153	U1093	G1033	U973	A913	C853	G793	G733	G673	A613	C553	A493
G1274	C1214	A1154	C1094	U1034	U974	C914	G854	U794	G734	U674	G614	U554	A494
A1275	A1215	G1155	A1095	G1035	C975	C915	G855	A795	G735	C675	C615	U555	C495
U1276	G1216	U1156	A1096	G1036	C976	U916	A856	A796	G736	G676	U616	A556	C496
G1277	U1217	G1157	A1097	U1037	G977	U917	U857	U797	C737	G677	U617	U557	C497
A1278	C1218	A1158	G1098	U1038	U978	A918	G858	G798	G738	G678	A618	G558	C498
G1279	C1219	A1159	A1099	A1039	A979	U919	U859	C799	G739	C679	A619	C559	G499
U1280	G1220	G1160	G1100	A1040	G980	G920	U860	U800	A740	U680	G620	G560	G500
A1281	C1221	U1161	U1101	A1041	C981	A921	G861	A801	G741	A681	U621	U561	G501
A1282	G1222	A1162	G1102	G1042	C982	A922	A862	A802	G742	G682	U622	G562	A502
C1283	G1223	C1163	C1103	A1043	G983	A923	C863	C803	A743	A683	G623	G563	G503
G1284	A1224	G1164	G1104	U1044	A984	C924	C864	C804	C744	A684	A624	U564	G504
A1285	G1225	G1165	U1105	G1045	G985	U925	A865	G805	C745	A685	A625	A565	G505
U1286	A1226	A1166	A1106	U1046	A986	C926	U866	A806	G746	C686	A626	U566	G506
A1287	U1227	G1167	A1107	G1047	G987	C927	G867	A807	A747	G687	A627	G567	A507
A1288	G1228	U1168	U1108	U1048	C988	G928	U868	C808	A748	A688	A628	G568	G508
A1289	C1229	C1169	A1109	C1049	G989	A929	C869	C809	G749	A689	C629	C569	U509
A1290	C1230	U1170	G1110	G1050	A990	A930	C870	U810	C750	A690	G630	G510	G510
A1291	A1231	A1171	C1111	U1051	A991	G931	U871	G811	G751	C691	G631	U571	A511
A1292	U1232	U1172	C1112	C1052	A992	G932	G872	G812	G752	C692	A632	G572	A512
A1293	A1233	G1173	G1113	G1053	C993	G933	U873	A813	U753	A693	G633	C573	A513
G1294	C1234	G1174	A1114	C1054	A994	G934	A874	G814	G754	G694	G634	C574	G514
U1295	C1235	A1175	C1115	A1055	A995	C935	G875	A815	C755	G695	C635	U575	A515
G1296	G1236	U1176	U1116	G1056	C996	A936	A876	U816	G756	A696	G636	A576	G516
A1297	G1237	U1177	G1117	A1057	C997	C937	G877	A817	U757	G697	G637	U577	A517
G1298	A1238	C1178	G1118	G1058	C998	G938	C878	G818	G758	A698	A638	U578	A518
A1299	U1239	A1179	U1119	A1059	A999	C939	A879	C819	C759	G699	G639	G579	C519
A1300	G1240	A1180	C1120	G1060	G1000	G940	C880	U820	U760	C700	G640	A580	G520
U1301	G1241	C1181	G1121	A1061	A1001	U941	U881	A821	G761	U701	G641	A581	U521
C1302	A1242	U1182	A1122	G1062	C1002	U942	C882	G822	A762	A702	A642	G582	G522
U1303	G1243	G1183	G1123	C1063	C1003	U943	A883	U823	A763	A703	A643	C583	A523
U1304	U1244	G1184	U1124	C1064	A1004	A944	C884	U824	A764	G704	A644	A584	A524
C1305	G1245	G1185	G1125	A1065	U1005	G945	A885	C825	C765	C705	G645	U585	A525
U1306	G1246	G1186	A1126	G1066	C1006	U946	A886	U826	A766	A706	C646	G586	C526
U1307	U1247	A1187	G1127	G1067	A1007	C947	G887	C827	G767	A707	G647	A587	C527
C1308	G1248	A1188	G1128	A1068	G1008	C948	G888	C828	U768	G708	A648	G588	G528
G1309	A1249	G1189	A1129	G1069	C989	G949	C889	C829	C769	A709	G649	C589	U529
C1310	U1250	C1190	U1130	G1070	U950	G950	U890	C830	U770	C710	U650	C590	G530
C1311	G1131	G1191	G1131	A1071	A951	G951	A891	G831	G771	C711	G651	G591	G531
C1312	C1252	A1192	C1132	U1072	A1012	A952	A892	A832	G772	A712	C652	G592	A532
U1313	C1253	G1193	G1133	G1073	G1013	G953	G893	A833	G773	G713	G653	C593	C533
A1314	G1254	U1194	C1134	G1074	U1014	U954	A894	U834	A774	G714	A654	G594	A534
A1315	U1255	U1195	C1135	C1075	U1015	G955	G895	U835	U775	U715	A655	A595	U535
G1316	C1256	G1196	G1136	U1076	C1016	A956	C996	G836	G776	U716	U656	C596	A536



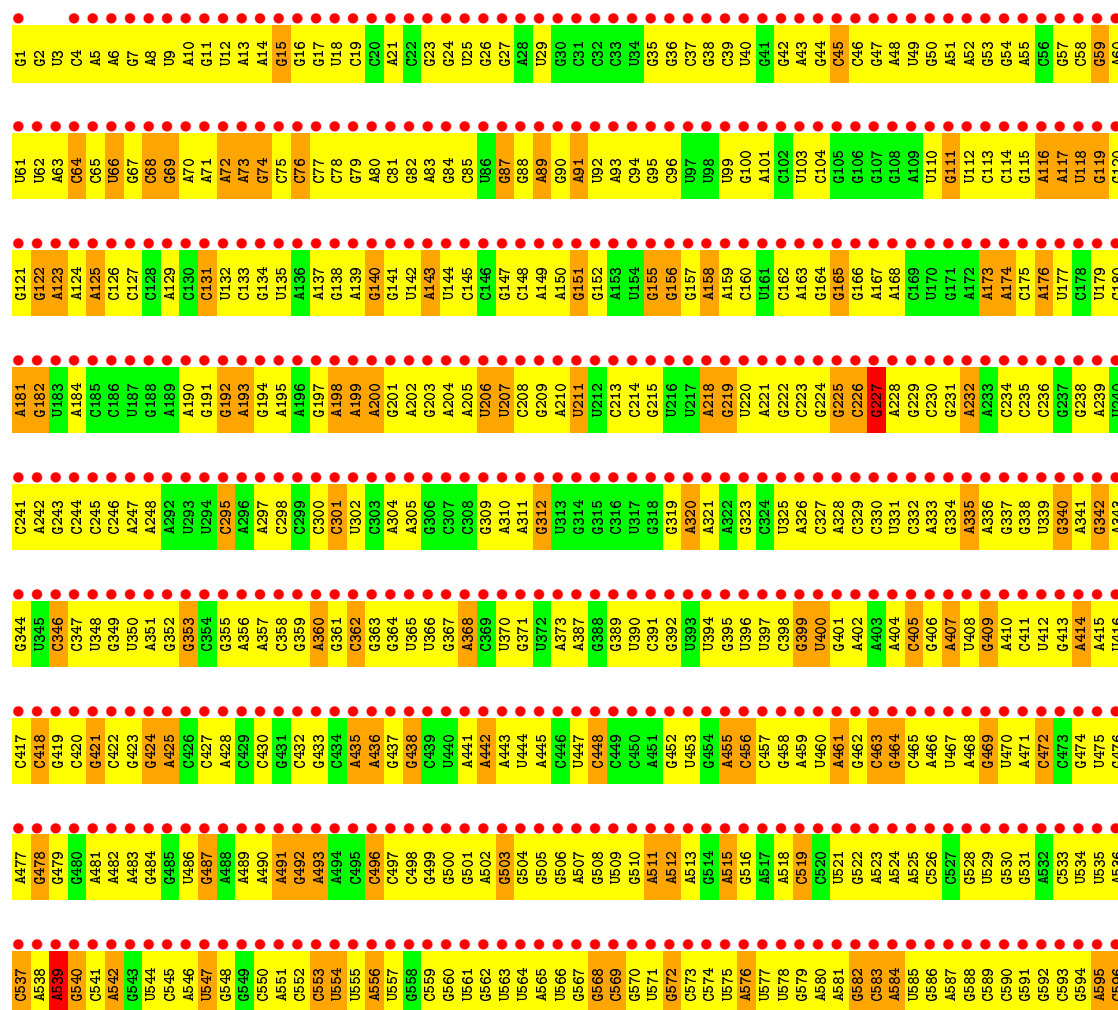
G3105	C2028	G1968	C1908	A3865	G1797	G1737	G1673	G1617	G1557	C1497	A1437	G1377	G1317
U3106	G2029	G1969	U1909	A3866	G1798	U1738	G1678	U1618	C1558	G1498	G1438	A1378	A1318
G3107	A2030	G1970	A1910	A3867	A1799	G1739	U1679	A1619	G1559	U1500	G1439	A1379	C1319
G3108	A2031	G1971	A1911	U3868	A1800	G1740	U1680	C1620	U1560	A1440	C1380	C1320	A1320
U3109	G2032	G1972	G1912	G3869	C1801	G1741	A1681	C1621	A1561	C1501	A1441	G1381	A1321
G3110	C2033	G1973	G1913	C3870	A1802	G1742	A1682	G1622	G1562	G1502	C1442	G1382	G1322
A2034	A2034	U1974	U1914	A3871	G1803	G1743	G1683	C1623	U1563	G1503	C1443	G1383	G1323
G3111	G2035	G1975	A1915	A3872	U1804	G1744	G1684	A1624	U1564	G1504	C1444	G1384	G1324
U3112	A2036	G1976	G1916	A3873	G1805	G1745	G1685	A1625	U1565	U1505	C1445	G1385	U1325
U3113	G2037	C1977	C1917	G3874	G1806	G1746	A1686	A1626	G1566	C1506	U1446	G1386	U1326
A2037	A2037	C1977	G1918	A3875	A1807	G1747	G1687	C1627	A1567	U1507	U1447	G1387	C1327
G3115	G2038	G1978	G1918	A3876	G1808	U1748	U1688	G1628	A1568	G1508	A1448	G1388	G1328
G3116	G2039	G1979	A1919	A3877	G1809	U1749	U1689	G1629	A1569	G1509	C1449	G1389	U1329
A3117	A2040	A1980	A1920	A3877	G1809	G1749	U1689	A1630	C1570	A1510	G1450	G1390	G1330
U3118	A2041	A1981	A1921	G3861	U1810	A1750	U1690	A1631	G1571	A1511	C1451	A1391	G1331
A3119	A2042	G1982	U1922	G1862	A1811	A1751	G1691	A1632	C1572	A1512	U1452	U1392	G1332
G3120	A2043	G1983	U1923	U1863	U1812	U1752	G1692	A1633	C1573	U1513	A1453	G1393	G1333
G3121	G2044	A1984	C1924	G1864	A1813	A1753	A1693	A1634	A1574	A1514	U1454	G1394	A1334
A2045	A2045	G1985	G1925	G1865	G1814	G1754	A1694	A1635	C1575	U1515	C1455	A1395	A1335
G3123	G2046	G1986	U1926	G1866	G1815	G1755	U1695	G1636	G1576	A1516	C1456	G1396	A1336
G3124	C2047	G1987	U1927	A1867	G1816	G1756	C1696	U1637	G1577	U1517	C1457	A1397	G1337
G3125	C2048	A1988	G1928	U1868	U1817	G1757	C1697	U1638	U1578	C1518	A1458	G1398	G1338
A3126	C2049	G1989	U1929	A1869	G1818	G1758	C1698	U1639	G1579	U1519	U1459	G1399	U1339
G3127	G2050	U1990	C1930	U1870	U1819	A1759	A1699	C1640	C1580	G1520	A1400	C1340	C1340
G3128	U2051	G1991	G1931	G1871	G1820	G1760	G1701	C1641	C1581	U1521	G1401	G1341	G1341
G3129	G2052	G1992	G1932	A1872	A1821	G1761	C1702	G1642	A1582	C1522	G1402	G1342	G1342
G3130	G2053	G1993	G1933	A1873	C1822	C1762	C1703	A1643	A1583	A1463	U1403	C1343	C1343
A3131	A2054	U1994	U1934	G1874	G1823	G1763	G1704	G1644	G1584	A1464	C1344	C1344	C1344
A3132	G2055	G1995	A1935	C1875	C1824	A1764	G1705	U1645	A1585	G1465	A1405	G1345	G1345
G3133	C2056	A1996	G1936	C1876	C1825	C1765	U1706	U1646	A1586	U1526	A1406	G1346	G1346
A3134	U2057	G1997	G1937	C1877	G1826	G1766	U1706	G1647	A1587	U1527	G1407	C1347	C1347
G3135	U2058	A1998	U1938	C1878	G1827	G1767	A1707	U1648	A1588	C1528	U1408	C1348	C1348
A3136	U2059	U1999	U1939	G1879	C1828	U1768	G1708	A1649	A1589	U1469	U1409	A1349	A1349
G3137	A2060	U2000	C1940	G1880	C1829	U1769	U1709	A1650	C1590	U1530	G1470	G1350	G1350
A3138	C2061	G2001	C1941	U1881	G1830	U1770	U1710	U1651	C1591	G1471	U1411	G1351	G1351
U3139	U2062	A2002	G1942	G1882	G1831	A1771	C1711	G1652	U1592	A1532	C1412	G1352	A1352
A2063	A2063	A2003	A1943	A1883	G1832	G1772	G1712	C1653	C1593	G1533	U1413	A1353	A1353
G3141	U2064	U2004	C1944	A1884	U1833	C1773	G1713	A1654	U1594	A1534	G1414	A1354	A1354
A2065	A2065	U2005	G1945	C1885	G1834	A1774	A1714	C1655	A1595	U1475	C1415	A1355	A1355
G2066	G2066	G2006	U1946	G1886	C1835	A1775	A1715	C1656	A1596	G1476	A1416	G1356	G1356
U2067	U2067	G2007	G1947	G1887	G1836	A1776	G1716	U1657	C1597	U1537	C1417	U1357	U1357
C2068	C2068	C2008	C1948	C1888	G1837	A1777	A1717	A1658	A1598	U1538	C1418	G1358	G1358
U2069	U2069	U2009	A1949	G1889	G1838	U1778	A1718	G1659	U1599	U1539	G1419	G1359	G1359
G3148	G2070	G2010	C1950	G1890	A1839	G1779	G1719	G1660	U1600	C1540	G1420	G1360	G1360
A3149	U2071	U2011	G1951	C1891	A1840	U1780	G1720	C1661	U1601	U1481	U1421	A1361	A1361
G3150	C2072	A2012	A1952	C1892	G1841	C1781	G1721	G1662	G1602	G1542	C1422	A1362	A1362
U3151	A2073	A2013	A1953	G1893	G1842	A1782	U1722	C1663	A1603	G1483	A1423	C1363	C1363
G3152	G2074	A2014	G1954	U1894	U1843	G1783	U1723	C1664	A1604	U1484	U1424	C1364	C1364
G3153	G2075	G2015	G1955	A1895	C1844	G1784	C1724	G1665	U1485	G1545	G1425	U1365	U1365
G3154	A2076	A2016	G1956	A1896	A1845	A1785	G1725	C1666	C1606	C1546	U1426	A1366	A1366
G3155	C3093	U2017	C1957	C1897	A1846	G1786	C1726	G1667	A1607	G1487	G1427	A1367	A1367
A3156	A3094	G2018	G1958	U1898	G1847	U1787	C1727	A1668	U1608	U1547	G1428	G1368	G1368
G3157	A3095	C2019	U1959	U1899	U1848	C1788	A1728	G1669	U1609	U1548	A1429	G1369	G1369
A3158	C3096	G2020	A1960	U1900	G1849	U1789	G1729	A1670	C1550	U1490	G1430	U1370	U1370
G3159	G3097	G2021	G1961	G1891	G1850	G1790	G1730	G1671	U1551	C1491	U1431	G1371	G1371
C3160	U3098	C2022	G1962	A1902	A1851	C1791	G1731	A1672	U1552	A1492	G1432	A1372	A1372
G3161	G3100	C2023	G1963	C1903	G1852	C1792	U1732	C1673	G1553	G1493	A1433	G1373	G1373
C3162	A3101	U2024	A1964	G3094	C1853	A1793	U1733	C1674	G1554	U1494	A1434	G1374	G1374
C3163	G3102	A2025	U1965	G1905	G1854	A1794	G1734	C1675	A1555	G1495	G1435	G1375	G1375
G3164	G3103	C2026	G1966	U1906	G1855	C1795	G1735	C1676	C1616	A1556	G1436	G1376	G1376
G3166	C3104	C2027	U1967	C1907	U1856	A1796	C1736	U1676					

Chain DB:  100%

A897	A898	A899	A900	A901	A902	A903	A904	A905	A906	A907	A908	A909	A910	A911	A912	A913	A914	A915	A916	A917	A918	A919	A920	A921	A922	A923	A924	A925	A926	A927	A928	A929	A930	A931	A932	A933	A934	A935	A936	A937	A938	A939	A940	A941	A942	A943	A944	A945	A946	A947	A948	A949	A950	A951	A952	A953	A954	A955	A956																																																																																																																																																																																																																																												
U837	A838	U839	U840	A841	A842	A843	A844	U845	A846	A847	A848	A849	A850	U851	U852	A853	A854	A855	A856	U857	U858	U859	U860	A861	A862	A863	A864	A865	U866	U867	U868	U869	U870	U871	U872	A873	A874	A875	A876	U877	U878	U879	U880	U881	U882	U883	U884	A885	A886	U887	U888	U889	U890	U891	A892	U893	U894	U895	A896																																																																																																																																																																																																																																												
G717	A718	A719	A720	G721	G722	G723	G724	G725	U726	U727	G728	G729	G730	A731	G732	G733	G734	G735	G736	G737	G738	G739	A740	G741	G742	A743	C744	G745	G746	A747	A748	C749	G750	G751	G752	G753	G754	C755	C756	U757	U758	C759	U760	G761	A762	A763	A764	C765	A766	U767	U768	C769	U770	G771	G772	G773	A774	U775	G776																																																																																																																																																																																																																																												
A777	G778	U779	U780	G781	U782	G783	U784	U785	U786	A787	G788	G789	A790	G791	U792	G793	A794	A795	A796	U797	U798	U799	U800	A801	A802	A803	A804	A805	A806	A807	A808	A809	U810	U811	G812	A813	G814	A815	A816	A817	A818	A819	U820	A821	G822	U823	U824	U825	U826	U827	U828	U829	U830	A831	A832	A833	A834	U835	U836																																																																																																																																																																																																																																												
U837	A838	U839	U840	A841	A842	A843	A844	U845	A846	A847	A848	A849	A850	U851	U852	A853	A854	A855	A856	U857	U858	U859	U860	A861	A862	A863	A864	A865	U866	U867	U868	U869	U870	U871	U872	A873	A874	A875	A876	U877	U878	U879	U880	U881	U882	U883	A884	A885	A886	U887	U888	U889	U890	U891	A892	U893	U894	U895	A896																																																																																																																																																																																																																																												
G1	G2	U3	C4	A5	A6	G7	A8	U9	A10	A11	U12	A13	A14	G15	G16	A17	A18	A19	A20	A21	G22	G23	G24	U25	G26	G27	A28	U29	G30	G31	G32	G33	U34	G41	A43	A44	G45	G46	G47	A48	U49	G50	A51	A52	G53	C54	A55	A56	G57	U58	U59	G60	A60																																																																																																																																																																																																																																																		
U61	U62	A63	C64	G65	U66	G67	U68	U69	A70	A71	A72	A73	G74	C75	C76	C77	G78	G79	A80	G81	G82	A83	G84	C85	U86	G87	U88	G89	U90	U91	U92	A93	C94	G95	C96	U97	U98	U99	G100	G101	G102	A103	C104	G105	G106	G107	A108	A109	U110	G111	U112	C113	C114	G115	A116	A117	U118	U119	G120																																																																																																																																																																																																																																												
G121	G122	A123	C124	A125	C126	C127	G128	A129	C130	A131	U132	C133	G134	U135	A136	A137	G138	A139	G140	G141	U142	A143	U144	C145	G146	G147	C148	A149	A150	G151	G152	C153	U154	G155	G156	U157	A158	A159	C160	A161	C162	A163	C164	G165	G166	A167	G168	U169	G170	G171	A172	A173	C174	C175	U176	U177	C178	U179	C180																																																																																																																																																																																																																																												
A181	G182	U183	A184	C185	C186	U187	G188	A189	A190	U191	A192	A193	G194	A195	A196	G197	A198	A199	A200	G201	G202	G203	A204	A205	U206	U207	C208	G209	A210	U211	U212	C213	C214	G215	U216	U217	A218	G219	U220	C221	G222	G223	G224	G225	C226	G227	A228	G229	C230	G231	A232	A233	A234	C235	C236	G237	G238	A239	U240																																																																																																																																																																																																																																												
C241	A242	G243	C244	C245	C246	A247	A248	A249	A250	U251	U252	U253	A254	A255	A256	A257	A258	A259	A260	A261	A262	A263	A264	A265	A266	A267	A268	A269	A270	A271	A272	A273	A274	A275	A276	A277	A278	A279	A280	A281	A282	A283	A284	A285	A286	A287	A288	A289	A290	A291	A292	A293	A294	A295	A296	A297	A298	A299	A300	A301	A302	A303	A304	A305	A306	A307	A308	A309	A310	A311	A312	A313	A314	A315	A316	A317	A318	A319	A320	A321	A322	A323	A324	A325	A326	A327	A328	A329	A330	A331	A332	A333	A334	A335	A336	A337	A338	A339	A340	A341	A342	A343	A344	A345	A346	A347	A348	A349	A350	A351	A352	A353	A354	A355	A356	A357	A358	A359	A360	A361	A362	A363	A364	A365	A366	A367	A368	A369	A370	A371	A372	A373	A374	A375	A376	A377	A378	A379	A380	A381	A382	A383	A384	A385	A386	A387	A388	A389	A390	A391	A392	A393	A394	A395	A396	A397	A398	A399	A400	A401	A402	A403	A404	A405	A406	A407	A408	A409	A410	A411	A412	A413	A414	A415	A416	A417	A418	A419	A420	A421	A422	A423	A424	A425	A426	A427	A428	A429	A430	A431	A432	A433	A434	A435	A436	A437	A438	A439	A440	A441	A442	A443	A444	A445	A446	A447	A448	A449	A450	A451	A452	A453	A454	A455	A456	A457	A458	A459	A460	A461	A462	A463	A464	A465	A466	A467	A468	A469	A470	A471	A472	A473	A474	A475	A476	A477	A478	A479	A480	A481	A482	A483	A484	A485	A486	A487	A488	A489	A490	A491	A492	A493	A494	A495	A496	A497	A498	A499	A500	A501	A502	A503	A504	A505	A506	A507	A508	A509	A510	A511	A512	A513	A514	A515	A516	A517	A518	A519	A520	A521	A522	A523	A524	A525	A526	A527	A528	A529	A530	A531	A532	A533	A534	A535	A536
G344	U345	C346	G347	U348	U349	U350	A351	G352	G353	C354	G355	A356	A357	C358	A359	A360	A361	C362	G363	U364	U365	U366	A367	A368	C369	C370	A371	G372	U373	U374	G375	C376	U377	U378	U379	U380	U381	U382	U383	U384	U385	U386	U387	U388	U389	U390	U391	U392	U393	U394	U395	U396	U397	U398	U399	U400	G401	A402	A403	A404	A405	A406	A407	U408	G409	A410	A411	C412	A413	U414	U415	U416	G417	A418	A419	A420	A421	A422	A423	A424	A425	A426	A427	A428	A429	A430	A431	A432	A433	A434	A435	A436	A437	A438	A439	A440	A441	A442	A443	A444	A445	A446	A447	A448	A449	A450	A451	A452	A453	A454	A455	A456	A457	A458	A459	A460	A461	A462	A463	A464	A465	A466	A467	A468	A469	A470	A471	A472	A473	A474	A475	A476	A477	A478	A479	A480	A481	A482	A483	A484	A485	A486	A487	A488	A489	A490	A491	A492	A493	A494	A495	A496	A497	A498	A499	A500	A501	A502	A503	A504	A505	A506	A507	A508	A509	A510	A511	A512	A513	A514	A515	A516	A517	A518	A519	A520	A521	A522	A523	A524	A525	A526	A527	A528	A529	A530	A531	A532	A533	A534	A535	A536																																																																																																							
A477	U478	G479	U480	A481	A482	A483	A484	A485	A486	A487	A488	A489	A490	A491	A492	A493	A494	A495	A496	C497	C498	A499	A500	G501	A502	G503	G504	G505	G506	A507	A508	U509	G510	A511	A512	A513	A514	A515	A516	A517	A518	A519	A520	A521	A522	A523	A524	A525	A526	A527	A528	A529	A530	A531	A532	A533	A534	A535	A536																																																																																																																																																																																																																																												
C537	A538	A539	C540	C541	A542	A543	U544	C545	A546	U547	G548	G549	C550	A551	C552	C553	U554	U555	A556	C557	G558	A559	G560	U561	G562	U563	U564	A565	U566	G567	A568	C569	U570	U571	G572	C573	C574	U575	A576	U577	U578	G579	A580	A581	G582	C583	A584	U585	U586	A587	A588	C589	U590	A591	A592	A593	A594	A595	C596																																																																																																																																																																																																																																												
U597	U598	A599	G600	A601	C602	C603	U604	A605	U606	U607	A608	U609	G610	A611	G612	A613	G614	C615	U616	U617	A618	A619	G620	U621	U622	G623	A624	A625	A626	A627	A628	C629	G630	A631	A632	A633	A634	C635	U636	U637	A638	C639	A640	A641	A642	A643	A644	U645	C646	G647	A648	U649	U650	C651	G652	A653	U654	A655	A656	A657	A658	A659	A660	A661	A662	A663	A664	A665	A666	A667	A668	A669	A670	A671	A672	A673	A674	A675	A676	A677	A678	A679	A680	A681	A682	A683	A684	A685	A686	A687	A688	A689	A690	A691	A692	A693	A694	A695	A696	A697	A698	A699	A700	U701	A702	A703	A704	C705	A706	U707	U708	A709	U710	U711	G712	A713	G714	U715	A716	A717	A718	A719	A720	A721	A722	A723	A724	A725	A726	A727	A728	A729	A730	A731	A732	A733	A734	A735	A736	A737	A738	A739	A740	A741	A742	A743	A744	A745	A746	A747	A748	A749	A750	A751	A752	A753	A754	A755	A756	A757	A758	A759	A760	A761	A762	A763	A764	A765	A766	A767	A768	A769	A770	A771	A772	A773	A774	A775	A776	A777	A778	A779	A780	A781	A782	A783	A784	A785	A786	A787	A788	A789	A790	A791	A792	A793	A794	A795	A796	A797	A798	A799	A800	A801	A802	A803	A804	A805	A806	A807	A808	A809	A810	A811	A812	A813	A814	A815	A816	A817	A818	A819	A820	A821	A822	A823	A824	A825	A826	A827	A828	A829	A830	A831	A832	A833	A834	A835	A836																																																								
U837	A838	U839	U840	A841	A842	A843	A844	U845	A846	A847	A848	A849	A850	U851	U852	A853	A854	A855	A856	U857	U858	U859	U860	A861	A862	A863	A864	A865	U866	U867	U868	U869	U870	U871	U872	A873	A874	A875	A876	U877	U878	U879	U880	U881	U882	U883	A884	A885	A886	U887	U888	U889	U890	U891	A892	U893	U894	U895	A896																																																																																																																																																																																																																																												
C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956																																																																																																																																																																																																																																												

G1737	G1677	G1617	G1557	G1497	G1437	G1377	G1317	U1257	U1197	A1137	U1077	G1017	G957
U1738	G1678	U1618	G1558	G1498	G1438	A1378	A1318	G1258	C1198	A1138	U1078	C1018	G958
G1739	U1679	A1619	G1559	A1499	G1439	A1379	G1319	A1259	U1199	A1139	A1079	U1019	G959
G1740	U1680	U1620	U1560	U1500	G1440	A1380	A1320	A1260	G1200	A1080	A1020	U1060	U960
G1741	A1681	C1621	G1561	G1501	A1441	G1381	A1321	G1261	U1201	U1141	G1081	A1021	G961
G1742	A1682	G1622	G1562	G1502	C1442	G1382	G1322	U1262	G1202	G1142	G1082	A1022	G962
G1743	G1683	C1623	U1563	G1503	C1443	G1383	G1323	G1263	A1203	A1143	G1083	U1023	G963
G1744	A1684	A1624	U1564	G1504	G1444	G1384	G1324	C1264	G1204	U1144	A1084	A1024	A964
G1745	A1685	A1625	G1565	U1505	A1445	G1385	U1325	G1265	G1205	C1195	G1085	G1025	G965
G1746	A1686	A1626	C1566	C1506	A1446	A1386	U1326	G1266	G1206	G1146	U1086	U1026	A966
G1747	A1687	C1627	A1567	A1507	U1447	G1387	U1327	A1267	G1207	G1147	C1087	G1027	G967
U1748	U1688	G1628	A1568	G1508	A1448	C1388	C1328	U1268	A1208	G1148	A1088	G1028	G968
U1749	U1689	G1629	A1569	A1509	A1449	C1389	U1329	G1269	A1209	G1149	C1089	C1029	U969
A1750	U1690	A1630	A1570	A1510	G1450	G1390	G1330	C1270	C1210	C1150	C1090	U1030	A970
A1751	G1691	C1631	G1571	A1511	C1451	A1391	G1331	C1271	G1211	U1151	G1091	A1031	A971
A1752	G1692	A1632	C1572	A1512	U1452	U1392	G1332	G1272	U1212	C1152	U1092	A1032	G972
A1753	A1693	C1633	G1573	U1513	A1453	G1393	G1333	G1273	A1213	A1153	U1093	U1033	U973
G1754	A1694	A1634	A1574	A1514	A1454	G1394	A1334	C1274	C1214	A1154	G1094	G1034	U974
G1755	U1695	G1635	C1575	U1515	C1455	A1395	A1335	A1275	A1215	G1155	A1095	G1035	C975
G1756	C1696	G1636	U1576	A1516	C1456	C1396	G1336	U1276	G1216	U1156	A1096	G1036	G976
C1757	U1697	A1637	A1577	A1517	A1457	A1397	G1337	G1277	U1217	U1157	A1097	U1037	G977
C1758	G1698	G1638	U1578	C1518	A1458	G1398	G1338	A1278	C1218	U1158	G1098	U1038	U978
A1759	A1699	A1639	G1579	G1519	A1459	C1399	U1339	G1279	C1219	U1159	A1099	A1039	A979
G1760	G1700	C1640	C1580	U1520	A1460	A1400	G1340	U1280	G1220	G1160	A1040	G1040	G980
G1761	C1701	C1641	C1581	U1521	C1461	G1401	G1341	A1281	G1221	U1161	U1041	G1041	C981
C1762	C1702	G1642	A1582	C1522	G1462	G1402	G1342	A1282	G1222	A1162	G102	G1042	G982
G1763	C1703	A1643	A1583	A1523	A1463	U1403	C1343	G1283	A1223	C1163	G1043	U1044	G983
A1764	G1704	G1644	G1584	C1524	A1464	A1404	C1344	G1284	G1224	G1164	A1044	A1044	A984
G1765	U1705	A1645	A1585	A1525	G1465	A1405	G1345	A1285	G1225	G1165	U1045	G1045	G985
U1766	A1706	G1646	A1586	U1526	C1466	A1406	G1346	U1286	A1226	A1166	A1046	U1046	A986
G1767	A1707	U1647	U1587	G1527	U1467	A1407	C1347	A1287	A1227	A1167	A1047	G1047	G987
U1768	G1708	C1648	A1588	C1528	A1468	A1408	C1348	A1288	G1228	G1168	U1048	U1048	G988
U1769	U1709	A1649	G1589	A1529	A1469	U1409	A1349	A1289	C1229	U1169	A1049	C1049	G989
U1770	U1710	A1650	U1590	U1530	G1470	U1410	G1350	A1290	G1230	U1170	G1110	G1050	A990
A1771	C1711	U1651	A1591	A1531	G1471	C1411	G1351	G1291	A1231	A1171	C1111	U1051	A991
C1772	G1712	G1652	U1592	A1532	C1472	A1412	G1352	A1292	U1232	U1172	U1112	G1052	A992
G1773	G1713	C1653	G1593	G1533	U1473	U1413	A1353	A1293	A1233	G1173	G1113	G1053	C993
A1774	A1714	A1654	U1594	A1534	A1474	G1414	A1354	G1294	C1234	G1174	A1114	C1054	A994
A1775	A1715	C1655	C1595	C1535	U1475	A1415	A1355	U1295	C1235	A1175	C1115	U1055	A995
A1776	G1716	U1656	A1596	G1536	G1476	A1416	G1356	G1296	G1236	U1176	U1116	U1056	C996
A1777	A1717	A1657	A1597	U1537	U1477	C1417	U1357	A1297	G1237	U1177	G1117	A1057	C997
U1778	A1718	A1658	C1598	A1538	U1478	C1418	G1358	G1298	A1238	A1178	G1118	G1058	C998
G1779	G1719	G1659	G1599	U1539	A1479	G1419	G1359	A1299	A1239	A1179	U1119	A1059	A999
A1780	G1720	C1660	C1540	C1540	G1480	A1420	G1360	A1300	G1240	A1180	G1120	C1060	G1000
C1781	C1721	C1661	U1601	G1542	U1481	U1421	G1361	U1301	G1241	C1181	G1121	A1061	A1001
A1782	G1722	G1662	G1602	G1542	U1482	C1422	A1362	C1302	A1242	U1182	A1122	G1062	C1002
G1783	U1723	C1663	A1603	G1543	G1483	A1423	C1363	U1303	G1243	C1183	U1123	C1063	C1003
C1784	G1724	A1664	A1604	A1544	U1484	U1424	C1364	U1304	U1244	G1184	U1124	C1064	A1004
A1785	C1725	C1665	G1605	G1545	U1485	G1425	U1365	C1305	G1245	C1185	G1125	A1065	U1005
G1786	C1726	G1666	C1606	C1546	A1486	U1426	A1366	U1306	G1246	G1186	A1126	G1066	C1006
U1787	C1727	A1667	U1607	U1547	C1487	G1427	A1367	U1307	U1247	A1187	C1127	G1067	A1007
A1788	U1728	G1668	U1608	A1548	G1488	G1428	G1368	C1308	G1248	A1188	G1128	A1068	G1008
U1789	U1729	A1669	C1569	C1549	G1489	A1429	G1369	G1309	G1249	G1189	A1129	G1069	C1009
G1790	G1730	A1670	U1610	U1550	U1490	G1430	U1370	C1310	A1250	C1190	U1130	G1070	U1010
C1791	U1731	A1671	U1611	U1551	C1491	U1431	G1371	C1311	A1251	G1191	G1131	A1011	A1011
U1792	U1732	A1672	C1552	A1492	A1492	G1432	A1372	G1312	C1252	A1192	C1132	U1072	A1012
A1793	U1733	C1673	G1553	A1493	A1493	A1433	G1373	U1313	C1253	G1193	G1133	G1073	G1013
A1794	C1734	C1674	G1554	G1494	A1494	U1434	G1374	A1314	G1254	U1194	C1134	G1074	G1014
G1795	G1735	C1675	A1555	A1495	G1495	G1435	C1375	A1315	A1255	U1195	C1135	C1075	U1015
A1796	C1736	U1676	A1556	A1496	G1496	G1436	C1376	G1316	C1256	G1196	G1136	U1076	C1016

G2570	A2510	A2450	A2390	G2330	G2270	G2210	G3105	C2028	G1968	C1908	A3865	C1797
G2571	G2511	G2451	A2391	A2331	G2271	U2211	U3106	G2029	G1969	U1909	A3866	G1798
U2572	A2512	U2452	G2392	A2332	A2272	U2212	G3107	U2030	G1970	A1910	G3867	A1799
G2573	A2513	G2453	G2393	A2333	G2273	G2213	G3108	A2031	G1971	A1911	U3868	A1800
G2574	G2514	G2454	G2394	G2334	G2274	G2214	U3109	G2032	G1972	G1912	G3869	C1801
U2575	G2515	A2455	G2395	G2335	U2275	G2215	G3110	C2033	G1973	G1913	G3870	A1802
U2576	U2516	U2456	G2396	G2336	G2276	G2216	G3111	A2034	U1974	U1914	A3871	G1803
A2577	G2517	U2457	A2397	A2337	A2277	G2217	G3112	G2035	U1975	A1915	A3872	U1804
G2578	G2518	U2458	G2398	A2338	G2278	G2218	U3113	G2036	U1976	G1916	G3873	G1805
A2579	G2519	G2459	A2399	A2339	G2279	U2219	A3114	A2037	G1977	C1917	G3874	A1806
C2580	A2520	G2460	G2400	G2340	A2280	A2220	G3115	C2038	U1978	G1918	A3875	A1807
G2581	G2521	G2461	A2401	G2341	G2281	G2221	G3116	G2039	G1979	A1919	A3876	G1808
G2582	G2522	G2462	U2402	G2342	G2282	U2222	A3117	A2040	U1980	A1920	A3877	G1809
U2583	G2523	G2463	C2403	G2343	G2283	U2223	U3118	A2041	A1981	A1921	G1861	U1810
U2584	G2524	G2464	A2404	G2344	U2284	U2224	A3119	A2042	G1982	U1922	C1862	A1811
G2585	G2525	G2465	A2405	A2345	U2285	G2225	G3120	A2043	G1983	U1923	U1863	A1812
G2586	U2526	G2466	G2406	G2346	G2286	A2226	U3121	G2044	A1984	C1924	G1864	A1813
U2587	G2527	A2467	G2407	G2347	G2287	G2227	U3122	A2045	G1985	G1925	G1865	G1814
G2588	G2528	G2468	G2408	G2348	A2288	U2228	G3123	C2046	G1986	U1926	G1866	G1815
U2589	G2529	G2469	A2409	G2349	G2289	G2229	G3124	C2047	G1987	U1927	A1867	G1816
G2590	C2530	U2470	U2410	G2350	A2290	G2230	G3125	G2048	A1988	U1928	A1868	U1817
U2591	U2531	U2471	A2411	G2351	U2291	G2231	A3126	C2049	C1989	U1929	A1869	G1818
G2592	G2532	U2472	A2412	A2352	G2292	G2232	G3127	G2050	U1990	G1930	U1870	U1819
A2593	G2533	G2473	G2413	G2353	G2293	G2233	U3128	U2051	G1991	G1931	G1871	G1820
U2594	U2534	G2474	A2414	G2354	U2294	G2234	G3129	G2052	G1992	G1932	A1872	A1821
C2595	G2535	C2475	G2415	A2355	G2295	G2235	G3130	G2053	G1993	G1933	A1873	C1822
G2596	G2536	A2476	U2416	A2356	U2296	U2236	A3131	A2054	U1994	U1934	G1874	G1823
U2597	G2537	G2477	U2417	G2357	G2297	G2237	A3132	G2055	G1995	A1935	C1875	C1824
C2598	C2538	G2478	A2418	G2358	U2298	G2238	G3133	C2056	A1996	A1936	C1876	G1825
U2599	G2539	U2479	G2419	G2359	A2299	G2239	A3134	U2057	A1997	G1937	G1877	U1826
A2600	G2600	G2480	G2420	C2360	G2300	C2240	A3135	U2058	U1998	U1938	C1878	G1827
G2601	U2641	G2481	C2421	G2361	A2301	U2241	C3136	U2059	U1999	U1939	C1879	C1828
C2602	U2642	A2482	A2422	G2362	G2302	C2242	G3137	A2060	U2000	G1940	G1880	C1829
G2603	A2643	G2483	G2423	G2363	C2303	C2243	U3138	C2061	G2001	G1941	G1881	C1830
G2604	G2644	G2484	G2424	G2364	G2304	C2244	U3139	U2062	A2002	G1942	U1882	G1831
G2605	A2645	U2485	G2425	U2365	G2305	A2245	G3140	A2063	A2003	A1943	G1832	G1832
G2606	G2646	G2486	G2426	U2366	A2306	G2246	G3141	U2064	U2004	C1944	A1884	U1833
C2607	G2647	G2487	A2427	A2367	A2307	G2247	C3142	A2065	U2005	C1945	C1885	C1834
A2608	G2648	G2488	U2428	G2368	A2308	A2248	U3143	G2066	G2006	U1946	G1886	C1835
G2609	G2649	G2489	A2429	U2369	G2309	U2249	A3146	U2067	G2007	G1947	G1887	C1836
U2610	C2650	U2490	A2430	G2370	G2310	G2250	C3147	C2068	C2008	C1948	C1888	G1837
A2611	A2651	C2491	C2431	A2371	U2311	U2251	G3148	U2069	U2009	A1949	G1889	G1838
G2612	G2652	G2492	A2432	A2372	A2312	A2252	G3149	G2070	G2010	C1950	G1890	A1839
A2613	G2653	U2493	G2433	C2373	G2313	A2253	C3150	G2071	U2011	G1951	C1891	A1840
G2614	C2654	C2494	G2434	G2374	A2314	C2254	U3151	C2072	A2012	A1952	C1892	G1841
U2615	G2655	G2495	G2435	G2375	A2315	G2255	G3152	A2073	A2013	A1953	G1893	G1842
G2616	U2656	G2496	U2436	G2376	G2316	G2256	G3153	U2074	A2014	A1954	U1894	U1843
U2617	G2657	A2497	G2437	U2377	G2317	A2257	G3154	U2075	G2015	G1955	C1895	C1844
A2618	U2658	U2498	A2438	G2378	U2318	G2258	G3155	C3093	A2016	G1956	A1845	G1845
G2619	U2659	C2499	U2439	G2379	G2319	G2259	G3156	A3094	U2017	C1957	C1897	A1846
G2620	G2660	U2500	G2440	U2380	G2320	G2260	G3157	A3095	G2018	G1958	U1898	G1847
G2621	G2661	U2501	A2441	A2381	C2321	G2261	A3158	C3096	C2019	U1959	A1899	U1848
G2622	G2662	G2502	C2442	C2382	U2322	G2262	G3159	G3097	G2020	A1960	U1900	G1849
A2623	U2663	G2503	C2443	C2383	C2263	G2263	C3160	U3098	G2021	A1961	G1850	G1850
G2624	G2664	G2504	G2444	G2384	G2264	C2264	G3161	C3099	C2022	G1962	A1902	A1851
U2625	C2665	G2505	C2445	U2385	A2265	A2265	C3162	G3100	C2023	G1963	C1903	G1852
U2626	A2666	G2506	C2446	G2386	G2326	A2266	C3163	A3101	U2024	A1964	G1904	C1853
G2627	G2667	U2507	G2447	U2387	U2327	A2267	G3164	G3102	U2025	U1965	G1905	G1854
C2628	G2668	U2508	A2448	G2388	G2328	G2268	G3165	C3103	C2026	G1966	U1906	G1855
U2629	A2669	A2509	G2449	G2389	G2329	G2269	G3166	C3104	C2027	U1967	C1907	U1856



G1377	G1317	U1257	U1197	A1137	U1077	G1017	G957	A897	U837	A777	G717	A657	U597
A1378	A1318	G1288	C1198	A1138	A1078	C1018	G958	C998	A838	G778	A718	G658	U598
A1379	A1319	A1289	U1199	A1139	G1079	U1019	C959	G999	U839	G779	A719	G659	G600
C1380	C1319	A1260	G1200	A1140	A1080	U1020	C960	U900	U840	U780	A720	G660	A601
G1381	A1321	G1261	G1201	U1141	A1081	A1021	G961	A900A	C841	G781	C721	G661	C602
G1382	G1322	U1262	U1202	G1142	G1082	A1022	C962	A901	A842	U782	G722	G662	C603
C1383	G1323	G1263	A1203	A1143	C1083	U1023	G963	U902	G843	G783	C723	G663	U604
G1384	G1324	C1264	G1204	U1144	A1084	A1024	A964	G903	G844	U784	C724	G664	G605
C1385	U1325	G1265	G1205	C1145	G1085	A1025	G965	U904	U845	U785	C725	A665	U606
A1386	G1326	G1266	G1206	G1146	C1086	U1026	A966	G905	A846	U786	G726	U666	G607
G1387	C1327	A1267	G1207	G1147	C1087	U1027	G967	U906	C847	U787	G727	U667	C607
C1388	G1328	U1268	A1208	G1148	A1088	G1028	C968	U907	A848	G788	G728	A668	G608
G1389	U1329	G1269	G1209	G1149	C1089	C1029	U969	C909	G849	G789	A729	G669	U609
G1390	G1330	C1270	C1210	C1150	C1090	U1030	A970	U910	C850	A790	C730	U670	G610
A1391	G1331	G1271	G1211	U1151	C1091	A1031	A971	A911	C851	G791	A731	A671	C611
U1392	G1332	C1272	U1212	C1152	U1092	A1032	C972	A912	U852	U792	G732	C672	G612
G1393	G1333	G1273	G1213	A1153	C1093	G1033	U973	A913	C853	G793	G733	G673	A613
G1394	A1334	C1274	U1214	A1154	C1094	U1034	U974	C914	C854	A794	G734	G674	G614
A1395	A1335	A1275	A1215	G1155	A1095	G1035	C975	C915	C855	A795	G735	G675	C615
G1396	G1336	U1276	G1216	U1156	A1096	G1036	C976	U916	A856	A796	G736	G676	U616
A1397	G1337	G1277	U1217	U1157	A1097	U1037	G977	U917	U857	A797	G737	G677	U617
G1398	C1338	A1278	C1218	U1158	A1098	U1038	U978	A918	C858	G798	G738	G678	A618
C1399	U1339	G1279	G1219	U1159	A1099	A1039	A979	U919	U859	C799	G739	G679	A619
A1400	C1340	U1280	G1220	G1160	G1100	A1040	G980	G920	U860	U800	A740	U680	G620
G1401	G1341	A1281	C1221	U1161	U1101	G1041	C981	A921	C861	A801	G741	A681	U621
G1402	U1342	A1282	G1222	A1162	G1102	G1042	C982	A922	A862	A802	G742	G682	U622
U1403	C1343	C1283	G1223	C1163	G1103	A1043	G983	A923	C863	C803	A743	A683	G623
C1404	C1344	G1284	A1224	A1164	G1104	U1044	A984	C924	C864	C804	C744	C684	A624
A1405	G1345	A1285	G1225	G1165	U1105	G1045	G985	U925	A865	G805	C745	U685	A625
A1406	C1346	U1286	A1226	A1166	A1106	U1046	A986	C926	U866	A806	G746	C686	G626
G1407	C1347	A1287	G1227	A1167	A1107	G1047	G987	C927	C867	A807	A747	G687	A627
A1408	C1348	A1288	G1228	G1168	U1108	U1048	G988	G928	U868	C808	A748	A688	A628
U1409	A1349	A1289	C1229	C1169	A1109	C1049	G989	A929	C869	C809	C749	A689	C629
U1410	G1350	A1290	C1230	U1170	G1110	G1050	A990	A930	C870	U810	G750	A690	G630
C1411	G1351	C1291	A1231	U1171	U1111	U1051	A991	G931	C871	G811	G751	C691	G631
U1412	G1352	A1292	U1232	G1172	U1112	C1052	A992	G932	C872	G812	G752	C692	A632
U1413	A1353	A1293	A1233	G1173	C1113	G1053	C993	G933	U873	A813	U753	A693	G633
G1414	A1354	G1294	C1234	G1174	A1114	C1054	A994	G934	A874	G814	C754	G694	G634
C1415	A1355	C1295	C1235	U1175	C1115	A1055	A995	C935	C875	A815	C755	G695	C635
A1416	G1356	G1296	G1236	U1176	U1116	U1056	C996	A936	A876	U816	C756	U696	G636
C1417	U1357	A1297	G1237	U1177	G1117	A1057	C997	C937	C877	A817	U757	G697	G637
C1418	C1358	G1298	A1238	C1178	G1118	G1058	C998	G938	C878	G818	G758	A698	A638
G1419	G1359	A1299	A1239	A1179	U1119	A1059	A999	C939	C879	C819	C759	G699	G639
A1420	G1360	A1300	G1240	A1180	C1120	C1060	G1000	G940	C880	U820	U760	C700	C640
U1421	G1361	U1301	G1241	C1181	G1121	A1061	A1001	U941	U881	A821	G761	U701	G641
C1422	A1362	C1302	A1242	U1182	A1122	G1062	C1002	U942	C882	G822	A762	A702	A642
A1423	C1363	U1303	G1243	C1183	G1123	C1063	C1003	U943	A883	U823	A763	A703	A643
U1424	C1364	U1244	U1244	G1184	U1124	C1064	A1004	A944	C884	U824	A764	G704	A644
G1425	U1365	G1245	G1245	C1185	G1125	A1065	U1005	G945	A885	C825	C765	G705	G645
U1426	A1366	U1306	G1246	G1186	A1126	G1066	C1006	U946	A886	U826	A766	A706	C646
G1427	A1367	U1307	U1247	A1187	C1127	G1067	A1007	C947	C887	C827	G767	U707	G647
G1428	G1368	G1308	G1248	A1188	G1128	A1068	G1008	C948	C888	C828	U768	G708	A648
A1429	C1369	G1309	G1249	G1189	A1129	G1069	C1009	G949	C889	C829	C769	A709	G649
G1430	U1370	C1310	A1250	C1190	U1130	G1070	U1010	G950	U890	C830	U770	C710	U650
U1431	G1371	C1311	G1251	G1191	G1131	U1071	A1011	G951	A891	G831	C771	A711	C651
G1432	A1372	G1312	C1252	A1192	C1132	U1072	A1012	A952	A892	A832	G772	A712	G652
A1433	G1373	U1313	C1253	G1193	G1133	G1073	G1013	G953	C893	A833	G773	G713	G653
U1434	G1374	A1314	G1254	U1194	C1134	C1074	G1014	U954	C894	A834	A774	G714	A654
G1435	C1375	A1315	A1255	U1195	U1015	C1075	U1015	G955	C895	U835	U775	U715	G655
G1436	C1376	G1316	C1256	G1196	G1136	U1076	C1016	A956	C896	G836	G776	U716	U656

G2210	U3167	G3105	C2028	G1968	G1908	A3865	C1797	G1737	G1617	G1557	C1497	A1437
U2211	G3168	U3106	G2029	G1969	U1909	A3866	G1798	U1738	U1618	C1558	G1498	G1438
U2212	A3169	G3107	U2030	G1970	A1910	G3867	A1799	G1739	A1619	G1559	A1499	G1439
G2213	A3170	G3108	A2031	G1971	A1911	U3868	A1800	G1740	C1620	U1560	U1500	G1440
G2214	A3171	U3109	G2032	G1972	G1912	G3869	A1801	G1741	G1621	A1561	C1501	C1441
G2215	U3172	G3110	C2033	G1973	G1913	G3870	A1802	G1742	A1682	G1562	G1502	C1442
G2216	A3173	G3111	A2034	U1974	U1914	A3871	A1803	G1743	C1623	U1563	G1503	C1443
G2217	G3174	G3112	G2035	G1975	A1915	A3872	U1804	G1744	C1624	U1564	G1504	C1444
G2218	C3175	U3113	G2036	U1976	G1916	G3873	G1805	G1745	A1625	G1565	U1505	A1445
U2219	A3176	A3114	A2037	G1977	G1917	G3874	A1806	A1746	A1686	G1566	C1506	U1446
A2220	C3177	G3115	C2038	U1978	G1918	A3875	A1807	G1747	C1627	A1567	U1507	U1447
G2221	C3178	G3116	G2039	G1979	A1919	A3876	A1808	U1748	G1628	A1568	G1508	A1448
U2222	A3179	A3117	A2040	U1980	A1920	A3877	G1809	G1749	G1629	A1569	A1509	C1449
U2223	U3180	U3118	A2041	A1981	A1921	G1861	U1810	A1750	A1630	C1570	A1510	G1450
U2224	C3181	A3119	A2042	G1982	U1922	C1862	A1811	U1751	C1631	G1571	C1451	C1451
G2225	U3182	G3120	A2043	G1983	U1923	U1863	U1812	A1752	C1632	C1572	A1512	A1452
A2226	A3183	G3121	G2044	A1984	C1924	G1864	A1813	A1753	C1633	G1573	U1513	A1453
C2227	C3184	U3122	A2045	G1985	C1925	G1865	A1814	G1754	A1634	A1574	C1514	U1454
U2228	U3185	G3123	C2046	G1986	U1926	G1866	G1815	G1755	G1635	C1575	U1515	C1455
G2229	U3186	G3124	C2047	G1987	U1927	A1867	G1816	C1756	G1636	G1576	A1516	C1456
G2230	U3187	G3125	C2048	G1988	G1928	A1868	U1817	C1757	U1637	C1577	C1517	A1457
G2231	U3188	A3126	C2049	U1989	U1929	A1869	A1818	C1758	G1638	U1578	C1518	A1458
G2232	U3189	G3127	G2050	U1990	C1930	U1870	U1819	A1759	A1639	G1579	G1519	U1459
G2233	G3190	G3128	U2051	G1991	G1931	A1871	A1820	G1760	C1640	C1580	G1520	G1460
G2234	A3191	C3129	G2052	G1992	G1932	A1872	A1821	G1761	C1641	C1581	U1521	C1461
G2235	C3192	G3130	G2053	G1993	G1933	A1873	C1822	C1762	G1642	A1582	C1522	C1462
U2236	G3193	A3131	A2054	G1994	U1934	G1874	G1823	G1763	A1643	A1583	A1523	A1463
C2237	U3194	A3132	G2055	G1995	C1935	C1875	A1824	A1764	G1644	G1584	C1524	A1464
G2238	U3195	G3133	C2056	A1996	A1936	C1876	G1825	C1765	U1645	A1585	A1525	G1465
C2239	G3196	A3134	U2057	A1997	G1937	C1877	U1826	U1766	A1646	A1586	U1526	G1466
C2240	U3197	G3135	U2058	A1998	U1938	C1878	G1827	G1767	U1647	A1587	G1527	U1467
U2241	A2181	C3136	U2059	U1999	U1939	G1879	C1828	U1768	C1648	A1588	C1528	A1468
C2242	A2182	C3137	A2060	U2000	C1940	G1880	U1829	U1769	A1649	A1589	G1529	A1469
C2243	C2183	G3138	C2061	G2001	G1941	U1881	C1830	U1770	A1650	C1590	U1530	G1470
C2244	U2184	U3139	U2062	A2002	G1942	G1882	G1831	A1771	U1651	U1591	C1531	G1471
A2245	G2185	G3140	A2063	A2003	A1943	A1883	G1832	C1772	G1652	U1592	A1532	C1472
A2246	G2186	G3141	U2064	U2004	C1944	A1884	U1833	C1773	C1653	G1593	G1533	U1473
A2247	A2187	C3142	A2065	U2005	C1945	C1885	G1834	A1774	A1654	U1594	A1534	A1474
A2248	A2188	U3143	G2066	G2006	U1946	G1886	C1835	A1775	C1655	A1595	C1535	U1475
U2249	A2189	A3146	U2067	G2007	G1947	G1887	C1836	A1776	U1656	A1596	G1536	G1476
G2250	A2190	C3147	C2068	C2008	C1948	C1888	G1837	U1777	A1657	C1597	U1537	C1477
U2251	A2191	G3148	U2069	U2009	A1949	G1889	G1838	U1778	A1658	C1598	A1538	U1478
A2252	U2192	G3149	G2070	G2010	C1950	G1890	A1839	A1779	G1659	G1599	U1539	G1479
C2253	C2193	C3150	G2071	U2011	G1951	C1891	A1840	U1780	G1660	U1600	C1540	U1480
C2254	A2194	U3151	C2072	A2012	A1952	C1892	G1841	C1781	C1661	U1601	G1541	U1481
G2255	C2195	G3152	A2073	A2013	A1953	G1893	G1842	U1782	G1662	G1602	C1542	U1482
G2256	U2196	G3153	U2074	A2014	A1954	U1894	U1843	G1783	C1663	A1603	G1543	G1483
A2257	U2197	G3154	U2075	G2015	G1955	A1895	C1844	G1784	G1664	A1604	A1544	G1484
G2258	U2198	G3155	C3093	A2016	A1956	A1896	A1845	A1785	G1665	A1605	G1545	U1485
G2259	C2199	G3156	A3094	U2017	C1957	C1897	A1846	C1786	G1666	C1606	G1546	A1486
C2260	G2200	G3157	A3095	G2018	G1958	U1898	G1847	U1787	A1667	A1607	U1547	C1487
G2261	G2201	A3158	C3096	C2019	U1959	A1899	U1848	C1788	G1668	U1608	U1548	G1488
G2262	G2202	G3159	G3097	G2020	U1960	U1900	G1849	U1789	C1669	G1609	C1549	A1489
C2263	G2203	C3160	U3098	G2021	A1961	A1901	G1850	U1790	G1670	A1610	C1550	U1490
C2264	A2204	G3161	C2022	C2022	G1962	A1902	A1851	C1791	A1671	U1611	U1551	C1491
A2265	C2205	C3162	G3100	C2023	G1963	C1903	G1852	C1792	A1672	U1612	C1552	A1492
A2266	C2206	C3163	A3101	U2024	A1964	G1904	C1853	A1793	C1673	G1613	G1553	A1493
A2267	G2207	G3164	A3102	A2025	U1965	U1905	G1854	A1794	C1674	C1614	G1554	G1494
G2268	U2208	C3165	G3103	C2026	C1966	G1906	G1855	C1795	C1675	C1615	A1555	G1495
G2269	G2209	G3166	C3104	C2027	U1967	C1907	A1856	A1796	U1676	C1616	A1556	G1496



U2370	G2330	A2390	A2450	A2510	C2570	C2630	A2690	G2750	G2813	G2873
C2271	A2331	A2391	G2451	G2511	G2571	C2631	C2691	C2751	G2814	A2874
C2272	G2332	G2392	U2452	A2512	U2572	U2632	U2692	C2752	C2815	C2874
C2273	A2333	G2393	C2453	A2513	C2573	A2633	U2693	C2753	C2816	C2875
C2274	G2334	G2394	C2454	A2514	U2574	C2634	G2694	C2754	C2817	C2876
U2275	U2335	C2395	C2455	G2515	U2575	U2635	C2695	A2755	C2818	A2877
C2276	G2336	C2396	U2456	U2516	G2576	A2636	A2696	A2756	C2819	
A2277	A2337	U2397	A2457	C2517	A2577	C2637	G2697	C2757	C2820	
A2278	G2338	U2398	A2458	G2518	U2578	C2638	G2698	A2758	G2821	
C2279	A2339	C2399	C2459	C2519	C2579	A2639	G2699	U2759	U2822	
A2280	G2340	G2400	C2460	A2520	C2580	G2640	U2700	G2760	G2823	
C2281	U2341	U2401	G2461	A2521	A2581	A2641	A2701	A2761	C2824	
G2282	G2342	C2402	C2462	G2522	G2582	G2642	G2702	U2762	A2825	
G2283	C2343	C2403	G2463	G2523	U2583	G2643	G2703	U2763	G2826	
U2284	G2344	A2404	G2464	U2524	U2584	C2644	U2704	U2764	G2827	
U2285	A2345	G2405	G2465	U2525	C2585	C2645	A2705	C2765	C2828	
G2286	G2346	C2406	G2466	U2526	G2586	C2646	U2706	U2766	A2829	
G2287	U2347	C2407	A2467	G2527	G2587	G2647	G2707	C2767	U2830	
A2288	A2348	G2408	G2468	G2528	U2588	G2648	U2708	C2768	A2831	
A2289	G2349	C2409	G2469	G2529	C2589	A2649	C2709	C2769	G2832	
A2290	G2350	U2410	U2470	U2530	U2590	G2650	C2710	A2770	G2833	
U2291	G2351	U2411	U2471	U2531	C2591	U2651	G2711	C2771	A2834	
C2292	A2352	A2412	U2472	G2532	U2592	G2652	G2712	U2772	A2835	
G2293	G2353	G2413	C2473	U2533	U2593	A2653	A2713	G2773	U2836	
G2294	G2354	A2414	G2474	U2534	U2594	A2654	A2714	U2774	G2837	
C2295	A2355	G2415	C2475	C2535	C2595	C2655	C2715	U2775	U2838	
U2296	A2356	U2416	U2476	G2536	C2596	G2656	G2716	U2776	G2839	
U2297	G2357	U2417	C2477	G2537	G2597	G2657	G2717	A2777	U2840	
U2298	C2358	C2418	C2478	C2538	C2598	A2658	A2718	U2778	U2841	
A2299	U2359	G2419	U2479	U2539	U2599	C2659	U2719	G2779	G2842	
G2300	C2360	C2420	C2480	A2540	A2600	C2660	A2720	U2780	A2843	
A2301	G2361	C2421	G2481	U2541	C2601	C2661	A2721	A2781	G2844	
G2302	C2362	C2422	U2482	U2542	G2602	C2662	C2722	A2782	C2845	
C2303	G2363	G2423	U2483	A2543	G2603	U2663	G2723	U2783	G2846	
G2304	C2364	G2424	C2484	A2544	G2604	C2664	C2724	A2784	G2847	
C2305	U2365	G2425	U2485	A2545	C2605	U2665	U2725	C2785	A2848	
A2306	U2366	G2426	C2486	G2546	G2606	U2666	U2726	U2786	C2849	
A2307	A2367	A2427	G2487	C2547	C2607	C2667	G2727	G2790	U2850	
A2308	G2368	U2428	G2488	G2548	A2608	U2668	A2728	C2791	G2851	
G2309	U2369	A2429	C2489	G2549	G2609	C2669	A2729	C2792	G2852	
G2310	G2370	A2430	U2490	C2550	G2610	C2670	A2730	G2793	U2853	
U2311	C2371	C2431	C2491	A2551	C2611	C2671	C2731	G2794	G2854	
A2312	C2372	A2432	U2492	G2552	G2612	U2672	C2732	A2795	U2855	
G2313	A2373	G2433	U2493	G2553	A2613	C2673	A2733	U2796	C2856	
A2314	C2374	G2434	C2494	G2554	A2614	C2674	U2734	C2797	A2857	
G2315	G2375	C2435	G2495	G2555	U2615	U2675	C2735	A2798	C2858	
C2316	G2376	U2436	C2496	A2556	U2616	G2676	U2736	C2799	U2859	
G2317	U2377	G2437	A2497	G2557	G2617	U2677	A2737	C2800	A2860	
U2318	G2378	A2438	U2498	C2558	A2618	C2678	A2738	A2801	G2861	
C2319	G2379	U2439	C2499	U2559	G2619	G2679	G2739	U2802	U2862	
G2320	U2380	C2440	C2500	G2560	G2620	U2680	C2740	C2803	U2863	
C2321	A2381	U2441	U2501	G2561	G2621	A2681	G2741	G2804	C2864	
U2322	G2382	C2442	G2502	G2562	G2622	C2682	G2742	G2805	G2865	
G2323	C2383	C2443	G2503	U2563	A2623	C2683	G2743	G2806	A2866	
A2324	G2384	G2444	G2504	U2564	G2624	A2684	A2744	U2807	C2867	
C2325	U2385	C2445	G2505	C2565	U2625	A2685	A2745	U2808	G2868	
G2326	G2386	C2446	C2506	A2566	U2626	C2686	G2746	A2809	U2869	
U2327	U2387	G2447	U2507	G2567	G2627	C2687	C2747	A2810	C2870	
G2328	G2388	A2448	G2508	A2568	C2628	U2688	C2748	G2811	U2871	
C2329	G2389	G2449	A2509	A2569	U2629	C2689	A2749	A2812	U2872	

• Molecule 22: 23S RIBOSOMAL RNA

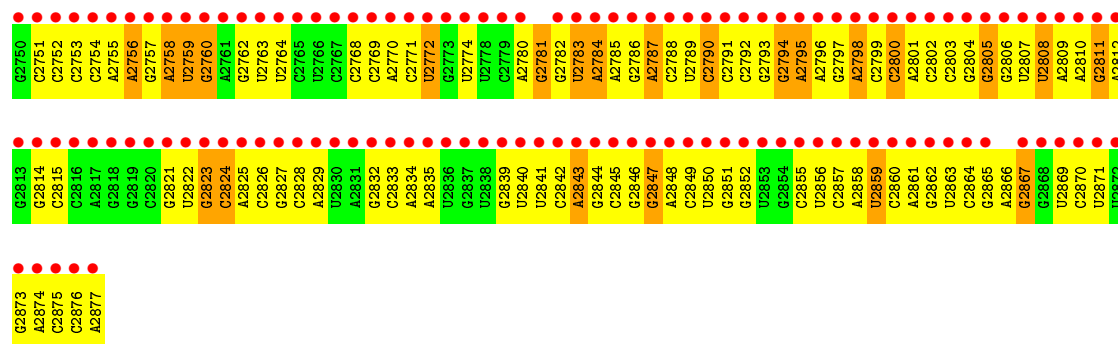


G1	U61
G2	U62
U3	A63
C4	G64
A5	C65
A6	U66
G7	G67
A8	C68
U9	G69
A10	A70
G11	A71
U12	A72
A13	A73
A14	G74
G15	C75
G16	C76
G17	C77
U18	C78
C19	G79
C20	A80
A21	C81
C22	G82
G23	A83
A24	G84
U25	C85
G26	U86
G27	G87
A28	G88
U29	A89
G30	G90
C31	A91
C32	U92
C33	A93
U34	C94
G35	G95
G36	C96
C37	U97
G38	U98
C39	U99
U40	G100
G41	A101
G42	G102
A43	U103
G44	C104
C45	G105
C46	G106
G47	G107
A48	G108
U49	A109
G50	U110
A51	G111
A52	U112
G53	C113
G54	C114
A55	G115
C56	A116
G57	A117
C58	U118
G59	G119
A60	G120

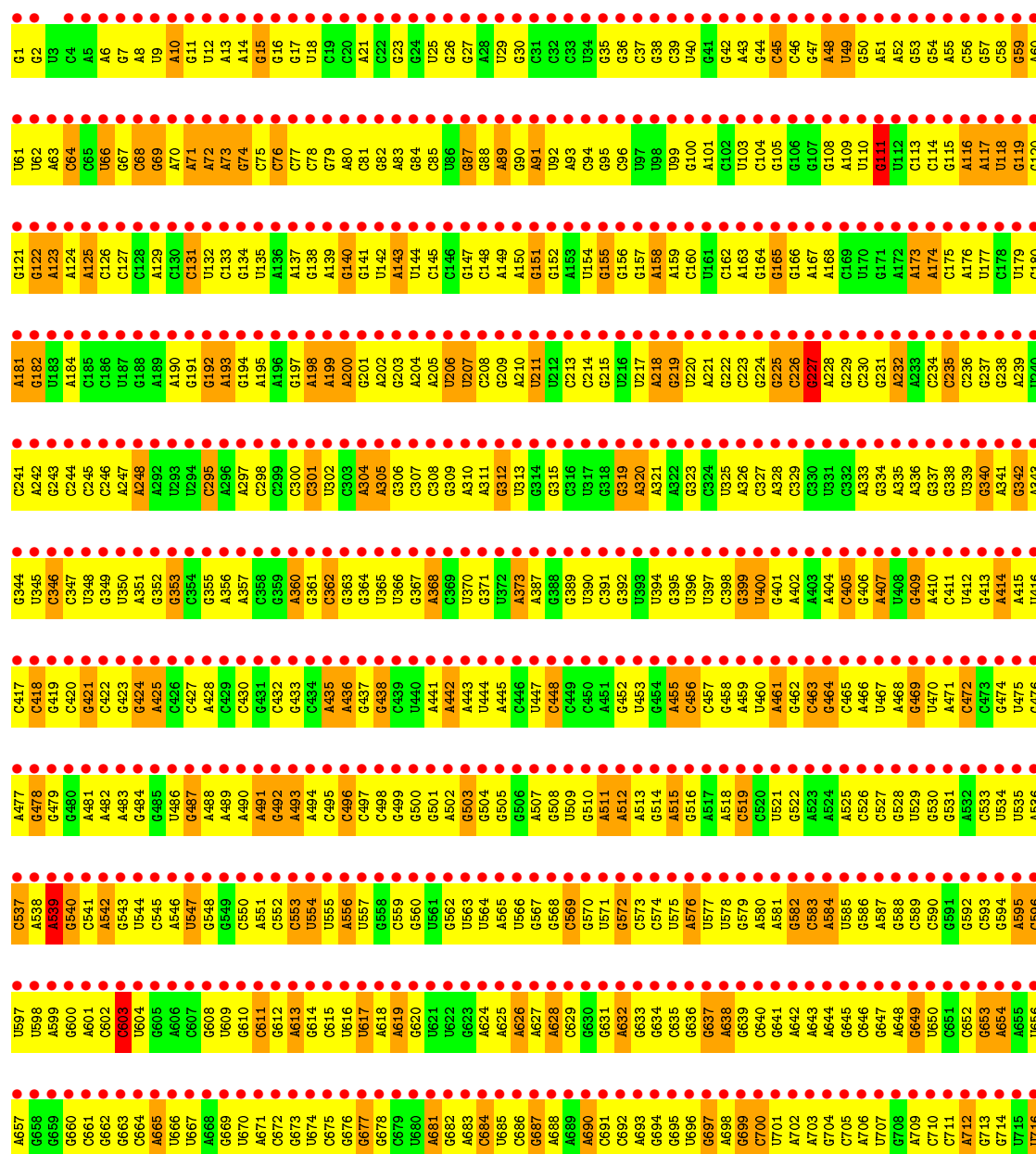
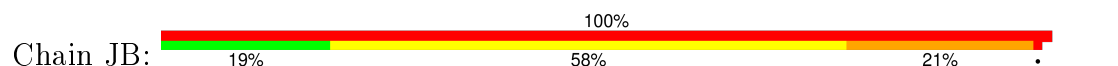
C1017	G957	A897	U837	A777	G717	A657	U597	C537	A477	G344	C241	A181	G121
C1018	G958	C896	A838	G778	A718	G658	U598	A538	G478	U345	A242	G182	G122
C1019	C959	C899	U839	U779	A719	G659	A599	A539	G479	C346	G243	U183	A123
A1020	U960	U960	U840	U780	A720	G660	G600	G480	G480	C347	C244	A184	A124
A1021	G961	A900A	C841	G781	G721	C661	A601	C541	A481	U348	C245	G185	A125
U1063	C962	A901	C842	U782	G722	G662	C602	A542	A482	G349	C246	G186	G126
G1024	G963	U902	G843	G783	G723	G663	G603	G543	A483	U350	A247	U187	C127
A1025	A964	G903	G844	U784	G724	C664	U604	U544	G484	A351	A248	G188	C128
U1026	G965	U904	U845	U785	C725	A665	G605	C545	G485	G352	A292	A189	A129
C1027	A966	U906	A846	U786	G726	U666	A606	A546	U486	G353	U293	A190	C130
G1028	G967	U907	C847	U787	G727	U667	C607	U547	G487	C354	U294	G191	G131
C1029	C968	U908	A848	G788	G728	A668	G608	G548	A488	U355	C295	G192	U132
U1030	U969	C910	G849	G789	A729	G669	U609	G549	A489	A356	A296	A193	C133
C1031	A971	C911	C850	A790	C730	U670	G610	C550	A490	A357	A297	G194	G134
A1032	C972	A912	U852	U792	A731	A671	G611	A551	A491	C358	C298	A195	U135
G1033	U973	A913	C853	G793	G732	C672	G612	C552	G492	G359	C299	A196	A136
U1034	U974	C914	G854	A794	G733	G673	A613	C553	A493	A360	C300	G197	A137
C1035	C975	U915	G855	A795	G734	U674	G614	U554	A494	G361	C301	A198	G138
G1036	C976	U916	A856	A796	G735	C675	C615	U555	G495	C362	U302	A199	A139
U1037	U977	U917	G857	A797	G736	G676	U616	A556	G496	G363	C303	A200	G140
A1038	U978	A918	G858	G798	G737	U677	U617	U557	C497	A364	A304	G201	G141
C1039	A979	U919	U859	C799	G738	C678	A618	G558	C498	U365	A305	A202	U142
A1040	G980	G920	U860	U800	A740	C679	A619	C559	G499	U366	G306	G203	A143
G1041	C981	A921	G861	A801	G741	A681	G621	U561	G501	G367	C307	A204	U144
U1042	C982	A922	A862	A802	G742	G682	U622	G562	A502	A368	C308	A205	C145
A1043	G983	A923	C863	C803	A743	A683	G623	U563	G503	C369	G309	U206	G146
C1044	A984	C924	C864	C804	A744	A684	G624	U564	G504	U370	A310	U207	G147
U1045	G985	U925	A865	G805	C745	U685	A625	A565	G505	G371	A311	C208	C148
G1046	A986	C926	U866	A806	G746	C686	G626	U566	G506	U372	G312	G209	A149
U1047	G987	C927	U867	A807	A747	G687	A627	C567	A507	A373	A210	A210	A150
U1048	G988	G928	U868	C808	A748	A688	G628	G568	G508	A374	G314	U211	G151
C1049	U989	A929	C869	C809	C749	A689	C629	G569	U509	G388	G315	U212	G152
G1050	A990	U930	U870	U810	C750	A690	G630	G570	G510	C389	C316	C213	A153
U1051	A991	G931	U871	G811	G751	C691	G631	U571	A511	U390	G317	C214	U154
C1052	A992	G932	G872	G812	G752	C692	A632	G572	A512	G391	U318	G215	G155
G1053	C993	G933	U873	A813	U753	A693	G633	C573	A513	G392	G319	U216	G156
C1054	A994	G934	A874	G814	G754	C694	G634	C574	G514	U393	A320	U217	G157
A1055	U995	C935	G875	A815	C755	G695	C635	U575	A515	U394	A321	A218	A158
U1056	C996	A936	A876	U816	C756	U696	G636	A576	G516	G395	A322	G219	A159
A1057	C997	C937	G877	A817	U757	G697	G637	U577	A517	U396	G323	U220	C160
G1058	U998	G938	C878	G818	G758	A698	A638	U578	A518	U397	C324	A221	U161
A1059	A999	C939	A879	C819	C759	G699	G639	G579	C519	G399	A326	G222	A163
C1060	U1000	C940	C880	U820	U760	C700	C640	A580	C520	U400	C327	G223	A163
A1061	A1001	U941	U881	A821	G761	U701	G641	A581	U521	G401	A328	G224	G164
C1062	C1002	U942	C882	G822	A762	A702	A642	G582	G522	A402	C329	C226	G165
G1063	C1003	U943	A883	U823	A763	A703	A643	C583	A523	A403	C330	A167	A168
C1064	A1004	A944	C884	U824	A764	G704	A644	A584	A524	A404	U331	A228	G169
A1065	U1005	G945	A885	C825	G765	C705	G645	U585	A525	C405	C332	G229	A170
G1066	C1006	U946	A886	U826	A766	A706	C646	G586	C526	G406	A333	C230	U170
U1067	A1007	C947	G887	C827	G767	U707	G647	A587	C527	A407	G334	G231	G171
A1068	U1008	C948	C888	C828	U768	G708	A648	G588	G528	U408	A335	A232	A172
G1069	G1009	G949	C889	C829	C769	A709	G649	C589	U529	A409	A336	A233	A173
U1070	U1010	U950	U890	C830	U770	C710	U650	C590	G530	A410	G337	C234	A174
A1071	A1011	A951	G891	G831	G771	A711	C651	G591	A531	A411	G338	G235	C175
U1072	U1012	A952	A892	A832	G772	A712	C652	G592	A532	U412	U339	C236	A176
G1073	G1013	G953	G893	A833	G773	G713	G653	C593	C533	G413	G340	G237	U177
C1074	U1014	U954	G894	A834	A774	G714	A654	G594	U534	A414	A341	G238	C178
G1075	U1015	G955	U895	U835	U775	U715	A655	A595	U535	A415	G342	A239	U179
U1076	C1016	A956	C896	G836	G776	U716	U656	C596	A536	U416	A343	U240	C180

A3865	C1797	G1737	G1617	G1557	G1497	A1437	G1377	G1317	U1257	U1197	A1137	U1077
A3866	G1798	U1738	U1618	C1558	G1498	G1438	A1378	A1318	G1288	C1198	A1138	A1078
G3867	A1799	G1559	A1619	C1559	A1499	G1439	A1379	C1319	A1289	U1199	A1139	G1079
G3868	U1800	A1560	A1620	A1560	U1500	G1440	C1380	A1320	A1260	U1190	A1140	A1080
G3869	G1741	A1681	G1621	A1561	C1501	A1441	G1381	A1321	G1261	G1201	U1141	A1081
G3870	G1742	A1682	G1622	A1562	G1502	A1442	G1382	A1322	U1262	U1202	G1142	G1082
G1803	G1743	U1563	C1623	U1563	G1503	G1443	C1383	G1323	G1263	A1203	A1143	C1083
A3871	G1744	U1564	G1624	U1564	G1504	G1444	C1384	G1324	G1264	G1204	U1144	C1084
G3872	C1745	G1565	A1625	G1565	U1505	A1445	C1385	G1325	G1265	G1205	U1145	G1085
G3873	A1805	A1685	A1625	G1566	G1506	U1446	A1386	U1326	G1266	G1206	G1146	C1086
A3874	G1806	A1686	C1627	A1567	A1507	U1447	G1387	C1327	A1267	G1207	G1147	C1087
A3875	G1747	A1687	G1628	A1568	G1508	A1448	C1388	U1328	U1268	A1208	U1148	A1088
A3876	U1748	A1688	G1629	A1569	G1509	G1449	C1389	U1329	A1269	G1209	G1149	A1089
A3877	G1749	U1689	A1630	C1570	A1510	G1450	G1390	G1330	C1270	G1210	C1150	C1090
G1861	A1750	U1690	A1630	C1570	A1510	G1450	G1390	G1330	C1270	G1210	C1150	C1090
G1862	A1811	G1751	C1631	G1571	A1511	G1451	A1391	G1331	G1271	G1211	U1151	C1091
U1863	A1812	U1752	C1632	G1572	A1512	U1452	A1392	G1332	G1272	G1212	C1152	U1092
G1864	A1813	G1753	C1633	A1573	U1513	A1453	G1393	G1333	G1273	U1213	A1153	U1093
G1865	G1814	G1754	A1694	A1574	C1514	U1454	G1394	A1334	C1274	G1214	A1154	C1094
G1866	G1815	G1755	G1635	C1575	U1515	A1455	A1395	A1335	A1275	A1215	G1155	A1095
A1867	G1816	C1756	G1636	A1576	A1516	C1456	C1396	G1336	U1276	G1216	U1156	A1096
A1868	U1817	G1757	U1637	A1577	C1517	A1457	A1397	G1337	U1277	U1217	U1157	A1097
A1869	G1818	G1638	G1638	U1578	C1518	A1458	G1398	G1338	A1278	C1218	A1158	G1098
U1870	A1759	G1639	G1639	G1579	G1519	U1459	C1399	U1339	G1279	G1219	U1159	A1099
G1871	G1820	C1640	C1640	C1580	G1520	G1460	A1400	G1340	U1280	G1220	G1160	G1100
A1872	G1761	G1641	C1641	U1581	U1521	A1461	G1401	G1341	A1281	G1221	U1161	U1101
A1873	C1762	G1642	G1642	A1582	C1522	G1462	G1402	U1342	A1282	G1222	A1162	G1102
G1874	G1763	A1643	A1643	A1583	A1523	A1463	U1403	C1343	G1283	G1223	C1163	C1103
C1875	A1764	G1644	G1644	G1584	C1524	A1464	C1344	C1344	A1284	A1224	C1164	G1104
C1876	G1765	U1645	U1645	A1585	A1525	G1465	A1405	G1345	A1285	G1225	G1165	U1105
C1877	U1646	A1586	G1646	U1586	U1526	A1466	A1406	G1346	U1286	A1226	A1166	A1106
C1878	G1767	U1647	U1647	A1587	G1527	U1467	G1407	C1347	A1287	A1227	A1167	A1107
G1879	U1768	C1648	C1648	A1588	G1528	A1468	A1408	C1348	A1288	G1228	G1168	U1108
G1880	U1769	A1649	A1649	G1589	C1529	U1469	A1409	A1349	A1289	C1229	C1169	A1109
U1881	G1830	U1770	A1650	U1590	U1530	G1470	U1410	G1350	A1290	C1230	U1170	G1110
G1882	A1771	G1651	U1651	U1591	C1531	A1471	G1411	G1351	G1291	A1231	A1171	U1111
G1883	C1772	G1652	G1652	U1592	A1532	U1472	A1412	G1352	A1292	U1232	U1172	U1112
A1884	C1773	G1653	C1653	G1593	G1533	U1473	U1413	A1353	A1293	A1233	G1173	G1113
C1885	A1774	A1654	A1654	U1594	A1534	A1474	G1414	A1354	G1294	C1234	G1174	A1114
G1886	A1775	C1655	C1655	A1595	C1535	U1475	C1415	A1355	U1295	G1235	A1175	C1115
G1887	U1776	U1656	U1656	A1596	G1536	G1476	A1416	G1356	U1296	G1236	U1176	U1116
C1888	G1837	A1657	A1657	A1597	U1537	C1477	C1417	C1357	A1297	G1237	U1177	G1117
G1889	U1778	A1658	A1658	G1598	A1538	U1478	C1418	C1358	G1298	A1238	C1178	G1118
C1890	G1779	G1659	G1659	G1599	U1539	G1479	A1419	G1359	A1299	A1239	A1179	U1119
A1891	A1840	U1780	G1660	U1600	C1540	G1480	A1420	G1360	A1300	G1240	A1180	C1120
C1892	G1841	C1781	C1661	U1601	G1541	U1481	U1421	G1361	U1301	G1241	C1181	G1121
G1893	U1842	A1782	G1662	G1602	G1542	C1482	C1422	A1362	C1302	A1242	A1182	A1122
U1894	G1783	C1783	C1663	A1603	G1543	G1483	A1423	C1363	U1303	G1243	C1183	G1123
A1895	C1844	G1784	G1664	A1604	A1544	U1484	U1424	C1364	U1304	U1244	G1184	U1124
A1896	A1845	A1785	G1665	A1605	G1545	U1485	G1425	U1365	G1305	G1245	G1185	G1125
C1897	U1846	C1786	G1666	C1606	G1546	U1486	U1426	A1366	U1306	G1246	G1186	A1126
U1898	G1847	U1787	A1667	A1607	U1547	C1487	G1427	A1367	U1307	U1247	A1187	C1127
A1899	U1848	C1788	G1668	U1608	U1548	G1488	G1428	G1368	U1308	U1248	A1188	G1128
U1900	G1849	U1789	A1669	G1609	C1549	A1489	A1429	G1369	G1309	G1249	G1189	A1129
A1901	G1850	G1790	G1670	A1610	G1550	U1490	G1430	U1370	C1310	A1250	G1190	U1130
A1902	A1851	C1791	A1671	U1611	U1551	C1491	G1431	G1371	G1311	G1251	G1191	C1131
C1903	G1792	U1792	A1672	U1612	G1552	A1492	G1432	A1372	G1312	C1252	A1192	G1132
G1904	C1853	A1793	C1673	G1613	G1553	A1493	A1433	G1373	U1313	C1253	G1193	G1133
G1905	G1854	A1794	C1674	G1614	G1554	G1494	U1434	G1374	A1314	G1254	G1194	C1134
U1906	G1855	C1795	C1675	C1615	A1555	G1495	A1435	C1375	A1315	A1255	U1195	C1135
C1907	U1856	A1796	U1676	C1616	A1556	G1496	G1436	C1376	G1316	C1256	G1196	G1136

A2690	C2630	C9570	A2450	A2390	G2330	G2270	G2210	U3167	G3105	C2028	G1968	C1908
C2691	C2631	G2571	G2451	A2391	A2331	G2271	U2211	G3168	U3106	G2029	G1969	U1909
A2692	A2632	U2572	U2452	G2392	G2332	A2272	G2212	A3169	G3107	U2030	G1970	A1910
U2693	C2633	C2573	C2453	G2393	A2333	C2273	G2213	A3170	G3108	U2031	C1971	A1911
G2694	G2634	G2574	C2454	G2394	G2334	C2274	G2214	A3171	U3109	G2032	G1972	G1912
G2695	U2635	G2575	A2455	G2395	U2335	U2275	G2215	A3172	G3110	C2033	G1973	G1913
A2696	U2636	U2576	U2456	G2396	G2336	C2276	G2216	A3173	C3111	A2034	U1974	U1914
C2697	C2637	G2577	A2457	A2397	A2337	A2277	G2217	C3174	G3112	G2035	U1975	A1915
G2698	G2638	C2578	U2458	U2398	C2338	A2278	G2218	A3175	U3113	G2036	U1976	G1916
A2699	A2639	A2579	C2459	C2399	A2339	G2279	U2219	A3176	G3114	A2037	C1977	G1917
U2700	G2640	C2580	G2460	G2400	G2340	A2280	A2220	C3177	G3115	C2038	U1978	G1918
A2701	A2641	A2581	G2461	G2401	G2341	C2281	G2221	C3178	G3116	A2039	G1979	A1919
G2702	G2642	G2582	C2462	U2402	U2342	C2282	U2222	C3179	A3117	G2040	A1980	A1920
G2703	G2643	U2583	G2463	C2403	C2343	G2283	U2223	U3180	U3118	A2041	A1981	A1921
U2704	A2644	U2584	G2464	A2404	G2344	U2284	U2224	C3181	A3119	A2042	U1982	U1922
A2705	G2645	C2585	G2465	A2405	G2345	U2285	G2225	U3182	G3120	A2043	G1983	U1923
U2706	G2646	G2586	G2466	C2406	G2346	G2286	A2226	A3183	G3121	G2044	C1924	C1924
G2707	G2647	G2587	A2467	G2407	G2347	G2287	G2227	C3184	U3122	A2045	G1985	C1925
U2708	G2648	U2588	G2468	G2408	A2348	A2288	U2228	U3185	G3123	C2046	U1986	U1926
C2709	A2649	C2589	G2469	A2409	G2349	A2289	G2229	U3186	G3124	C2047	G1987	U1927
G2710	U2650	U2590	U2470	U2410	G2350	A2290	G2230	A3187	G3125	C2048	U1988	G1928
U2711	U2651	C2591	U2471	A2411	G2351	U2291	G2231	U3188	A3126	C2049	C1989	U1929
G2712	G2652	U2592	U2472	A2412	A2352	C2292	G2232	G3189	G3127	G2050	U1990	C1930
A2713	A2653	A2593	G2473	G2413	G2353	C2293	G2233	G3190	G3128	U2051	G1991	G1931
A2714	A2654	U2594	G2474	A2414	G2354	U2294	G2234	A3191	G3129	G2052	G1992	G1932
G2715	C2655	C2595	C2475	G2415	A2355	C2295	G2235	C3192	G3130	G2053	G1993	G1933
G2716	G2656	G2596	U2476	U2416	A2356	U2296	U2236	G3193	A3131	A2054	U1994	U1934
G2717	G2657	C2597	C2477	U2417	A2357	G2297	G2237	C3194	G3132	G2055	A1935	A1935
A2718	A2658	C2598	U2478	A2418	G2358	U2298	G2238	G3195	G3133	C2056	A1936	A1936
U2719	C2659	U2599	C2479	C2419	U2359	A2299	G2239	G3196	U3134	U2057	A1937	G1937
A2720	G2660	C2600	C2480	C2420	C2360	G2300	G2240	U3197	A3135	U2058	A1938	U1938
G2721	G2661	G2601	G2481	C2421	G2361	A2301	U2241	A2181	C3136	U2059	U1939	U1939
C2722	G2662	G2602	A2482	C2422	G2362	G2302	C2242	A2182	G3137	A2060	U2000	C1940
G2723	U2663	G2603	U2483	G2423	G2363	C2303	C2243	C2183	C3138	C2061	G2001	C1941
G2724	G2664	G2604	A2484	G2424	G2364	G2304	C2244	C2184	U3139	U2062	A2002	G1942
G2725	G2665	G2605	U2485	G2425	C2365	C2305	A2245	U2185	G3140	A2063	A2003	A1943
U2726	G2666	G2606	G2486	G2426	U2366	A2306	A2246	G2186	G3141	U2064	C1944	C1944
G2727	C2667	C2607	G2487	A2427	A2367	A2307	A2247	A2187	G3142	A2065	U2005	C1945
A2728	U2668	A2608	G2488	U2428	G2368	A2308	A2248	A2188	U3143	G2066	G2006	U1946
A2729	G2669	G2609	C2489	A2429	U2369	G2309	G2249	A2189	A3146	U2067	G2007	G1947
G2730	G2670	G2610	U2490	A2430	G2370	G2310	G2250	A2190	C3147	C2068	C2008	A1948
G2731	C2671	A2611	C2491	A2431	A2371	U2311	U2251	A2191	G3148	U2069	U2009	A1949
C2732	U2672	G2612	G2492	A2432	C2372	A2312	A2252	U2192	G3149	G2070	G2010	C1950
A2733	G2673	A2613	C2493	G2433	G2373	G2313	A2253	C2193	G3150	G2071	U2011	G1951
U2734	C2674	G2614	C2494	G2434	C2374	A2314	C2254	A2194	U3151	C2072	A2012	A1952
G2735	U2675	U2615	G2495	C2435	G2375	A2315	G2255	C2195	G3152	U2073	A2013	A1953
U2736	G2676	U2616	C2496	U2436	G2376	G2316	G2256	U2196	G3153	A2074	A2014	A1954
G2737	G2677	G2617	A2497	G2437	U2377	G2317	A2257	U2197	G3154	U2075	G2015	G1955
A2738	U2678	C2618	U2498	A2438	G2378	U2318	G2258	U2198	G3155	C3093	A2016	G1956
G2739	G2679	G2619	C2499	U2439	G2379	G2319	G2259	C2199	G3156	A3094	U2017	C1957
C2740	U2680	G2620	C2500	G2440	U2380	G2320	G2260	G2200	G3157	A3095	G2018	G1958
G2741	A2681	G2621	U2501	U2441	A2381	C2321	G2261	G2201	A3158	C3096	C2019	U1959
G2742	G2682	G2622	G2502	C2442	C2382	U2322	G2262	G2202	G3159	G3097	G2020	A1960
G2743	C2683	A2623	G2503	C2443	C2383	U2323	C2263	G2203	C3160	U3098	G2021	A1961
A2744	A2684	G2624	G2504	C2444	G2384	G2324	G2264	A2204	G3161	U3099	C2022	G1962
G2745	U2685	U2625	G2505	G2445	U2385	A2325	A2265	C2205	G3162	G3100	G2023	G1963
G2746	C2686	U2626	C2506	G2446	G2386	C2326	A2266	C2206	G3163	A3101	U2024	A1964
C2747	G2687	G2627	U2507	C2447	G2387	U2327	A2267	G2207	C3164	G3102	A2025	G1965
G2748	A2688	A2628	G2508	A2448	G2388	G2328	G2268	U2208	G3165	C3103	C2026	C1966
A2749	C2689	U2629	A2509	G2449	G2389	C2329	G2269	G2209	G3166	C3104	C2027	U1967



● Molecule 22: 23S RIBOSOMAL RNA

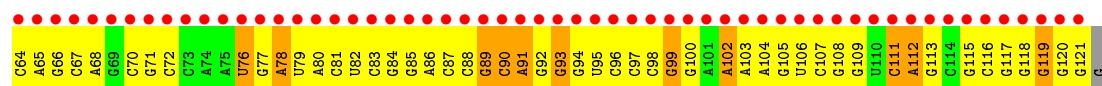


C1497	C1498	A1437	G1377	G1317	U1257	U1197	A1137	U1077	C1017	G957	A897	U837	A777	G717
G1498	G1499	G1438	A1378	A1318	G1258	C1198	A1138	A1078	C1018	G958	C898	A838	A778	A718
U1500	G1440	C1380	A1379	C1319	A1259	U1199	A1139	G1079	U1019	G959	G899	U839	G778	A719
C1501	G1441	G1381	C1380	A1320	G1260	G1200	A1140	A1080	A1020	U960	U900	U840	U779	A720
G1502	C1442	G1382	G1381	A1321	U1261	G1201	U1141	A1081	A1021	G961	A900A	A841	G781	C721
G1503	G1443	C1383	G1382	A1322	U1262	G1202	G1142	G1082	A1022	C962	U902	A842	U782	G722
G1504	C1444	G1383	G1383	A1323	G1263	A1203	A1143	G1083	U1023	G963	G843	G843	G783	G723
U1505	G1445	C1385	G1384	G1324	C1264	G1204	U1144	G1084	G1024	A964	G904	G844	U784	C724
C1506	A1445	A1386	G1385	U1325	G1265	G1205	C1145	G1085	A1025	G965	U905	U845	U785	C725
A1507	G1446	G1387	G1386	U1326	A1267	G1207	G1146	G1086	U1026	A966	U906	A846	U786	G726
G1508	C1448	C1388	G1387	C1328	U1268	A1208	G1147	C1087	G1027	G967	U907	C847	U787	U727
A1509	G1449	C1389	G1388	U1329	U1269	G1209	G1148	C1088	G1028	C968	C909	G848	G788	G728
A1510	G1450	G1390	G1389	U1330	C1270	G1210	G1149	C1089	U1030	U969	U910	G849	G789	A729
C1511	C1451	G1391	G1390	G1331	C1271	G1211	C1150	G1090	U1031	A970	C850	C850	A790	C730
A1512	A1452	A1392	A1391	G1332	G1272	U1212	U1151	C1091	A1032	A971	U911	U851	G791	A731
U1513	G1453	G1393	G1392	C1333	C1273	U1213	A1152	G1092	A1033	C972	A912	U852	U792	G732
A1514	U1454	A1394	G1393	G1334	G1274	C1214	A1153	U1093	G1034	U973	A913	C853	G793	G733
U1515	C1455	A1395	G1394	A1334	C1275	U1215	A1154	C1094	U1035	U974	C914	C854	A794	G734
A1516	C1456	A1396	A1395	A1335	A1275	A1215	G1155	A1095	G1035	C975	C915	G855	A795	G735
C1517	A1457	C1397	C1396	G1336	U1276	G1216	U1156	A1096	G1036	G977	U916	A856	A796	G736
G1518	U1458	G1398	G1397	G1337	G1277	U1217	G1157	A1097	U1037	G978	A918	U858	G798	G738
G1519	U1459	C1399	G1398	U1338	A1278	C1218	A1158	G1098	U1038	U978	U919	U859	C799	G739
G1520	G1460	A1400	G1399	U1339	G1279	C1219	U1159	A1099	A1039	A979	G920	U860	U800	A740
C1521	G1461	G1401	G1400	C1340	U1280	G1220	G1160	A1100	A1040	G980	G921	G861	A801	G741
C1522	C1462	G1402	G1401	G1341	U1281	C1221	U1161	U1101	G1041	C981	A921	A862	A802	G742
A1523	U1463	G1403	G1402	U1342	A1282	G1222	A1162	G1102	G1042	G982	A922	C863	G803	A743
C1524	A1464	U1404	C1403	C1343	G1283	G1223	C1163	G1103	A1043	A983	A923	C864	C804	C744
A1525	G1465	C1405	G1404	G1344	G1284	A1224	C1164	G1104	U1044	A984	C924	C865	G805	G745
U1526	G1466	A1406	A1405	G1345	A1285	G1225	G1165	U1105	G1045	G985	U925	U866	A806	G746
G1527	U1467	G1407	G1406	C1346	U1286	A1226	A1166	A1106	U1046	A986	C926	U867	A807	A747
C1528	U1468	C1408	G1407	C1347	A1287	G1227	A1167	A1107	G1047	G987	C927	U868	C808	A748
U1529	U1469	U1409	U1408	G1348	A1288	G1228	G1168	U1108	U1048	G988	C928	U869	C809	C749
U1530	U1470	G1410	U1409	A1349	A1289	C1229	C1169	A1109	C1049	G989	A929	C870	U810	C750
C1531	G1471	C1411	G1410	G1350	A1290	G1230	U1170	G1110	G1050	A990	A930	U871	G811	G751
A1532	C1472	U1412	C1411	G1351	G1291	A1231	A1171	U1111	U1051	A991	G931	G872	G812	G752
G1533	U1473	U1413	G1412	G1352	A1292	U1232	U1172	U1112	C1052	A992	G932	U873	A813	U753
A1534	A1474	C1414	U1413	A1353	A1293	C1233	G1173	G1113	G1053	C993	G933	U874	G814	G754
C1535	U1475	G1415	G1414	A1354	U1294	G1234	G1174	A1114	C1054	A994	C934	A875	A815	C755
G1536	G1476	A1416	C1415	A1355	U1295	C1235	U1175	C1115	A1055	A995	C935	A876	U816	C756
U1537	U1477	G1417	G1416	G1356	U1296	G1236	U1176	U1116	U1056	C996	A936	G877	A817	U757
A1538	U1478	C1418	U1417	U1357	A1297	G1237	U1177	G1117	A1057	C997	C937	C878	G818	G758
C1539	G1479	U1419	G1418	C1358	U1298	A1238	U1178	G1118	G1058	C998	G938	U879	C819	C759
U1540	G1480	U1420	G1419	G1359	A1299	G1239	A1179	U1119	A1059	A999	C939	C880	U820	U760
G1541	U1481	U1421	G1420	G1360	A1300	G1240	A1180	G1120	C1060	G1000	C940	U881	A821	G761
G1542	C1482	C1422	U1421	G1361	U1301	G1241	C1181	G1121	A1061	A1001	U941	C882	G822	A762
C1543	G1483	A1423	G1422	C1362	C1302	A1242	U1182	A1122	G1062	C1002	U942	U883	U823	C763
A1544	G1484	U1424	C1423	G1363	U1303	G1243	C1183	G1123	C1063	C1003	U943	C884	U824	A764
G1545	U1485	G1425	U1424	U1364	U1304	U1244	G1184	U1124	A1064	A1004	G944	A885	C825	G765
C1546	A1486	U1426	G1425	U1365	C1305	G1245	C1185	G1125	A1065	U1005	G945	U886	U826	A766
U1547	C1487	G1427	U1426	A1366	U1306	G1246	G1186	A1126	G1066	C1006	U946	C887	C827	G767
G1548	G1488	G1428	G1427	A1367	U1307	U1247	A1187	C1127	G1067	G1007	C947	C888	C828	U768
C1549	U1489	C1429	U1428	G1368	C1308	G1248	A1188	G1128	A1068	A1008	C948	C889	C829	C769
U1550	U1490	G1430	G1429	G1369	C1309	G1249	A1189	A1129	G1069	C1009	G949	U890	C830	U770
U1551	C1491	U1431	U1430	U1370	C1310	A1250	C1190	U1130	G1070	U1010	G950	U891	A831	G771
C1552	A1492	G1432	G1431	G1371	C1311	G1251	G1191	G1131	U1071	A1011	G951	A892	A832	G772
G1553	A1493	U1433	G1432	G1372	C1312	C1252	A1192	U1132	U1072	A1012	A952	G893	A833	G773
G1554	G1494	G1434	G1433	G1373	U1313	C1253	G1193	G1133	G1073	G1013	G953	G894	U834	G774
A1555	U1495	C1435	U1434	G1374	A1314	G1254	U1194	C1134	C1074	U1014	U954	A895	A835	U775
C1556	G1496	G1436	G1435	C1375	A1315	A1255	U1195	C1135	G1075	U1015	G955	C896	U836	G776

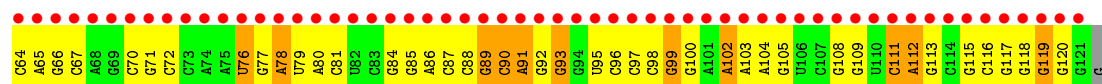
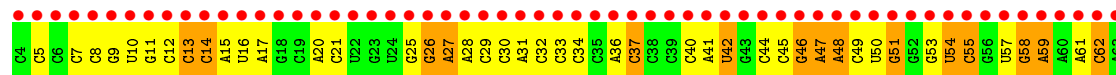
G2330	U2270	C2210	G3105	C2028	G1968	G1908	A3865	C1797	G1737	G1677	G1617	G1557
A2331	C2271	U2211	U3106	G2029	G1969	U909	A3866	G1798	U1738	G1678	U1618	C1558
G2332	A2272	G2212	G3107	U2030	G1970	A1910	G3867	A1800	G1739	U1679	A1619	C1559
A2333	C2273	G2213	G3108	A2031	C1971	A911	U3868	A1801	G1740	U1680	C1620	A1560
G2334	A2274	G2214	U3109	G2032	G1972	G1912	G3869	A1802	G1741	A1681	G1621	A1561
U2335	C2275	C2215	G3110	C2033	G1973	G1913	G3870	A1803	G1742	A1682	G1622	U1562
G2336	G2276	G2216	C3111	A2034	U1974	U1914	A3871	G1803	C1743	G1683	C1623	U1563
A2337	A2277	G2217	G3112	G2035	G1975	A915	A3872	U1804	G1744	A1684	A1624	U1564
C2338	C2278	G2218	C3175	G2036	U1976	G1916	G3873	G1805	C1745	A1685	A1625	G1565
A2339	U2279	U2219	A3176	A2037	C1977	C1917	G3874	A1806	G1746	A1686	A1626	G1566
G2340	A2280	G2220	G3115	C2038	U1978	G1918	A3875	A1807	G1747	C1687	C1627	A1567
G2341	C2281	G2221	G3116	G2039	G1979	A919	A3876	G1808	U1748	U1688	C1628	A1568
U2342	G2282	U2222	A3117	A2040	A1980	A1920	A3877	G1809	G1749	U1689	G1629	U1569
C2343	G2283	U2223	U3118	A2041	A1981	A921	G1861	U1810	A1750	U1690	A1630	C1570
A2344	U2284	U2224	A3119	A2042	C1982	U922	A1862	A1811	A1751	G1691	C1631	G1571
G2345	G2285	G2225	G3120	A2043	U1983	U923	U1863	U1812	U1752	C1692	A1632	C1572
G2346	G2286	A2226	G3121	G2044	A1984	C1924	A1864	A1813	A1753	A1693	C1633	G1573
G2347	G2287	C2227	U3122	G2045	G1985	C1925	G1865	A1814	G1754	A1694	A1634	A1574
A2348	U2288	U2228	G3123	C2046	U1986	U926	G1866	G1815	G1755	U1695	G1635	C1575
G2349	A2289	G2229	G3124	C2047	G1987	U927	A1867	G1816	C1756	C1696	G1636	G1576
A2350	G2290	G2230	G3125	C2048	A1988	G1928	A1868	U1817	C1757	U1697	U1637	G1577
G2351	U2291	G2231	A3126	C2049	C1989	U929	A1869	G1818	C1758	C1698	G1638	U1578
A2352	C2292	G2232	G3127	G2050	U1990	C1930	A1870	U1819	A1759	A1699	U1639	G1579
G2353	G2293	C2233	G3128	U2051	C1991	G1931	A1871	G1820	G1760	C1700	C1640	C1580
G2354	U2294	G2234	G3129	G2052	G1992	G1932	A1872	A1821	G1761	C1701	C1641	C1581
A2355	C2295	G2235	G3130	G2053	G1993	C1933	A1873	C1822	C1762	C1702	G1642	A1582
G2356	U2296	U2236	A3131	A2054	U1994	U934	G1874	G1823	G1763	C1703	A1643	A1583
A2357	G2297	C2237	A3132	G2055	G1995	A935	G1875	C1824	A1764	G1704	A1644	G1584
C2358	U2298	G2238	G3133	C2056	A1996	A936	A1876	A1825	G1765	U1705	U1645	A1585
U2359	G2299	C2239	A3134	U2057	A1997	G1937	C1877	U1826	U1766	A1706	G1646	A1586
C2360	U3000	C2240	A3135	U2058	A1998	U938	C1878	G1827	G1767	A1707	U1647	A1587
G2361	A2301	U2241	U3136	U2059	U1999	U939	G1879	C1828	U1768	C1708	C1648	U1588
A2362	G2302	C2242	C3137	A2060	U2000	C1940	G1880	U1829	U1769	U1709	A1649	G1589
C2363	C2303	C2243	C3138	C2061	G2001	G1941	U1881	C1830	U1770	U1710	A1650	C1590
G2364	G2304	C2244	U3139	U2062	A2002	G1942	A1882	G1831	A1771	C1711	U1651	U1591
U2365	C2305	A2245	G3140	A2063	A2003	A943	A1883	G1832	C1772	G1712	G1652	U1592
G2366	G2306	A2246	G3141	U2064	U2004	C1944	A1884	U1833	C1773	G1713	G1653	C1593
A2367	A2307	A2247	C3142	A2065	U2005	C1945	C1885	G1834	A1774	A1714	A1654	U1594
G2368	U2308	A2248	U3143	G2066	G2006	U946	G1886	C1835	A1775	A1715	C1655	A1595
U2369	G2309	C2249	A3146	U2067	G2007	G1947	G1887	C1836	A1776	G1716	U1656	A1596
G2370	C2310	G2250	C3147	C2068	C2008	C1948	C1888	G1837	A1777	A1717	A1657	A1597
A2371	U2311	U2251	G3148	U2069	U2009	A949	G1889	G1838	U1778	A1718	G1658	C1598
C2372	G2312	A2252	G3149	G2070	G2010	C1950	G1890	A1839	C1779	G1719	G1659	G1599
G2373	U2313	A2253	C3150	G2071	U2011	G1951	C1891	A1840	A1780	G1720	C1660	U1600
C2374	A2314	C2254	U3151	C2072	A2012	A952	G1892	G1841	C1781	G1721	C1661	U1601
A2315	G2315	G2255	G3152	A2073	A2013	A953	G1893	G1842	A1782	G1722	G1662	G1602
G2316	C2316	G2256	G3153	U2074	A2014	A954	U1894	U1843	G1783	U1723	C1663	A1603
G2317	G2317	A2257	G3154	U2075	G2015	G1955	A1895	C1844	C1784	G1724	G1664	A1604
G2318	U2318	G2258	G3155	C3093	A2016	G1956	A1896	A1845	G1785	G1725	C1665	A1605
G2319	G2319	G2259	G3156	A3094	U2017	C1957	C1897	A1846	C1786	C1726	G1666	C1606
U2380	C2320	C2260	G3157	A3095	G2018	G1958	U1898	G1847	U1787	C1727	A1667	A1607
A2381	C2321	G2261	A3158	C3096	C2019	U959	A1899	U1848	C1788	A1728	G1668	U1608
C2382	U2322	C2262	C3159	G3097	G2020	A960	U1900	G1849	U1789	C1729	A1669	G1609
C2383	C2323	C2263	C3160	U3098	G2021	A961	U1901	G1850	G1790	G1730	G1670	A1610
G2384	G2324	C2264	G3161	U3099	C2022	G1962	A1902	A1851	C1791	A1671	A1671	U1611
A2325	C2325	A2265	C3162	G3100	C2023	G1963	C1903	G1852	G1792	U1732	A1672	U1612
U2385	G2326	A2266	G3163	A3101	U2024	A964	G1904	C1853	A1793	U1733	C1673	G1613
G2386	U2327	A2267	C3164	G3102	A2025	U965	G1905	G1854	A1794	U1734	C1674	C1614
C2387	U2328	G2268	G3165	A3103	C2026	G1966	U1906	G1855	G1795	G1735	C1675	C1615
G2388	C2329	G2269	G3166	C3104	C2027	U1967	C1907	U1856	A1796	C1736	U1676	C1616



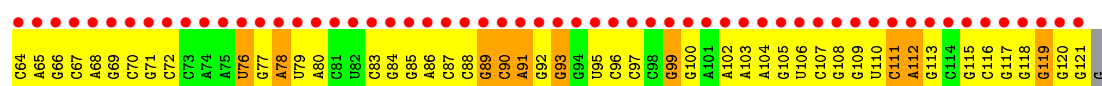
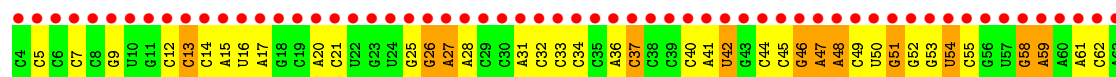




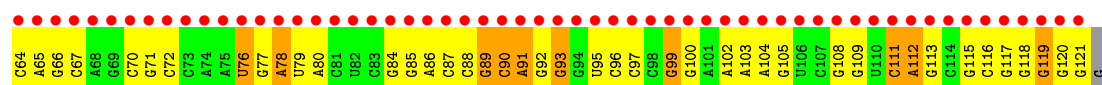
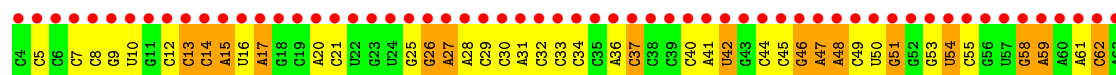
• Molecule 23: 5S RIBOSOMAL RNA



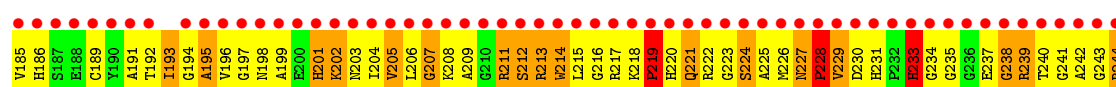
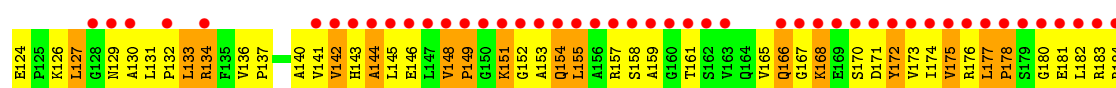
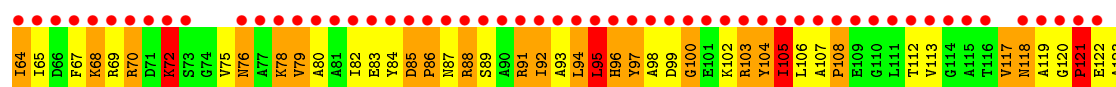
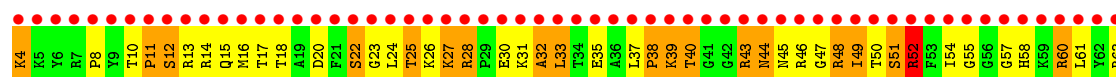
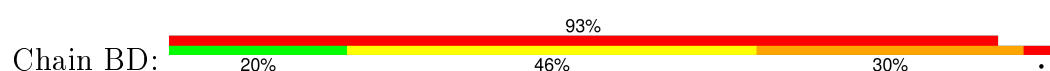
• Molecule 23: 5S RIBOSOMAL RNA



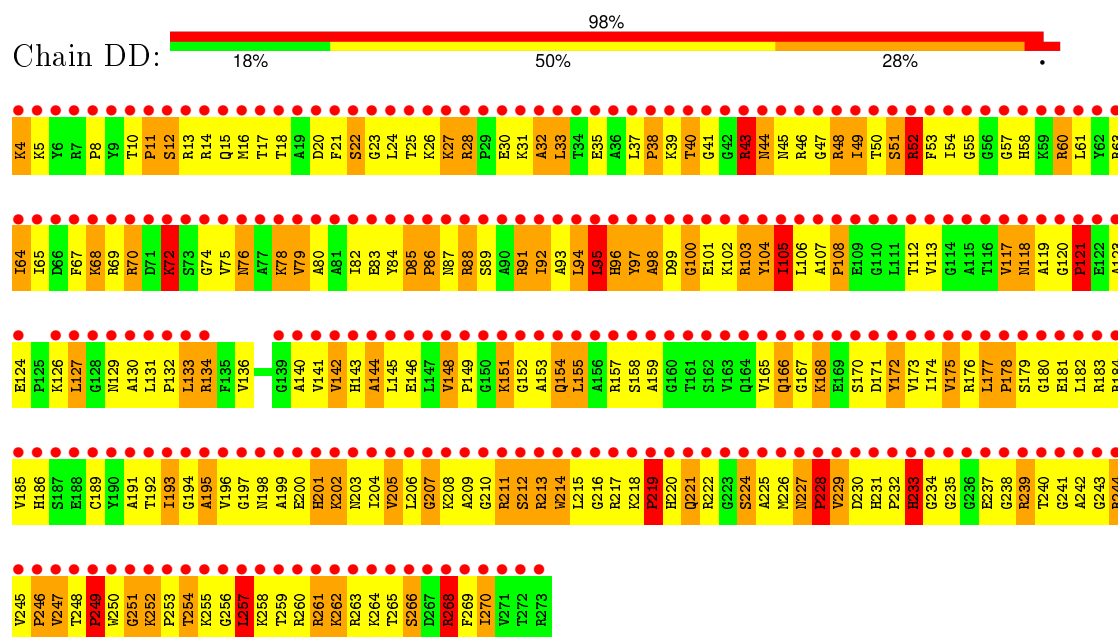
• Molecule 23: 5S RIBOSOMAL RNA



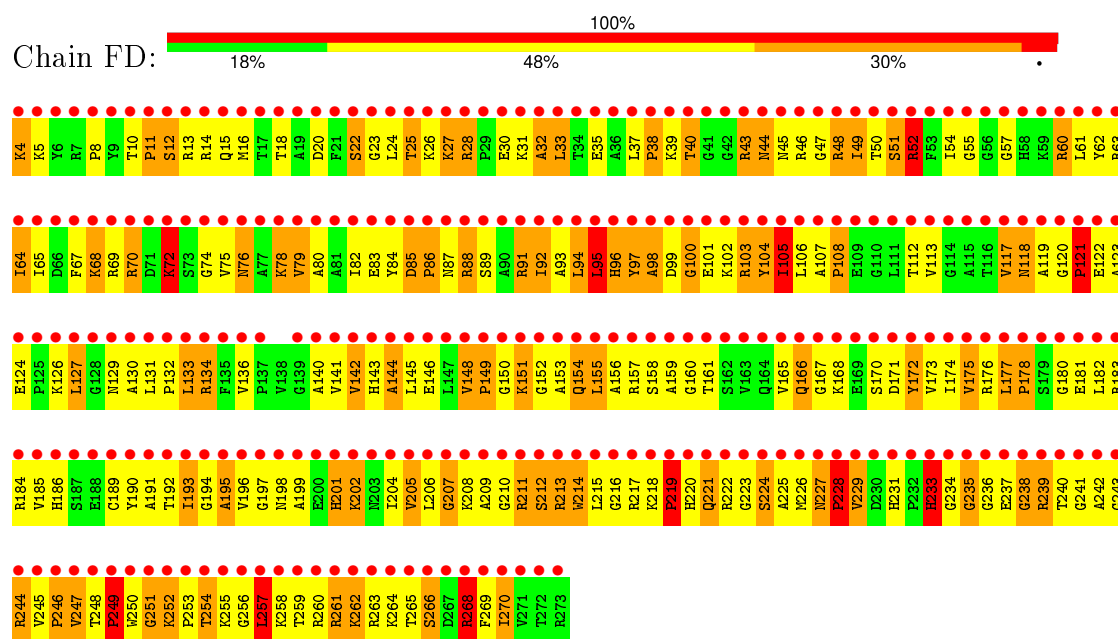
• Molecule 24: 50S ribosomal protein L2



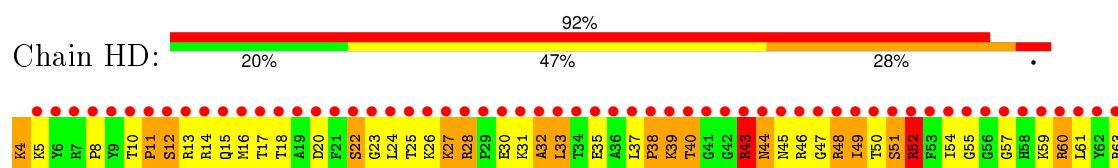
- Molecule 24: 50S ribosomal protein L2

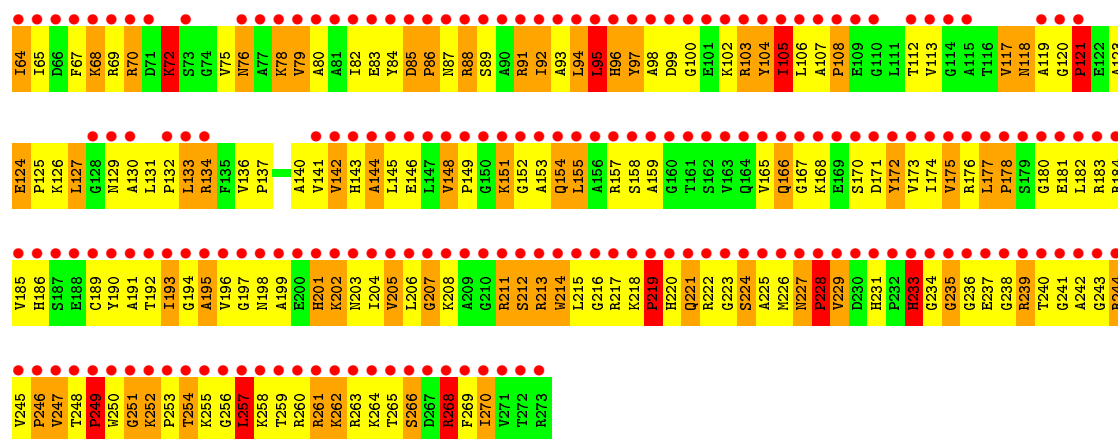


- Molecule 24: 50S ribosomal protein L2

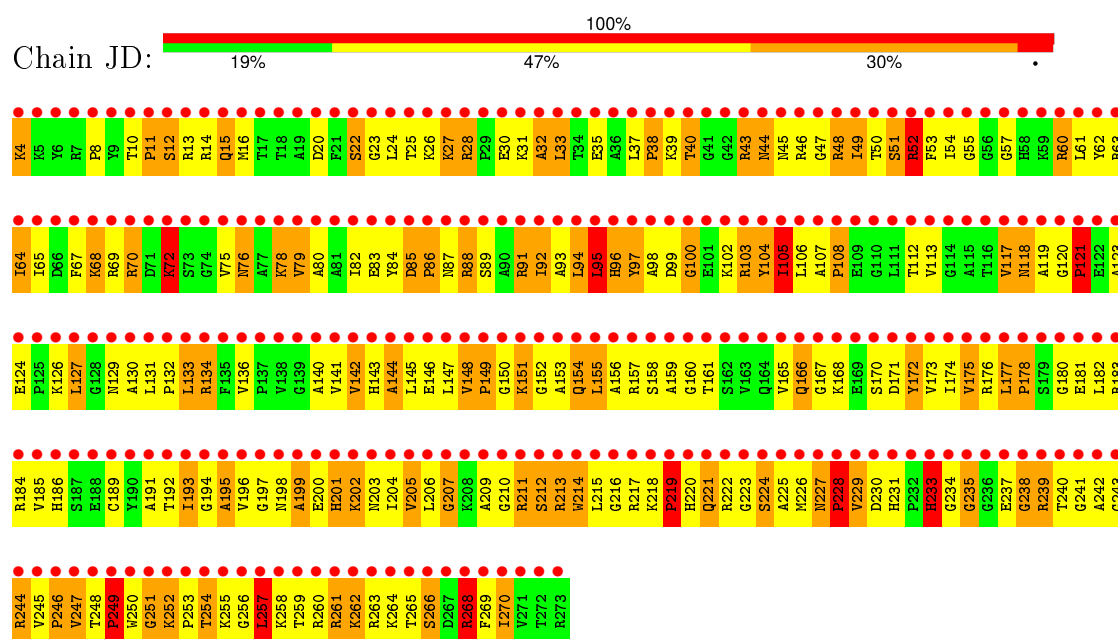


- Molecule 24: 50S ribosomal protein L2

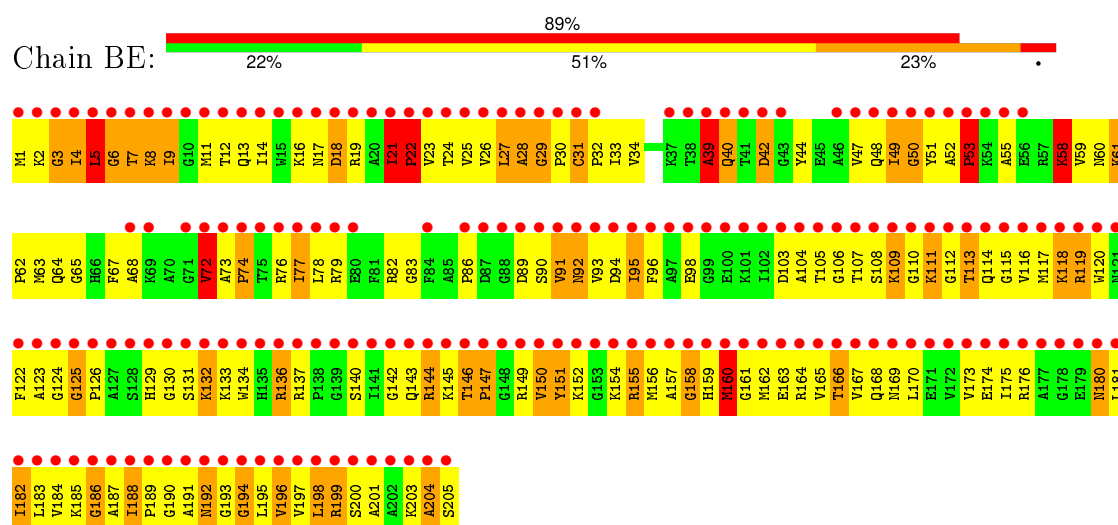




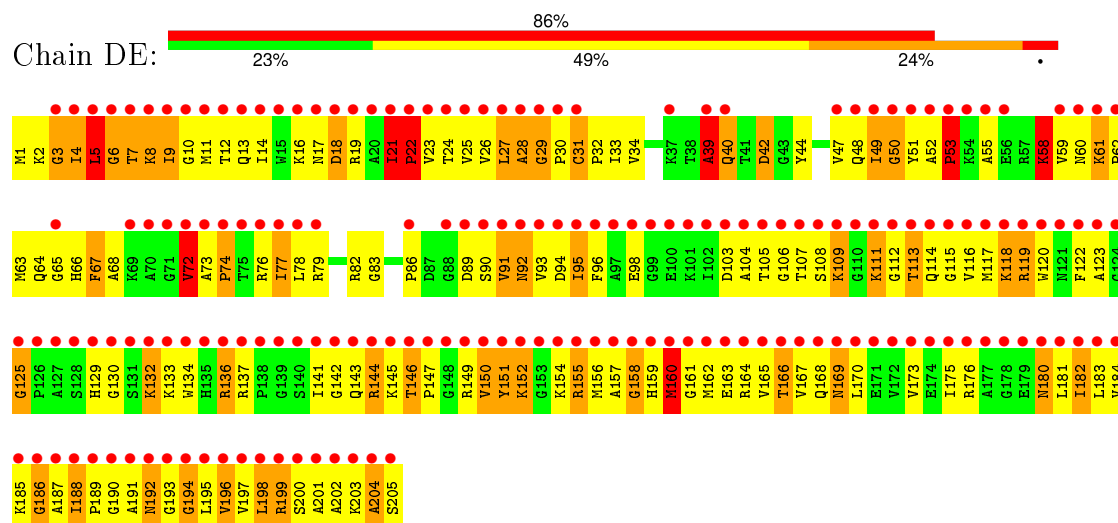
• Molecule 24: 50S ribosomal protein L2



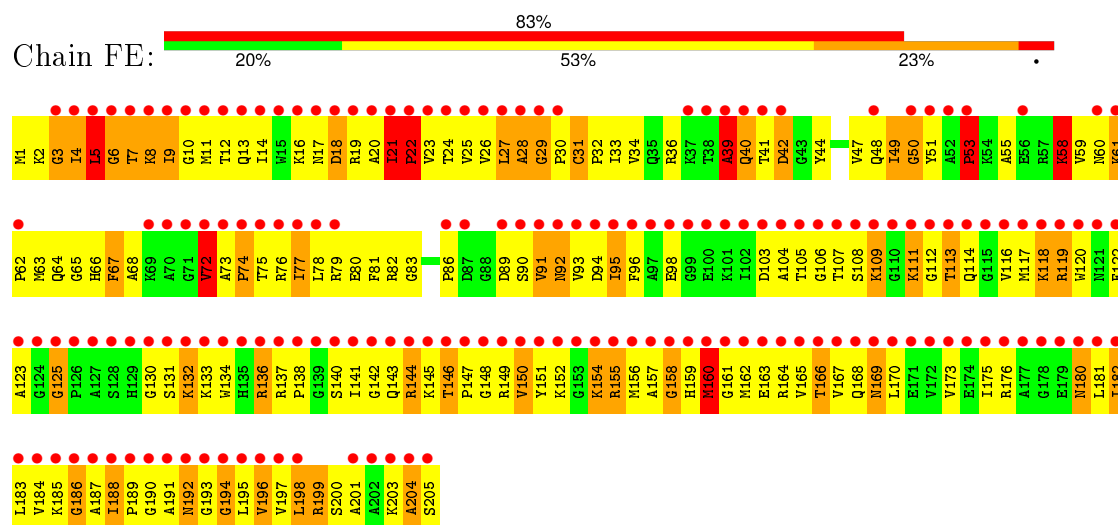
• Molecule 25: 50S ribosomal protein L3



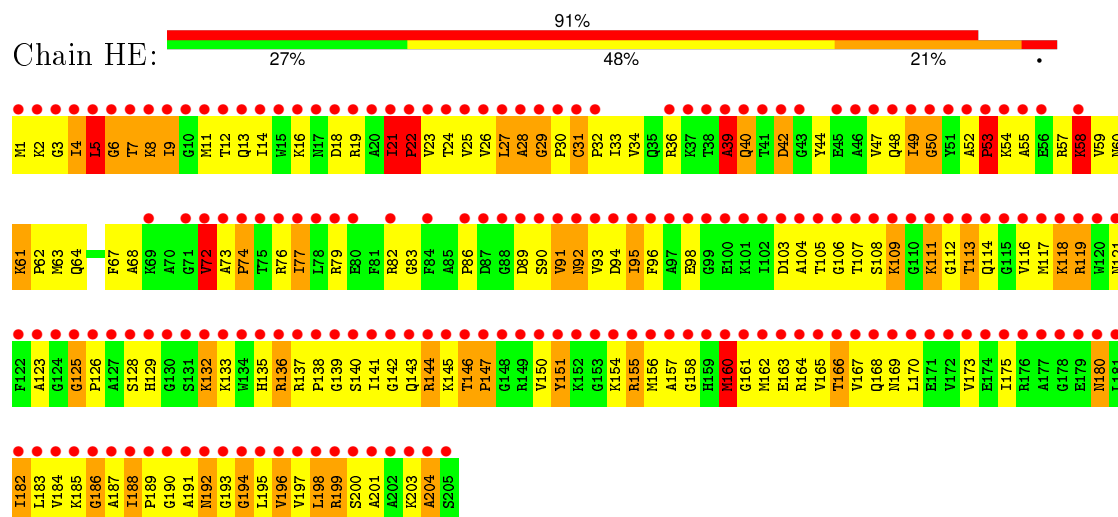
• Molecule 25: 50S ribosomal protein L3



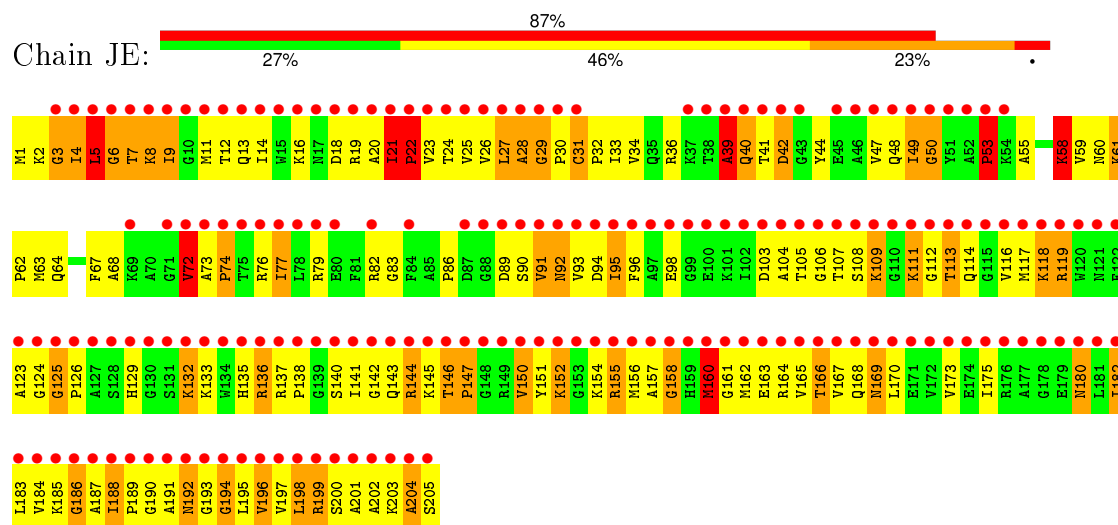
• Molecule 25: 50S ribosomal protein L3



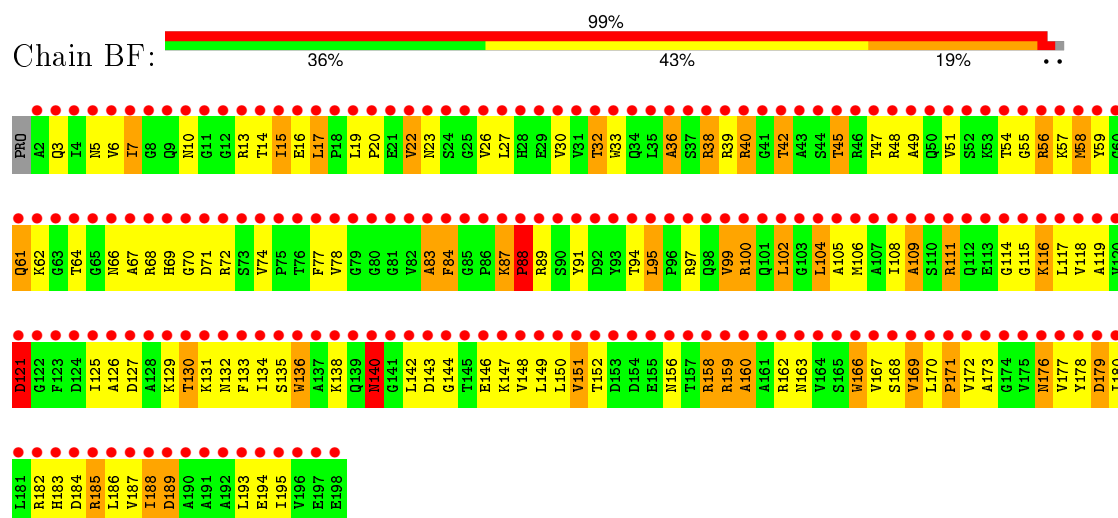
• Molecule 25: 50S ribosomal protein L3



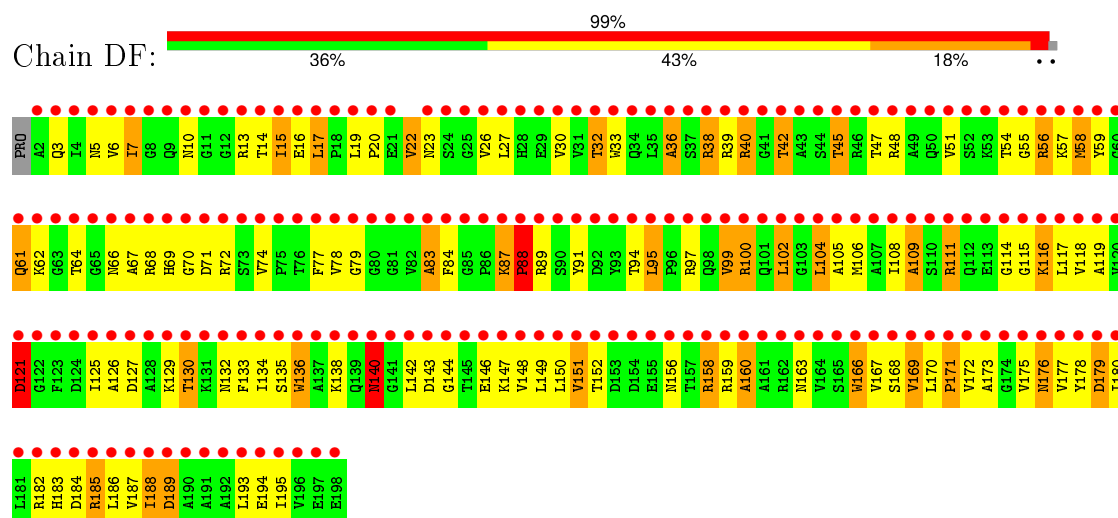
• Molecule 25: 50S ribosomal protein L3



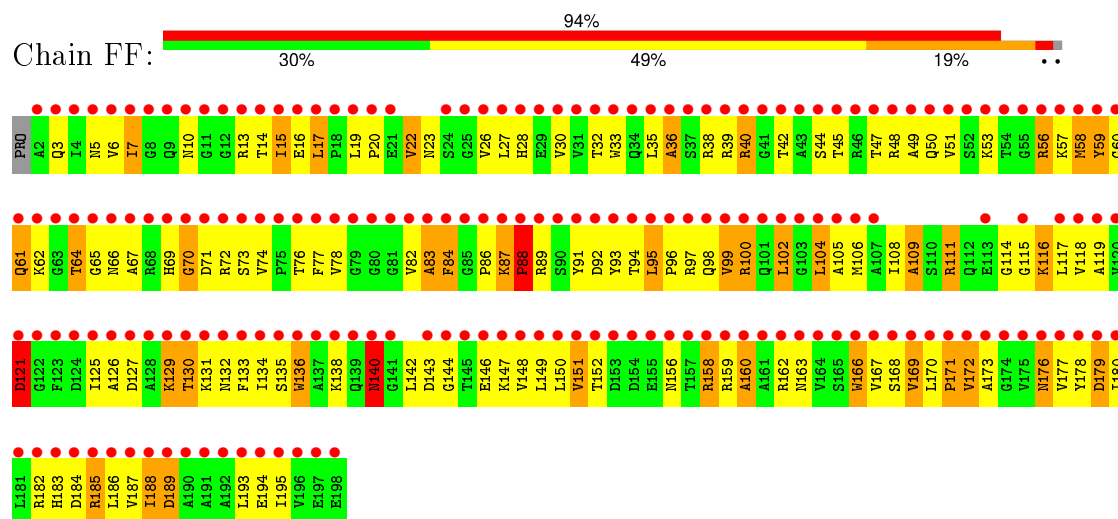
• Molecule 26: 50S ribosomal protein L4



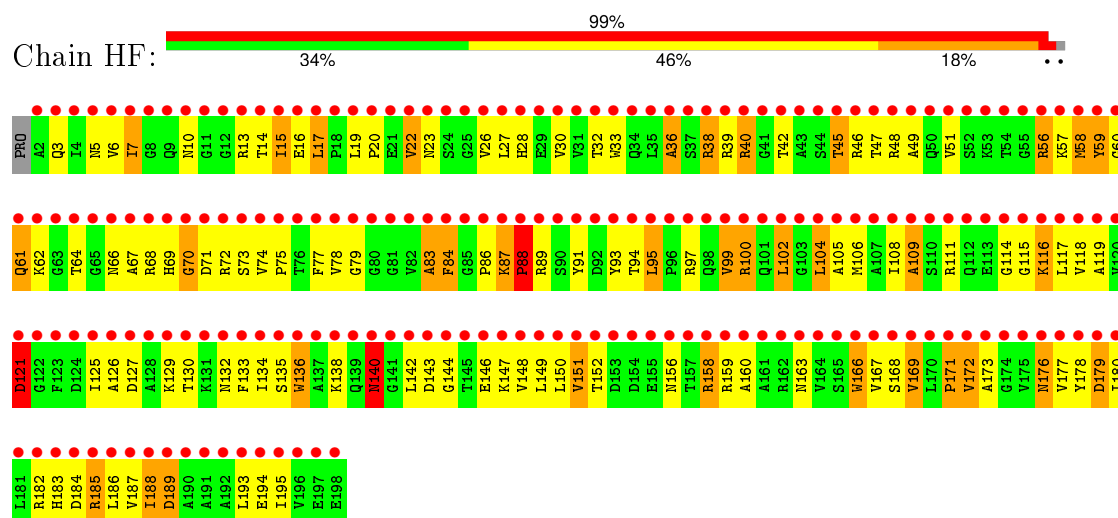
• Molecule 26: 50S ribosomal protein L4



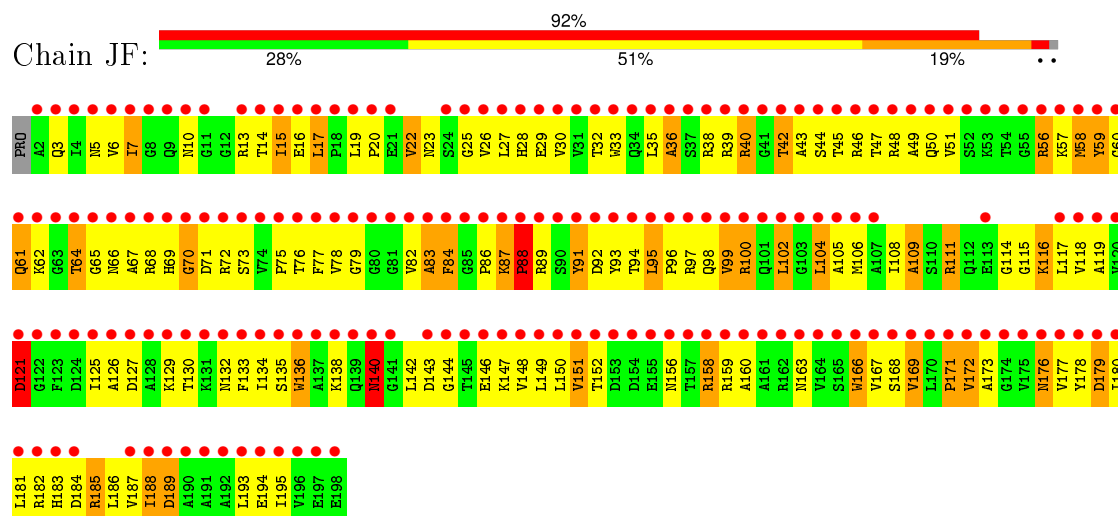
• Molecule 26: 50S ribosomal protein L4



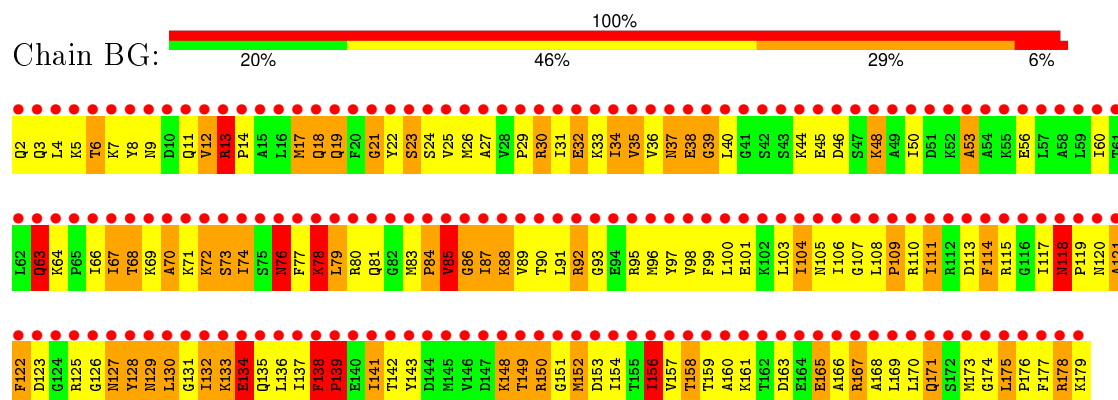
• Molecule 26: 50S ribosomal protein L4



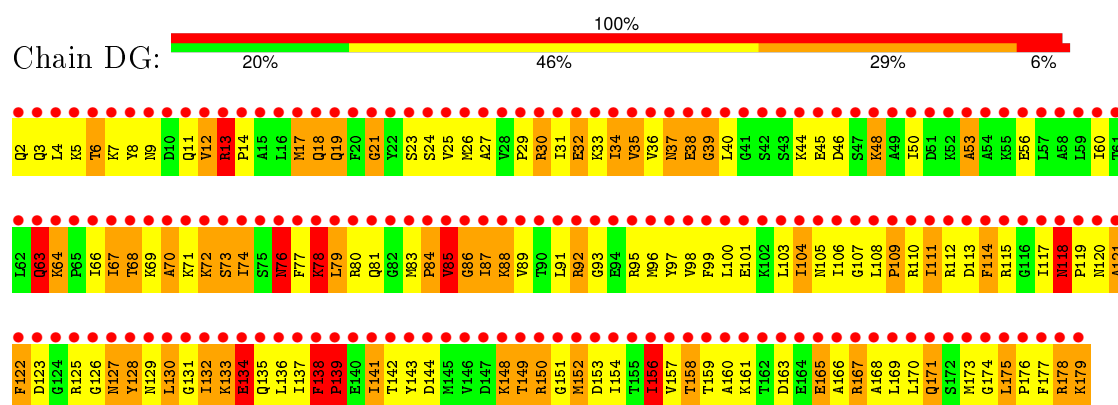
• Molecule 26: 50S ribosomal protein L4



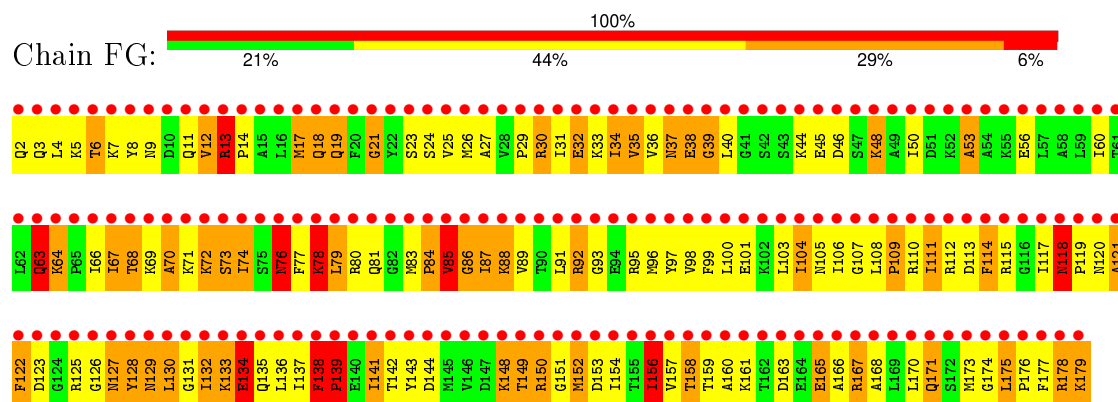
## ● Molecule 27: 50S ribosomal protein L5



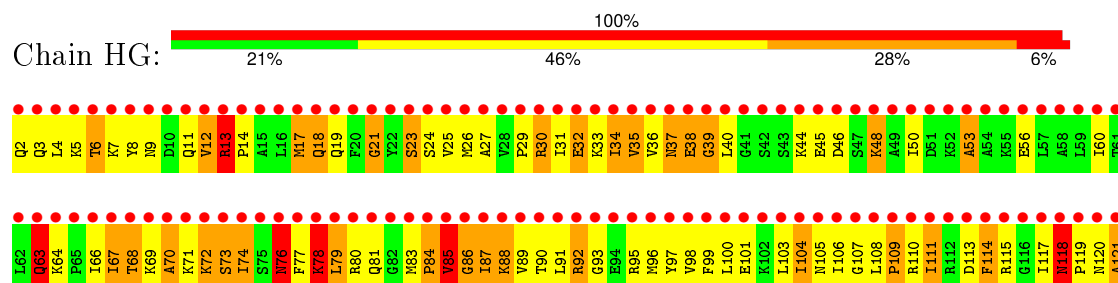
## ● Molecule 27: 50S ribosomal protein L5

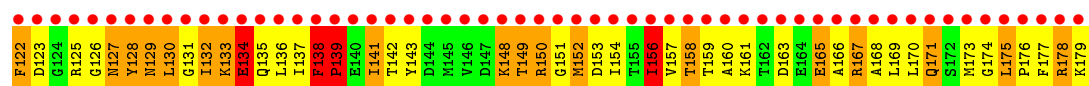


## ● Molecule 27: 50S ribosomal protein L5

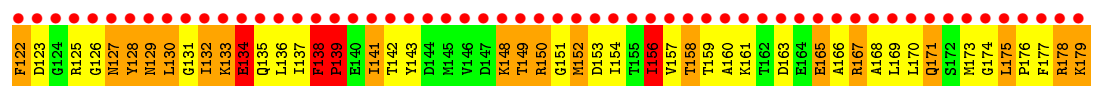
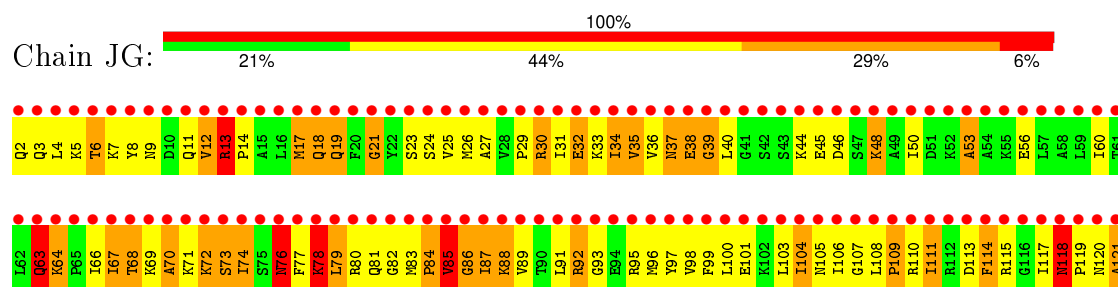


## ● Molecule 27: 50S ribosomal protein L5

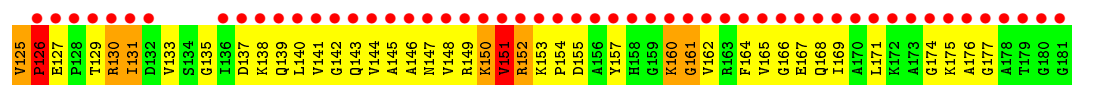
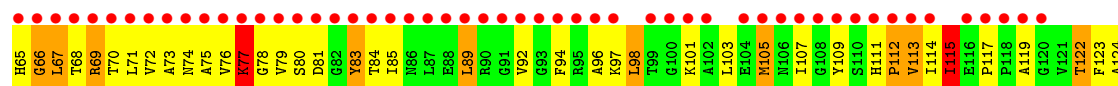
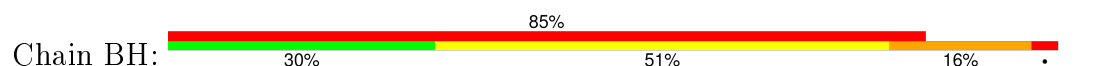




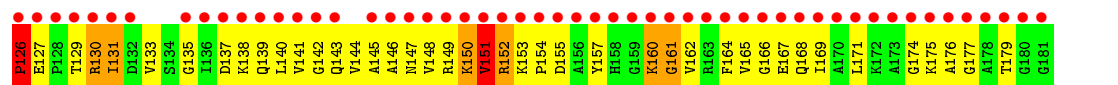
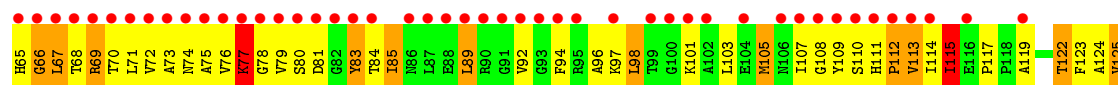
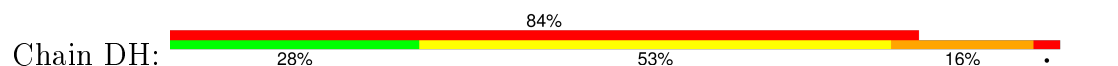
• Molecule 27: 50S ribosomal protein L5



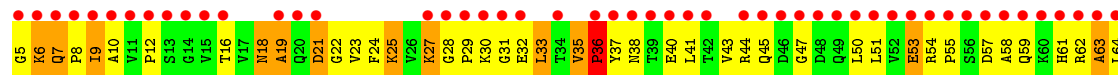
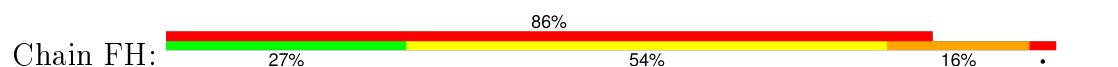
• Molecule 28: 50S ribosomal protein L6



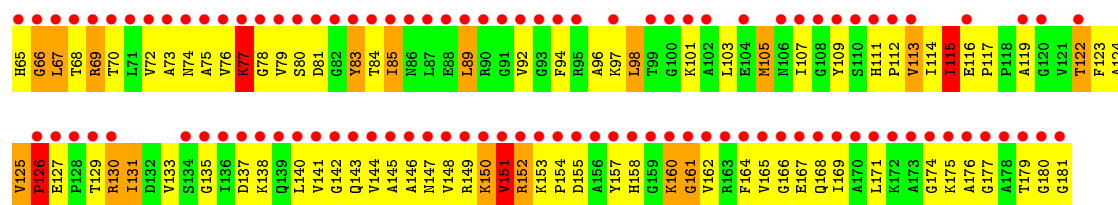
• Molecule 28: 50S ribosomal protein L6



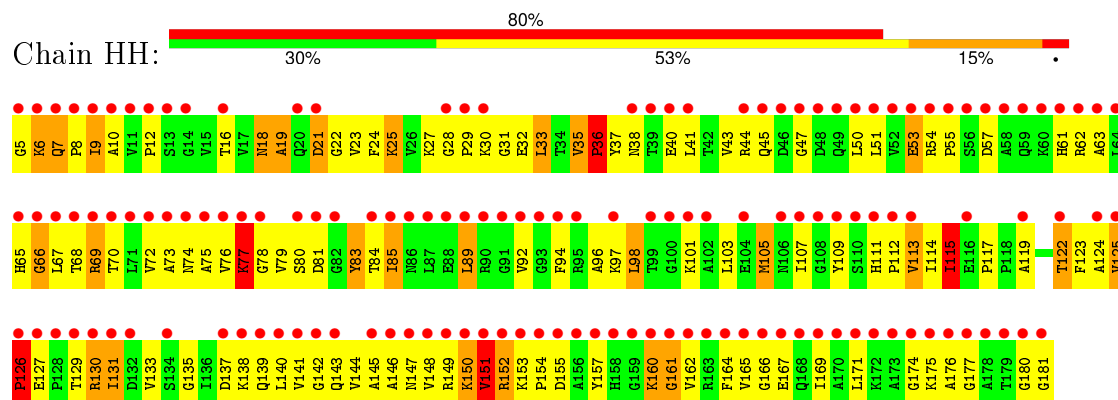
• Molecule 28: 50S ribosomal protein L6



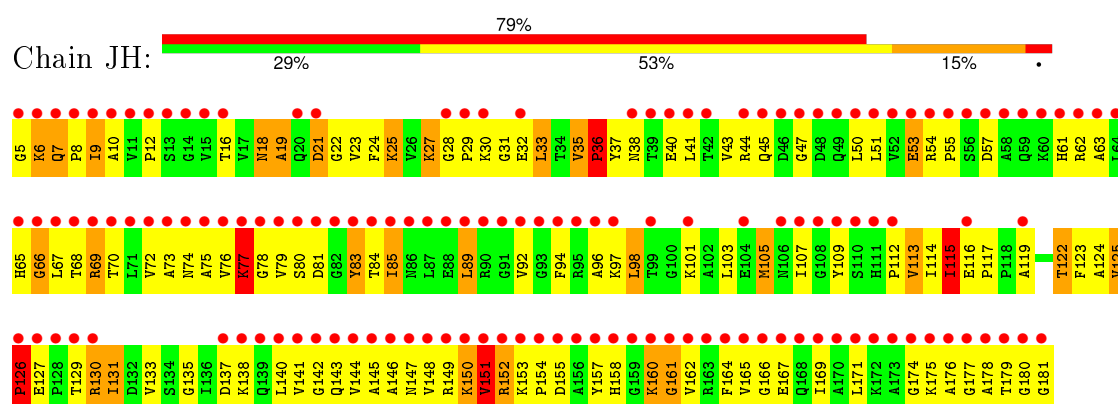




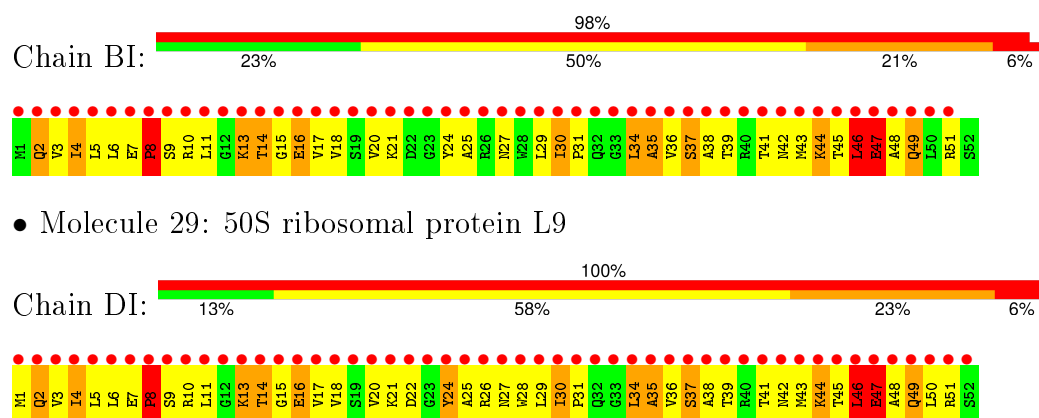
• Molecule 28: 50S ribosomal protein L6



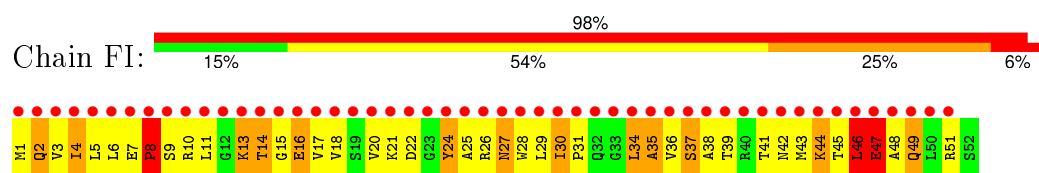
• Molecule 28: 50S ribosomal protein L6



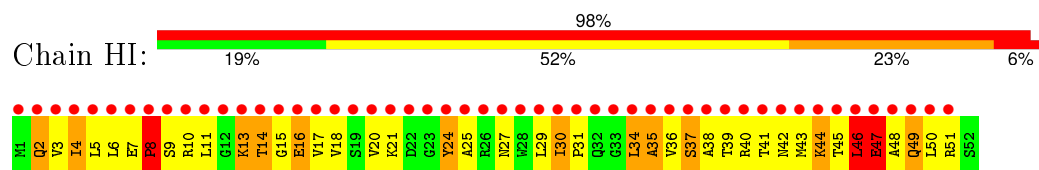
• Molecule 29: 50S ribosomal protein L9



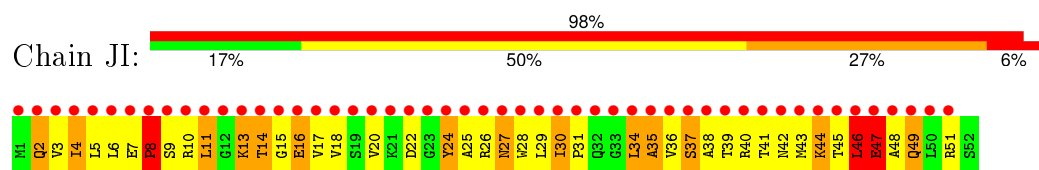
• Molecule 29: 50S ribosomal protein L9



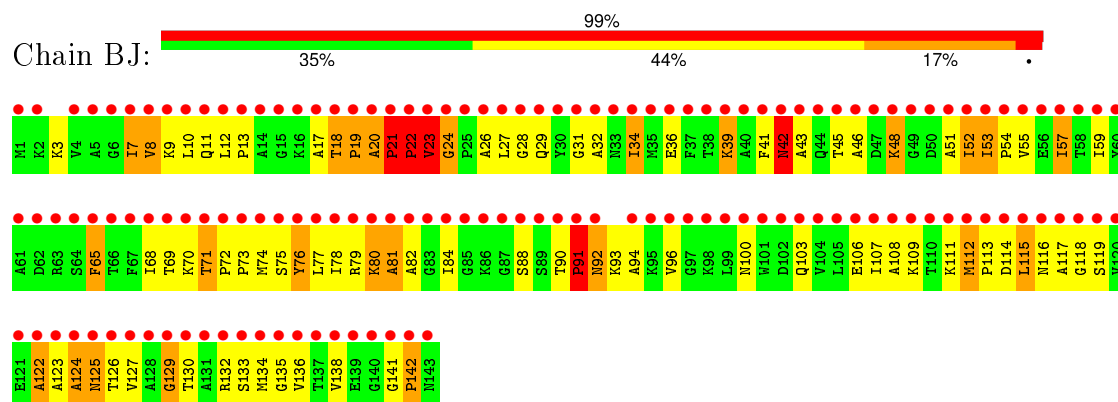
- Molecule 29: 50S ribosomal protein L9



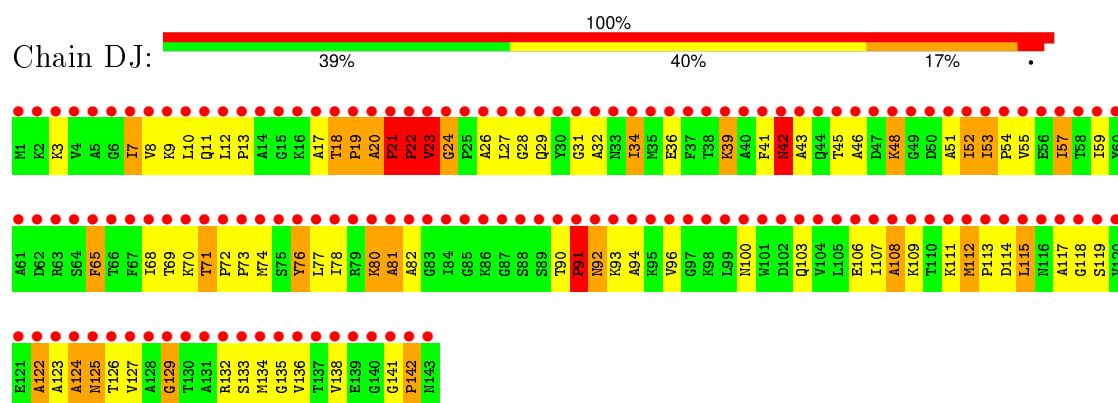
- Molecule 29: 50S ribosomal protein L9



- Molecule 30: 50S ribosomal protein L11

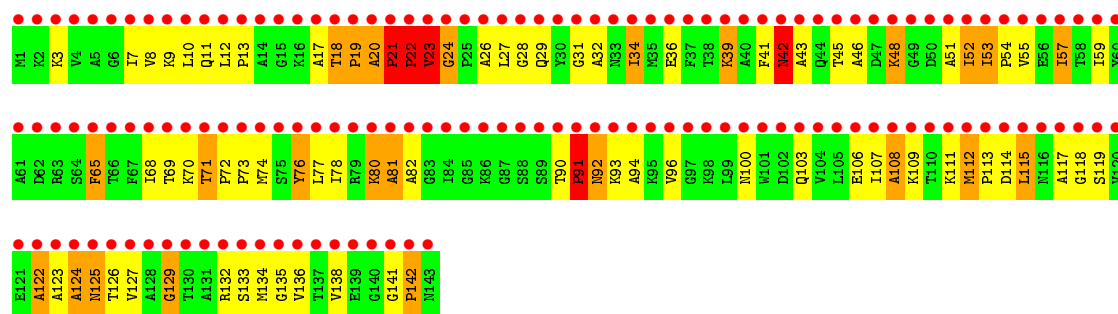


- Molecule 30: 50S ribosomal protein L11

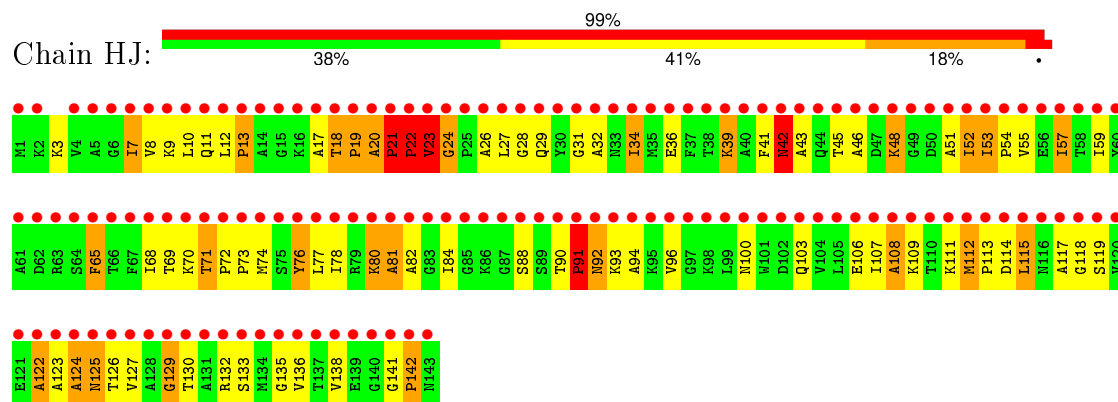


- Molecule 30: 50S ribosomal protein L11

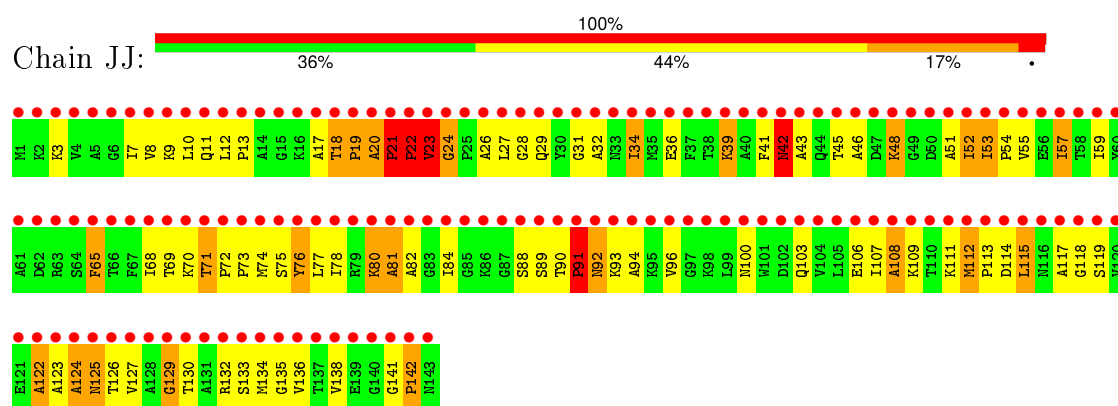




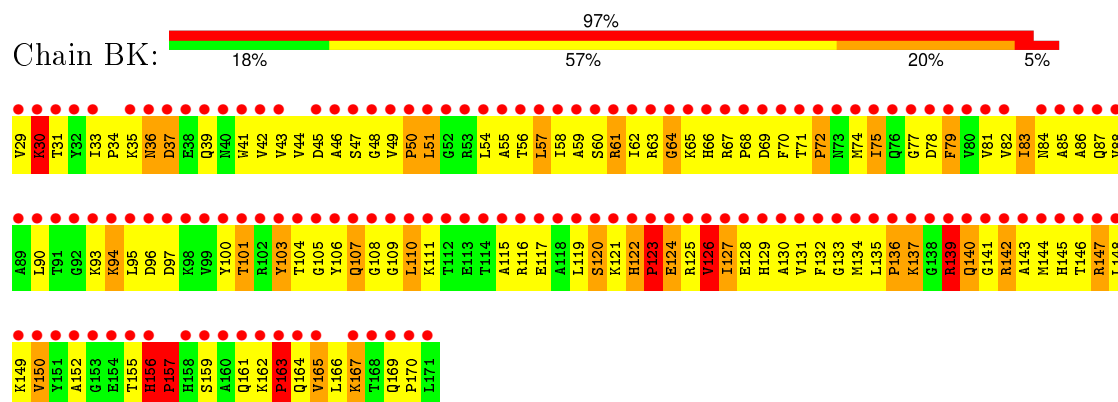
• Molecule 30: 50S ribosomal protein L11



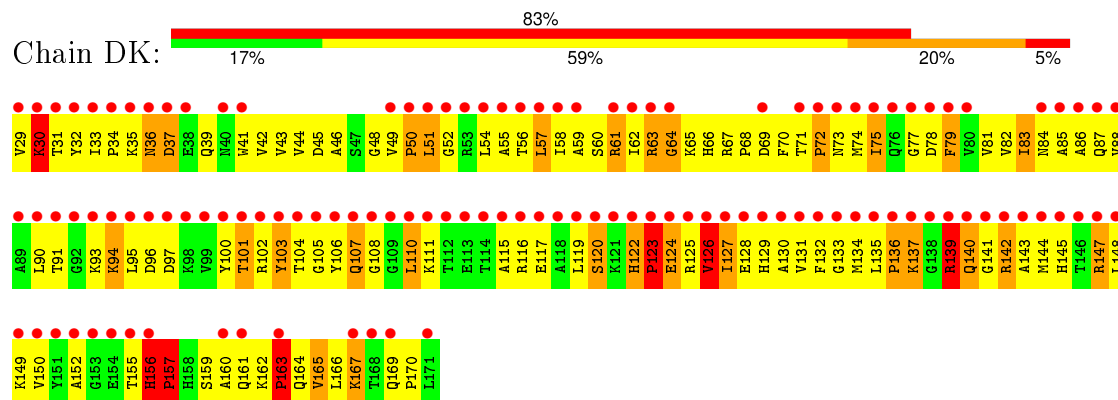
• Molecule 30: 50S ribosomal protein L11



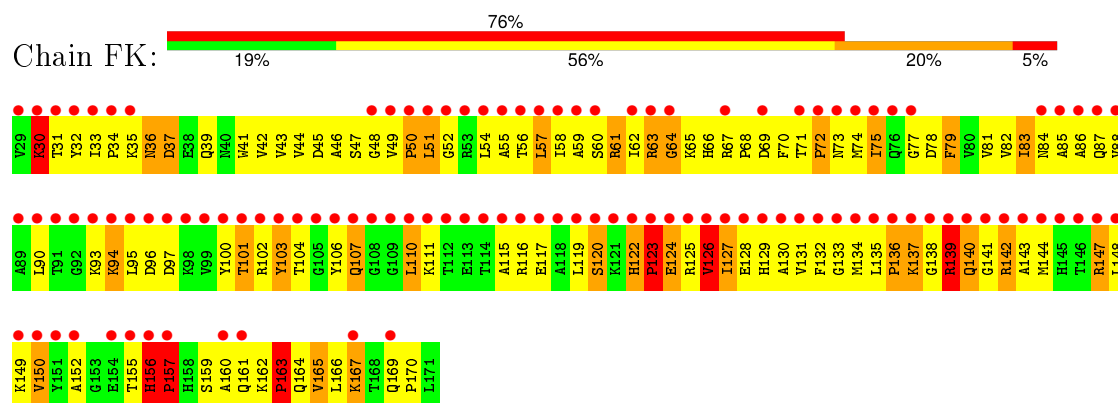
• Molecule 31: 50S ribosomal protein L13



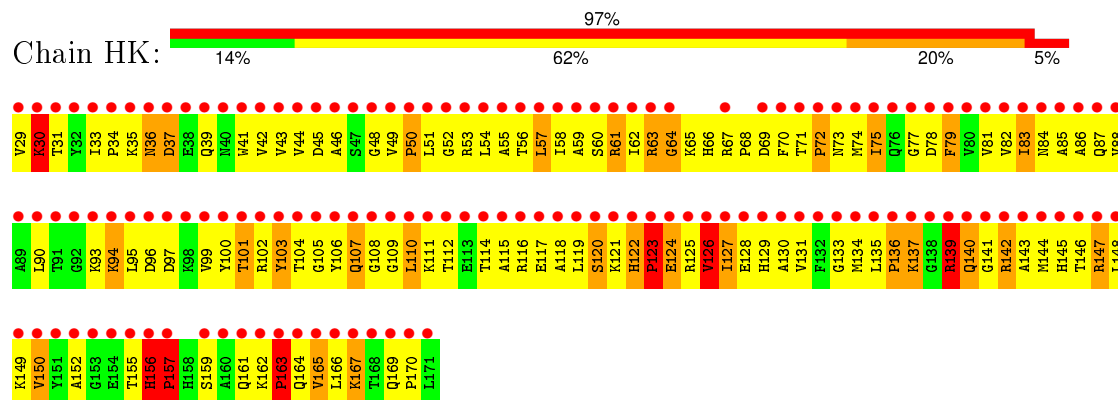
- Molecule 31: 50S ribosomal protein L13



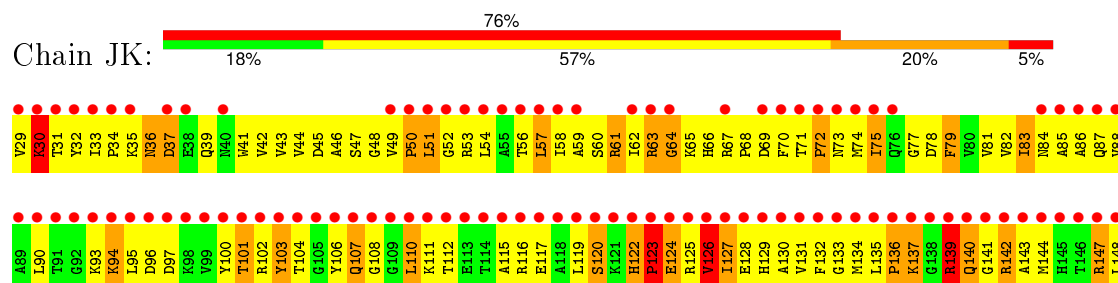
- Molecule 31: 50S ribosomal protein L13

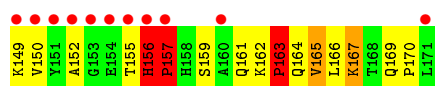


- Molecule 31: 50S ribosomal protein L13

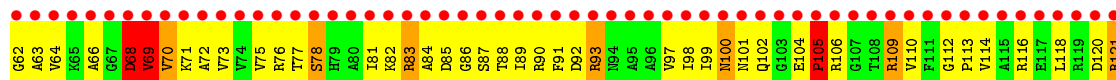
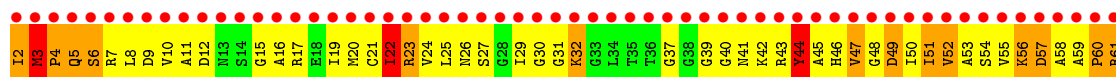


- Molecule 31: 50S ribosomal protein L13

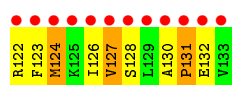
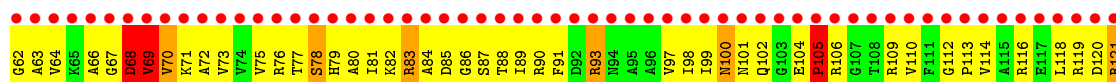




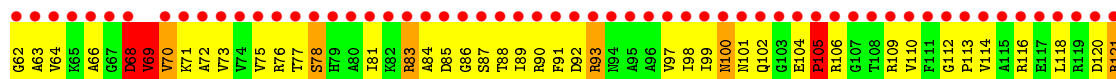
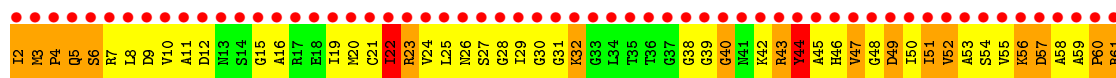
● Molecule 32: 50S ribosomal protein L14



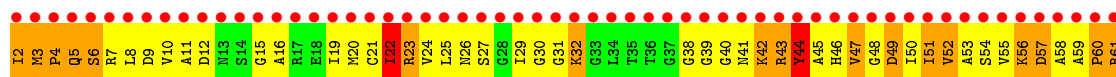
● Molecule 32: 50S ribosomal protein L14

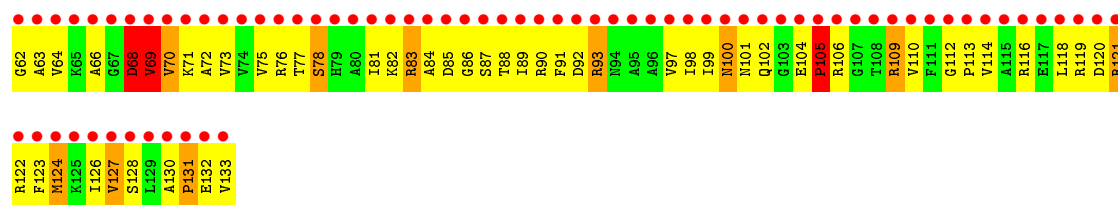


● Molecule 32: 50S ribosomal protein L14

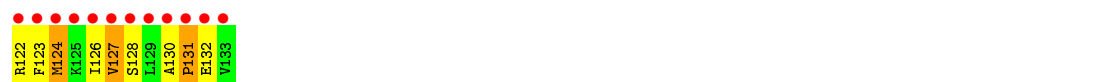
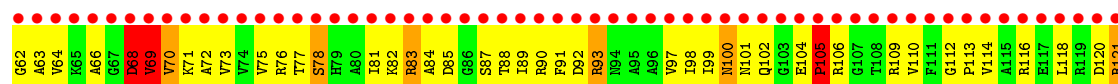
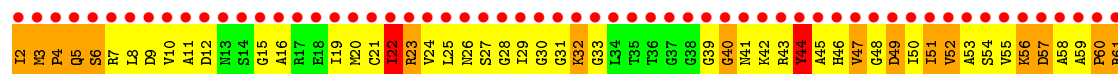


● Molecule 32: 50S ribosomal protein L14

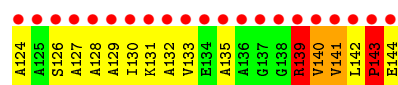
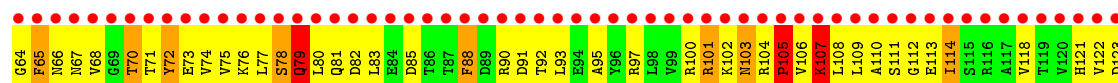
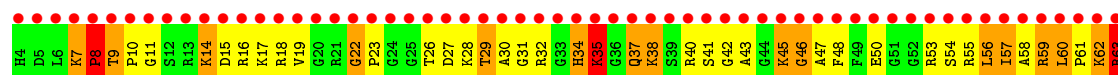




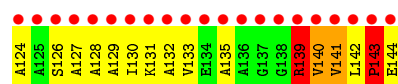
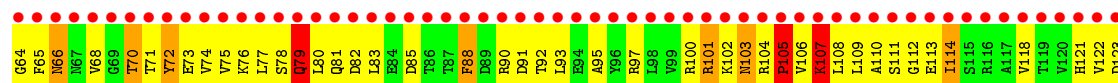
• Molecule 32: 50S ribosomal protein L14



• Molecule 33: 50S ribosomal protein L15

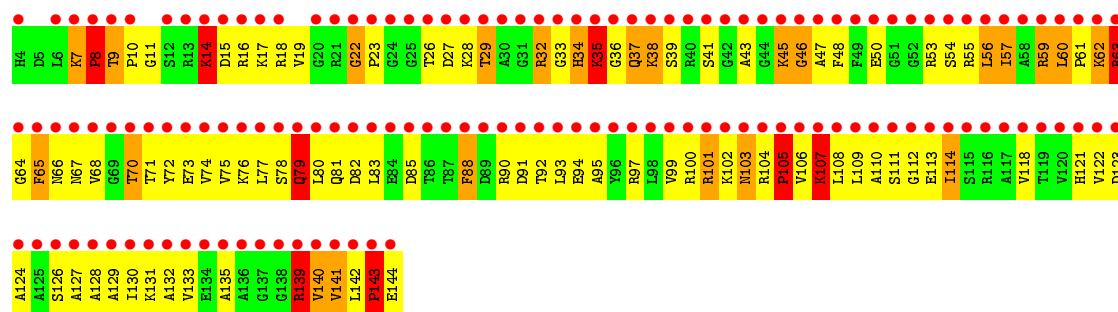


• Molecule 33: 50S ribosomal protein L15

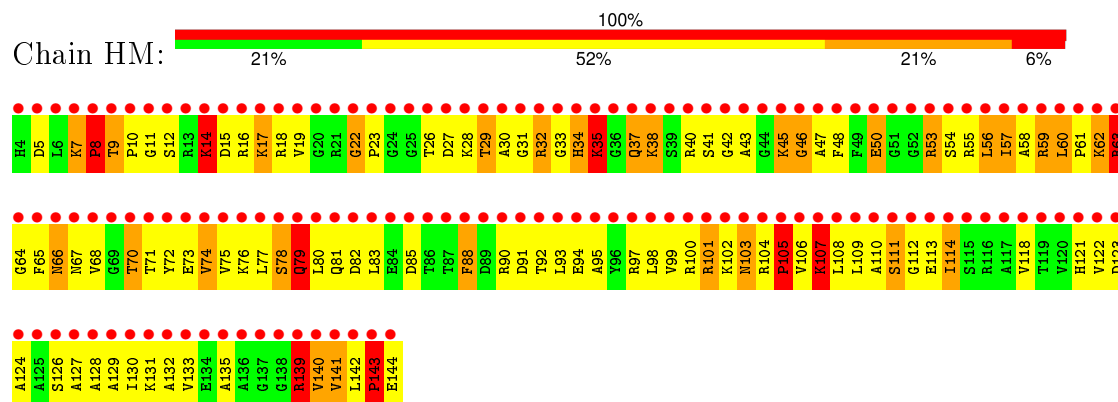


• Molecule 33: 50S ribosomal protein L15

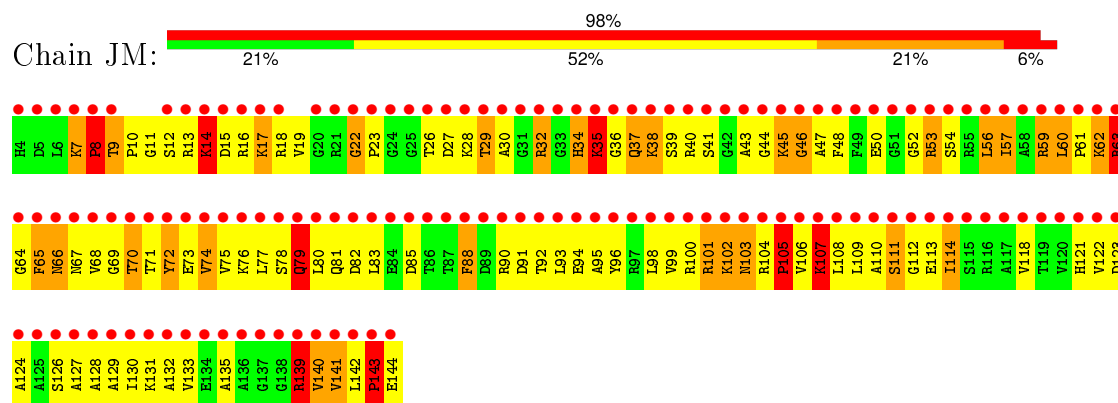




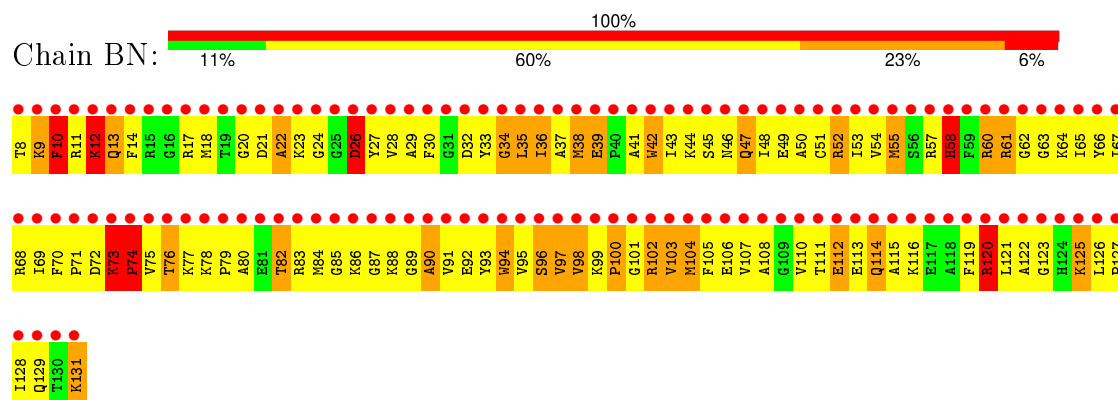
• Molecule 33: 50S ribosomal protein L15



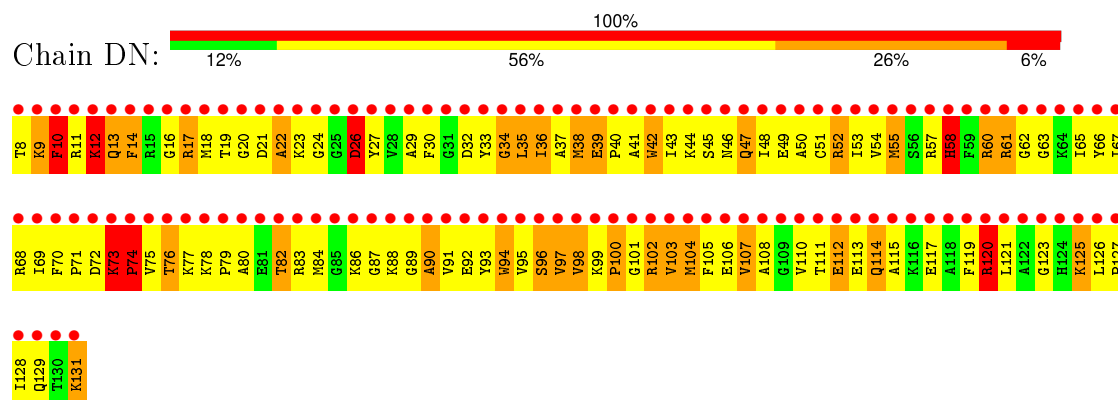
• Molecule 33: 50S ribosomal protein L15



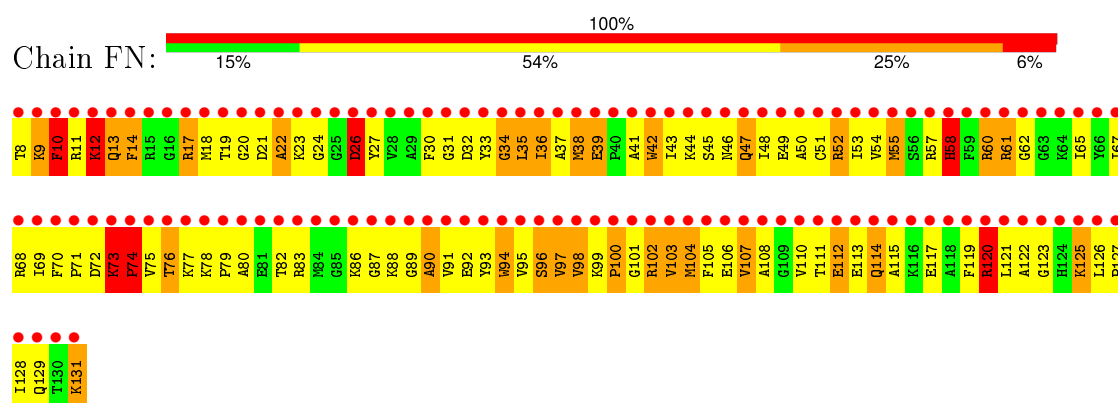
• Molecule 34: 50S ribosomal protein L16



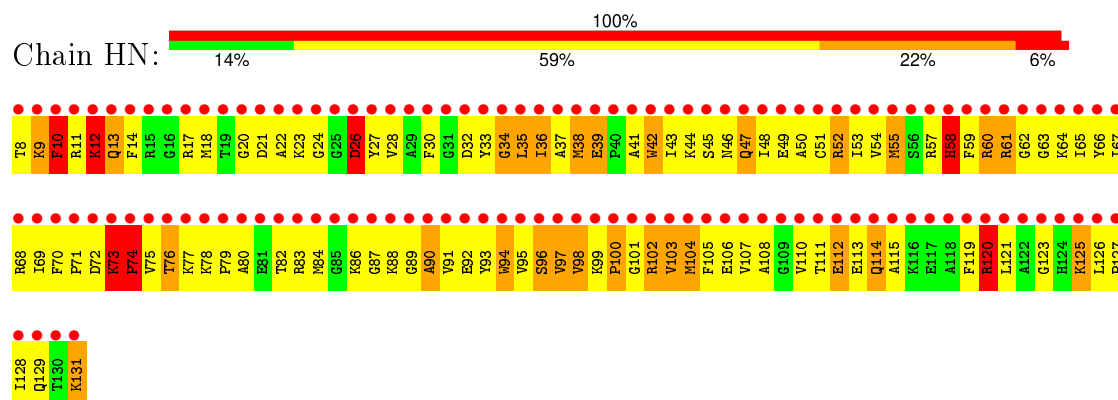
- Molecule 34: 50S ribosomal protein L16



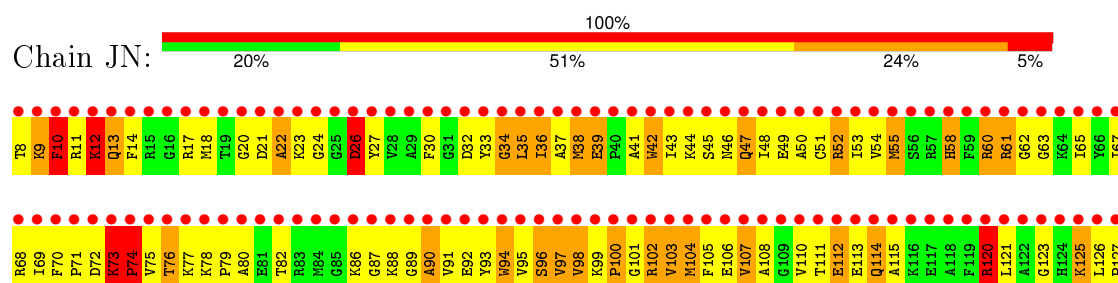
- Molecule 34: 50S ribosomal protein L16



- Molecule 34: 50S ribosomal protein L16



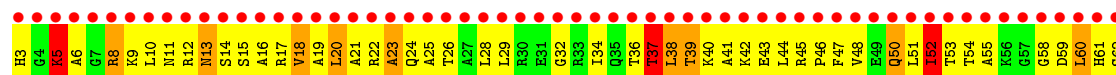
- Molecule 34: 50S ribosomal protein L16



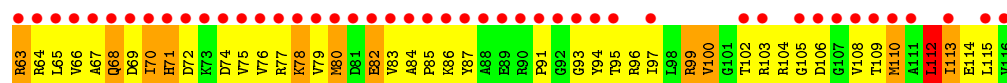
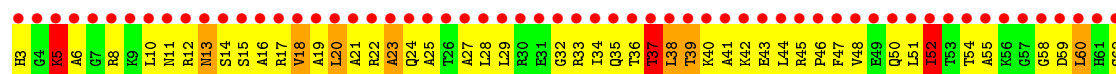




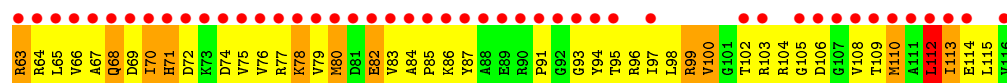
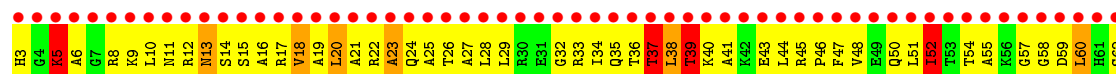
- Molecule 35: 50S ribosomal protein L17



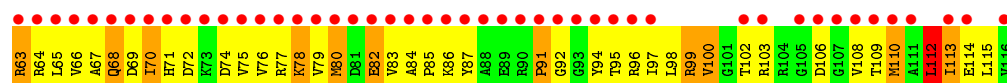
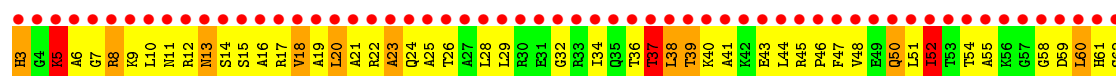
- Molecule 35: 50S ribosomal protein L17



- Molecule 35: 50S ribosomal protein L17

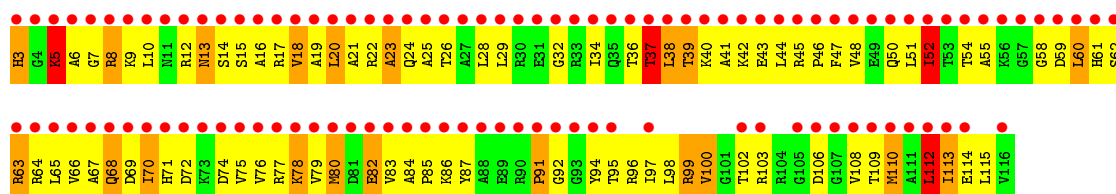


- Molecule 35: 50S ribosomal protein L17

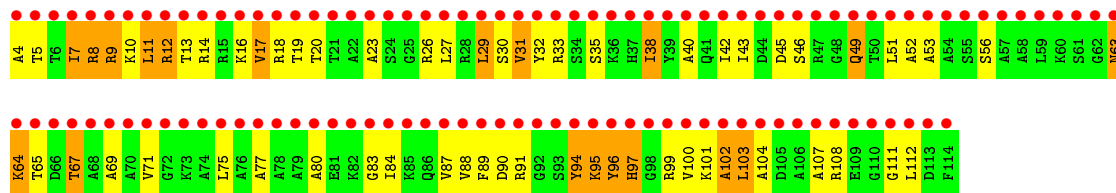


- Molecule 35: 50S ribosomal protein L17

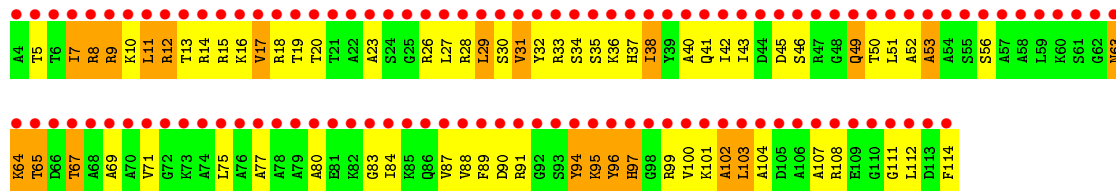




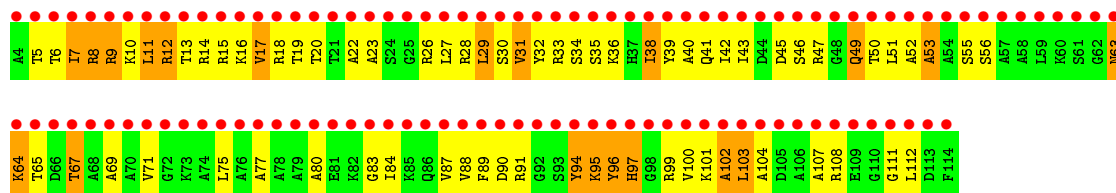
• Molecule 36: 50S ribosomal protein L18



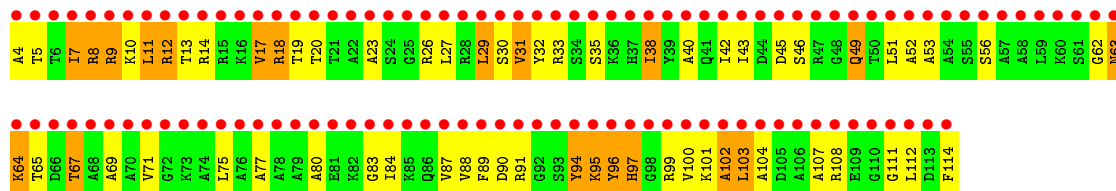
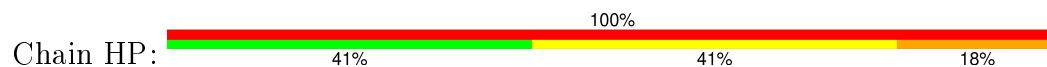
• Molecule 36: 50S ribosomal protein L18



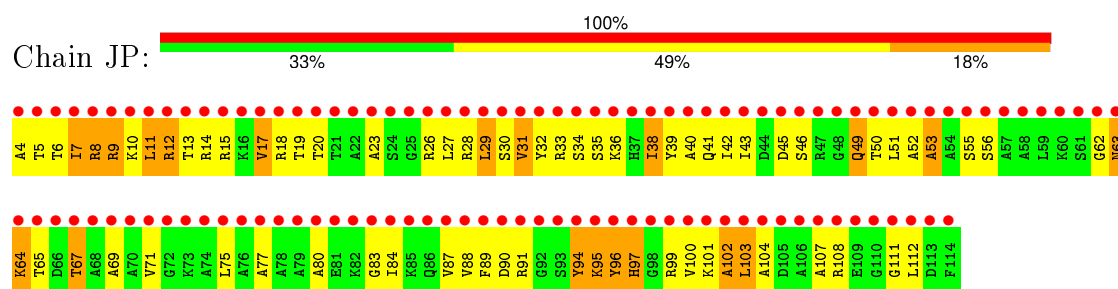
• Molecule 36: 50S ribosomal protein L18



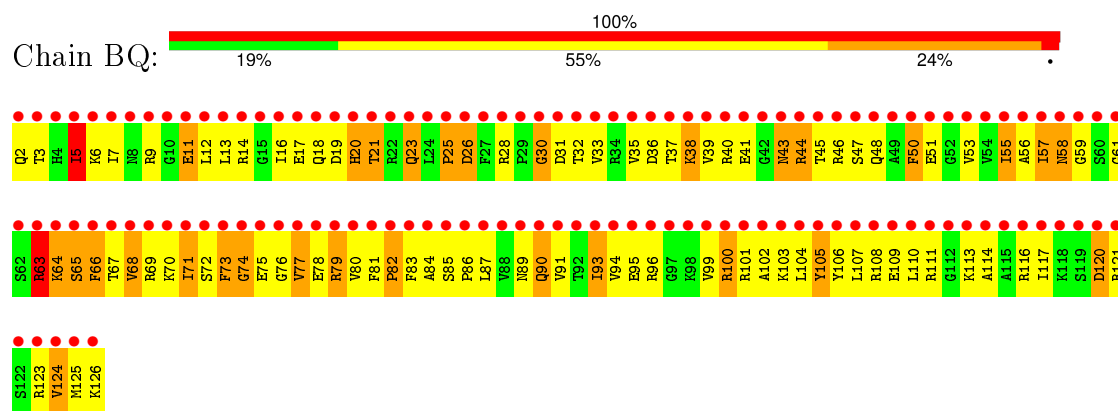
• Molecule 36: 50S ribosomal protein L18



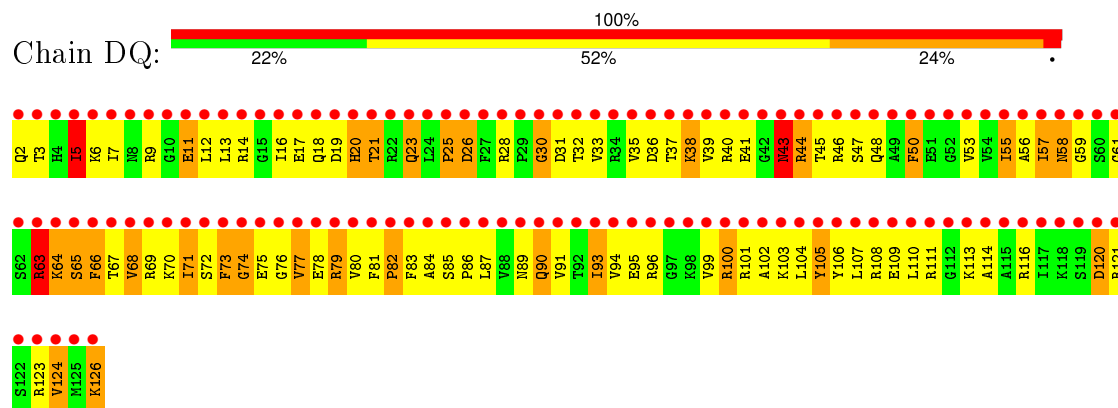
• Molecule 36: 50S ribosomal protein L18



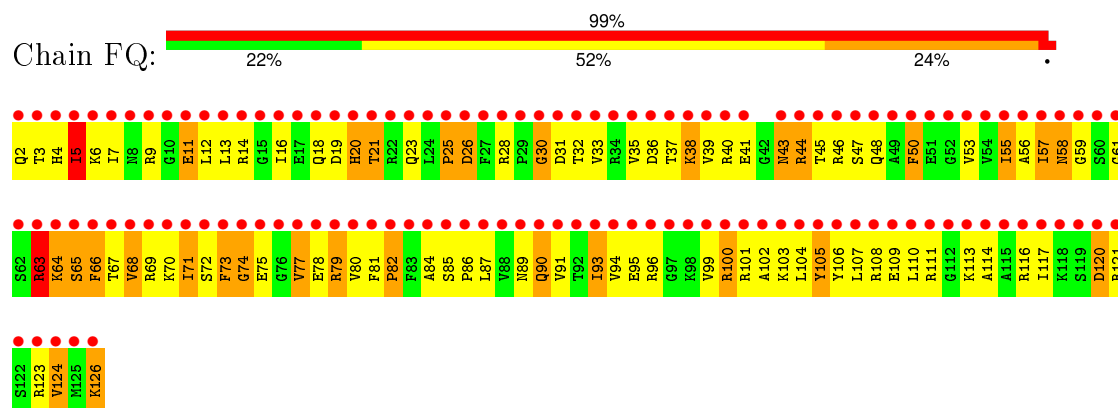
• Molecule 37: 50S ribosomal protein L19



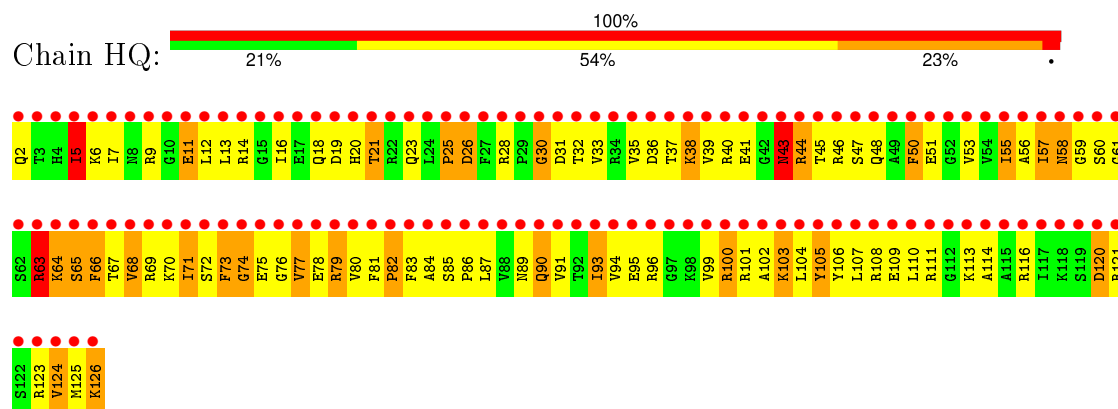
• Molecule 37: 50S ribosomal protein L19



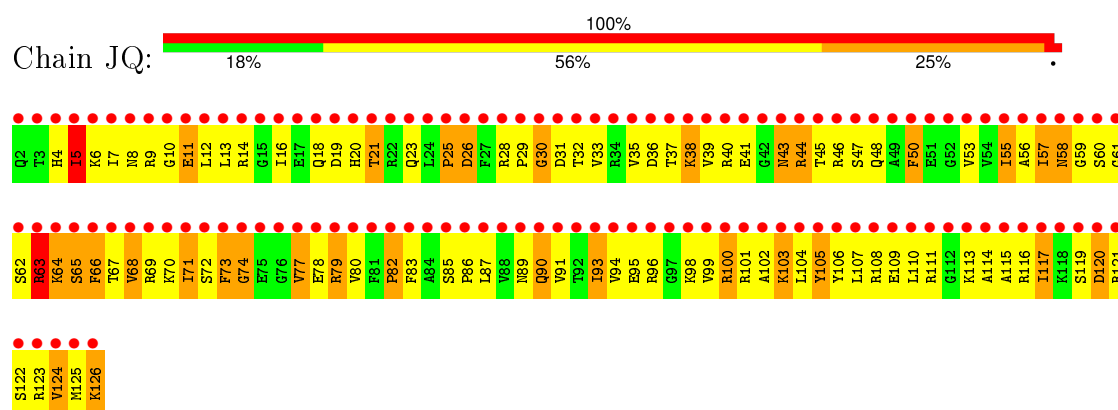
• Molecule 37: 50S ribosomal protein L19



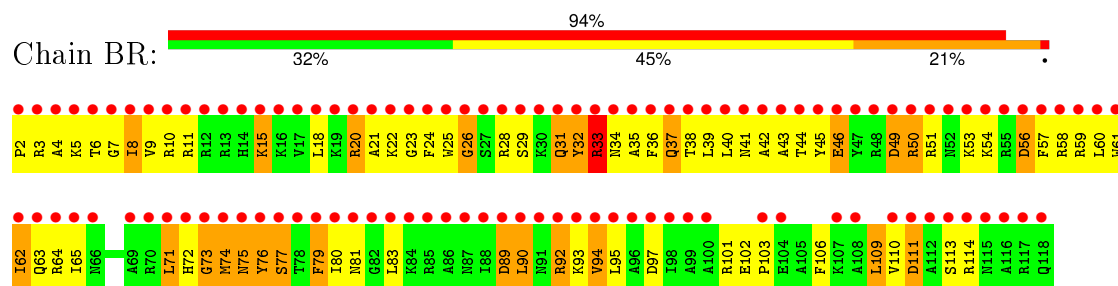
- Molecule 37: 50S ribosomal protein L19



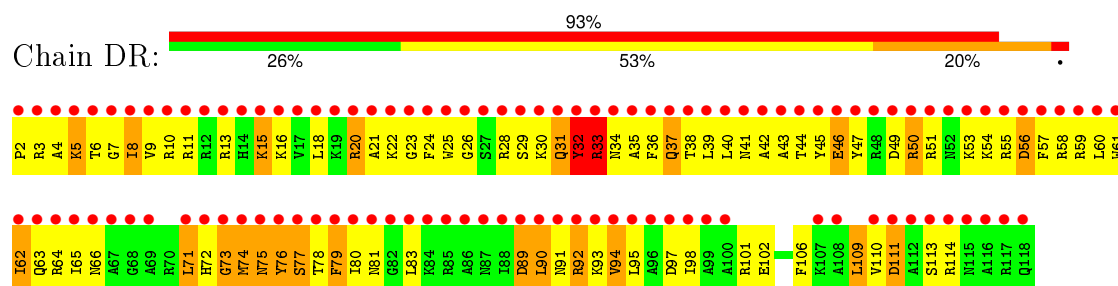
- Molecule 37: 50S ribosomal protein L19



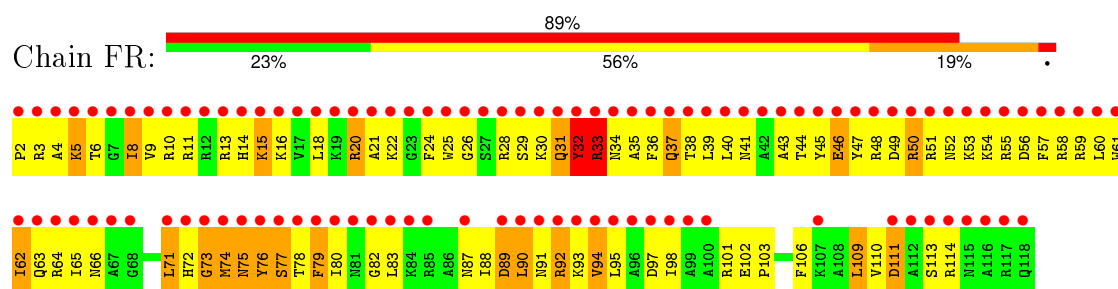
- Molecule 38: 50S ribosomal protein L20



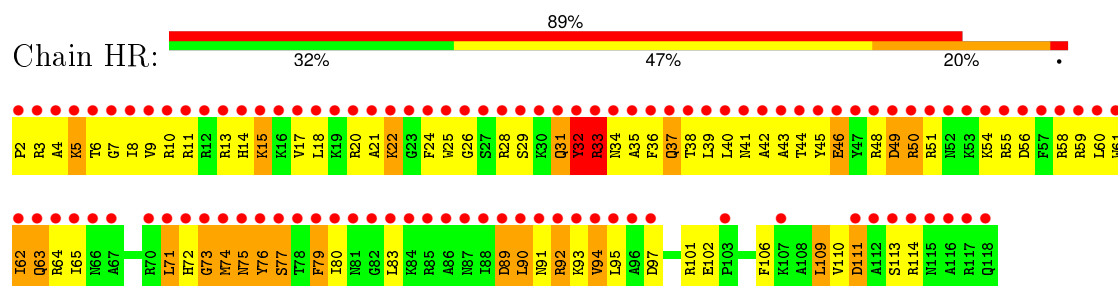
- Molecule 38: 50S ribosomal protein L20



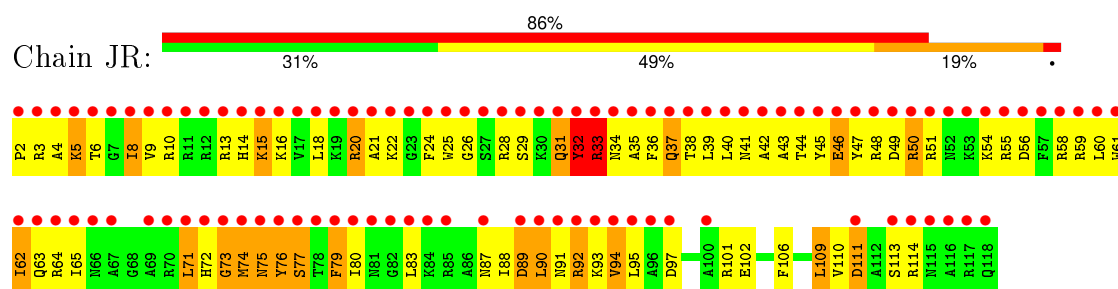
- Molecule 38: 50S ribosomal protein L20



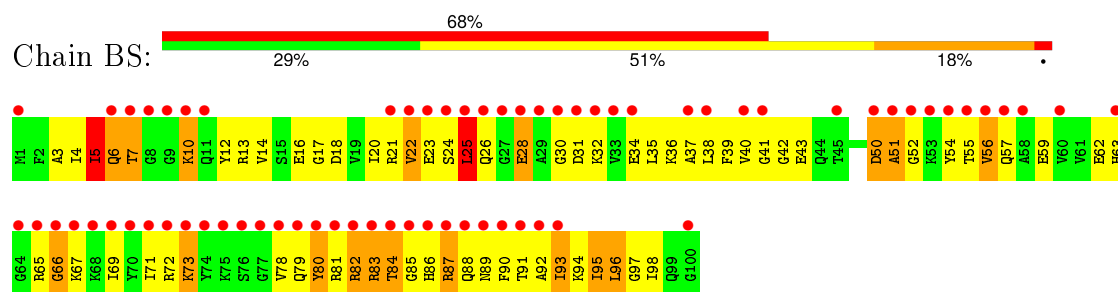
• Molecule 38: 50S ribosomal protein L20



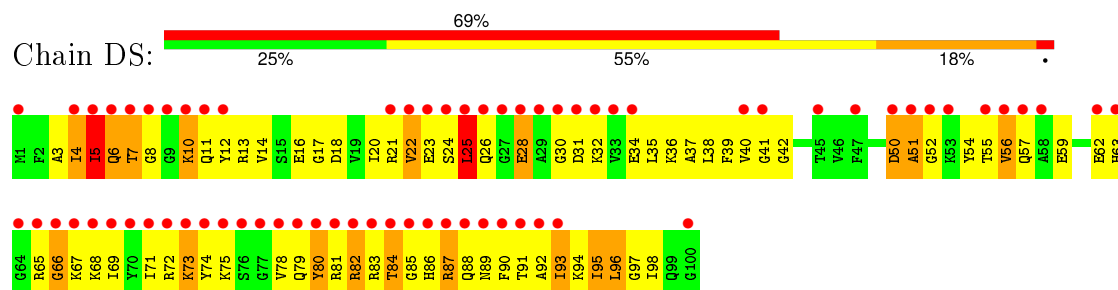
• Molecule 38: 50S ribosomal protein L20



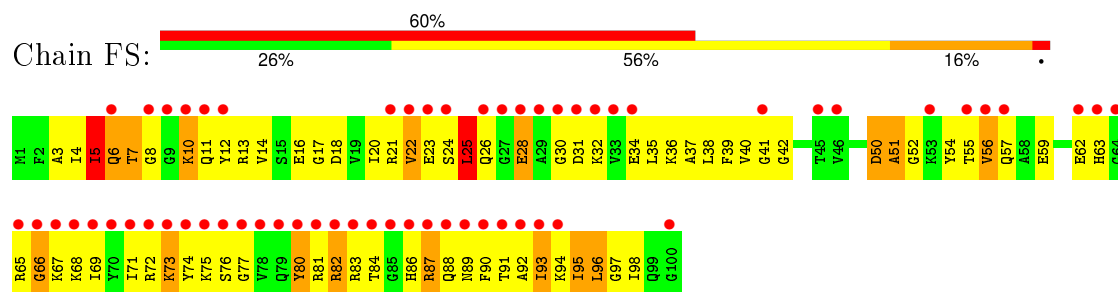
• Molecule 39: 50S ribosomal protein L21



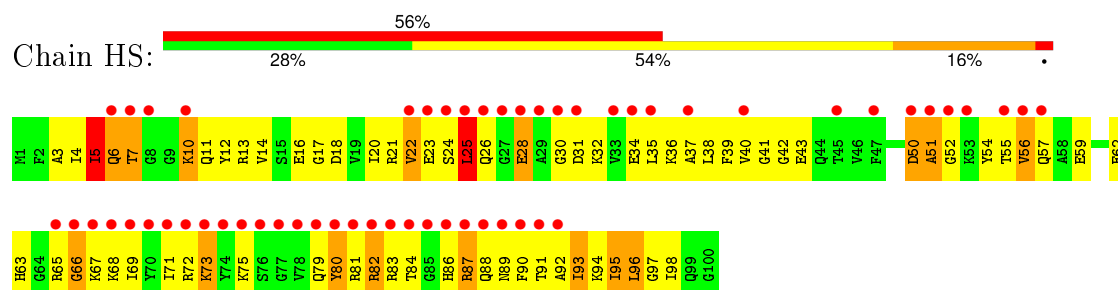
• Molecule 39: 50S ribosomal protein L21



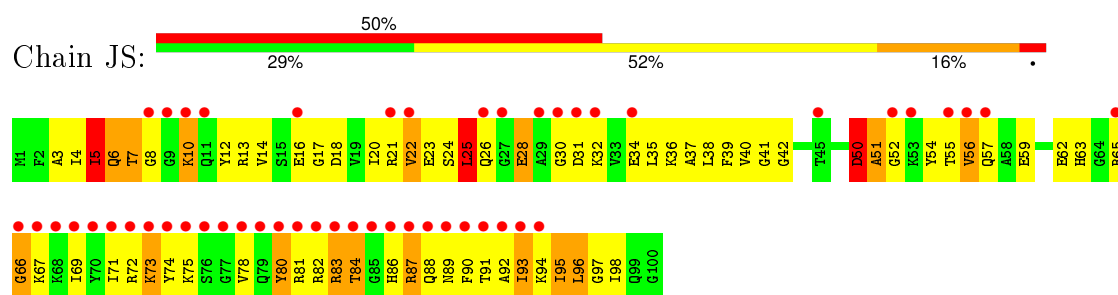
- Molecule 39: 50S ribosomal protein L21



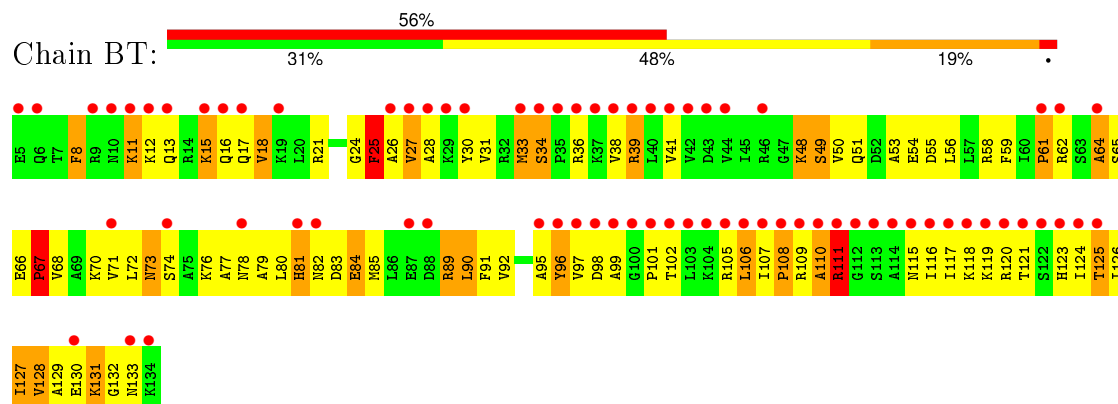
- Molecule 39: 50S ribosomal protein L21



- Molecule 39: 50S ribosomal protein L21

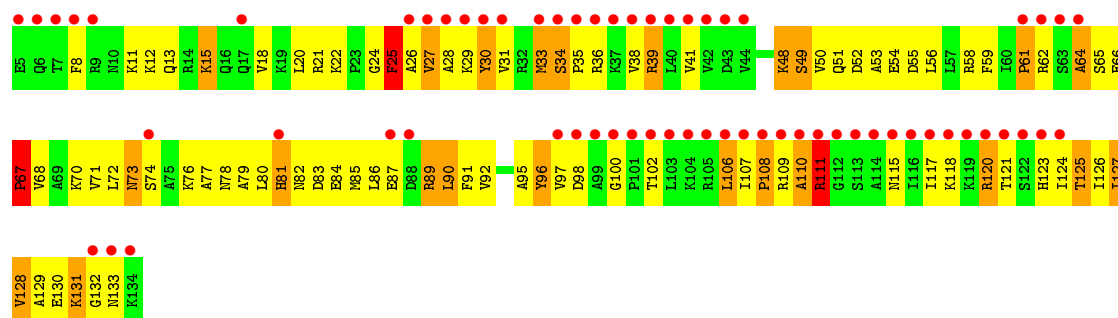


- Molecule 40: 50S ribosomal protein L22

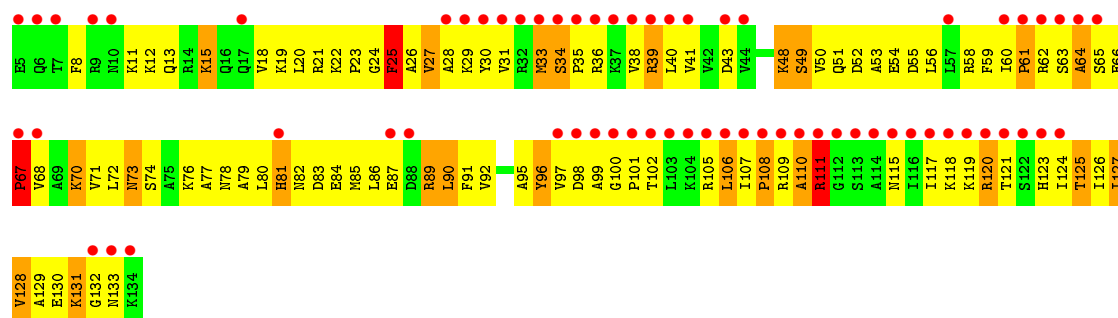


- Molecule 40: 50S ribosomal protein L22

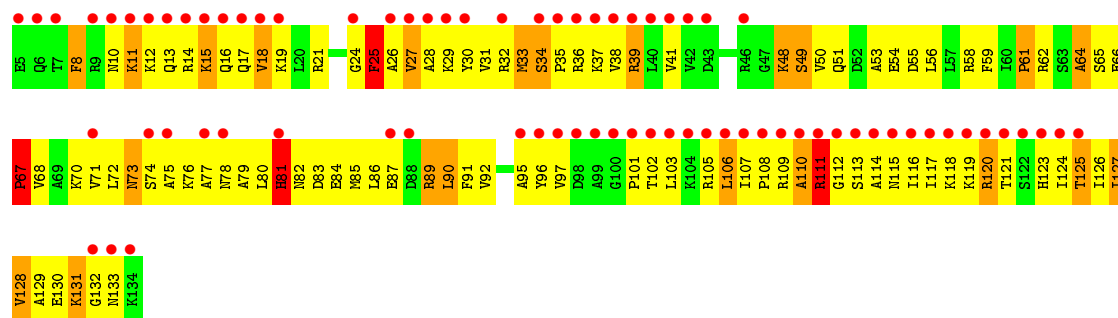




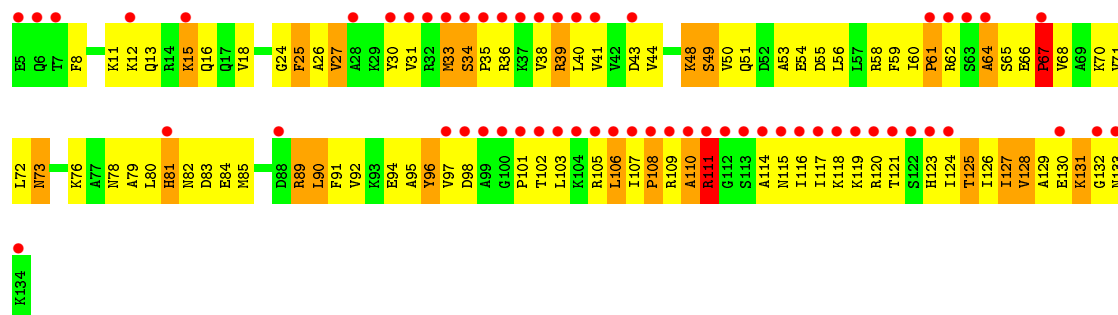
• Molecule 40: 50S ribosomal protein L22



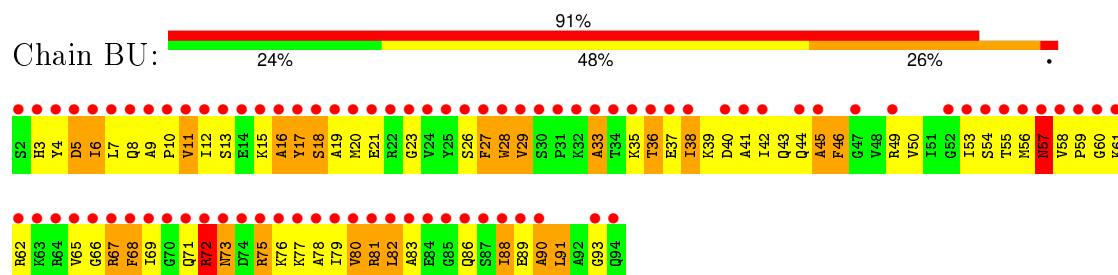
• Molecule 40: 50S ribosomal protein L22



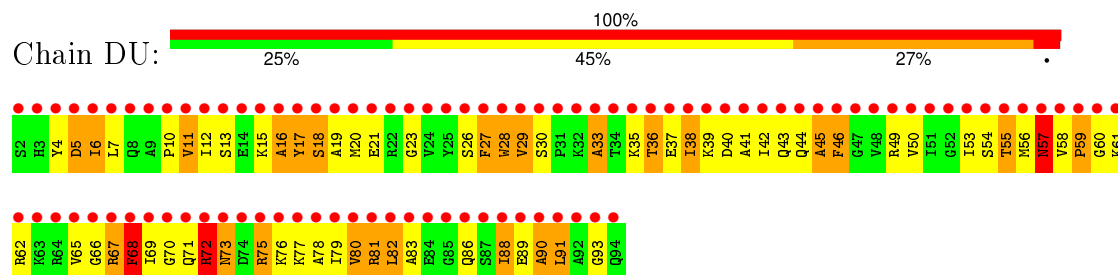
• Molecule 40: 50S ribosomal protein L22



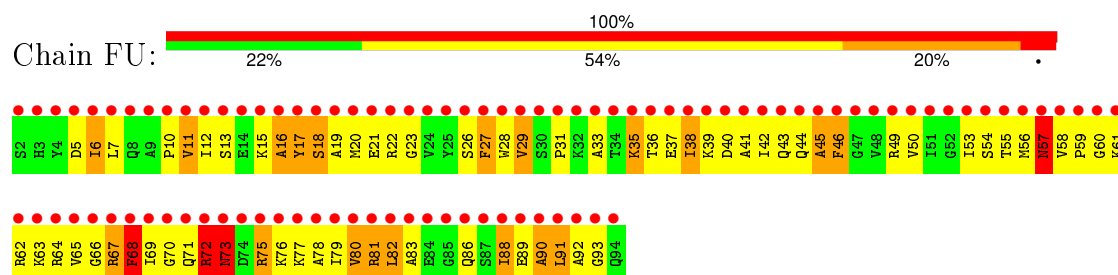
- Molecule 41: 50S ribosomal protein L23



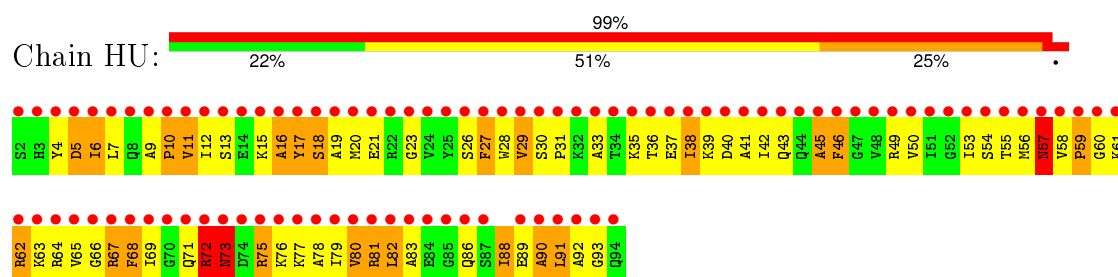
- Molecule 41: 50S ribosomal protein L23



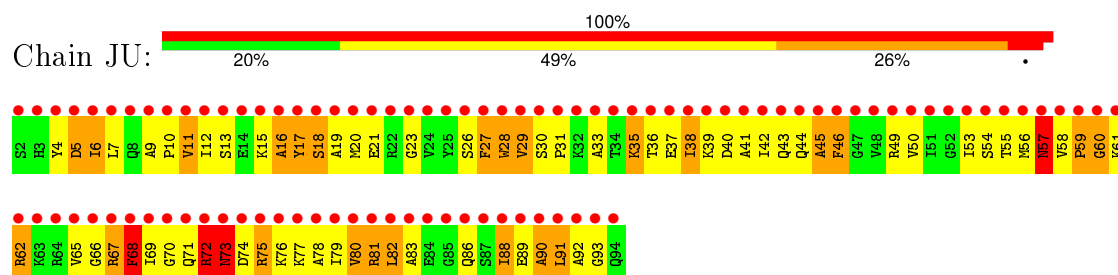
- Molecule 41: 50S ribosomal protein L23



- Molecule 41: 50S ribosomal protein L23

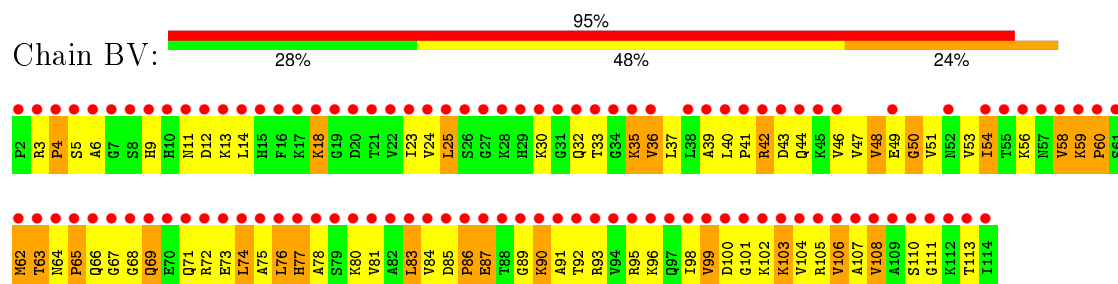


- Molecule 41: 50S ribosomal protein L23

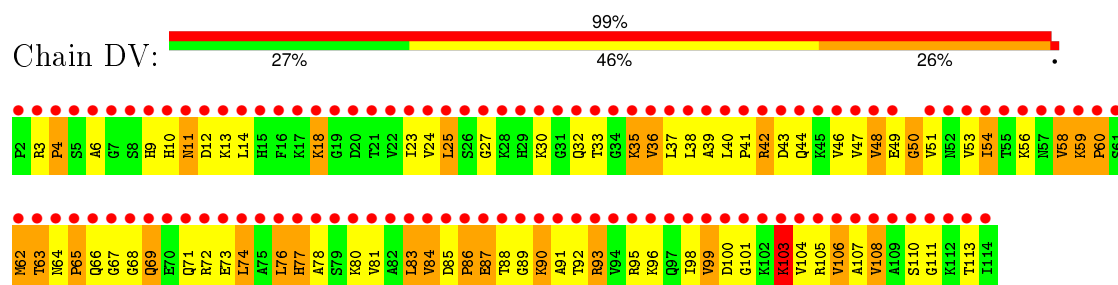




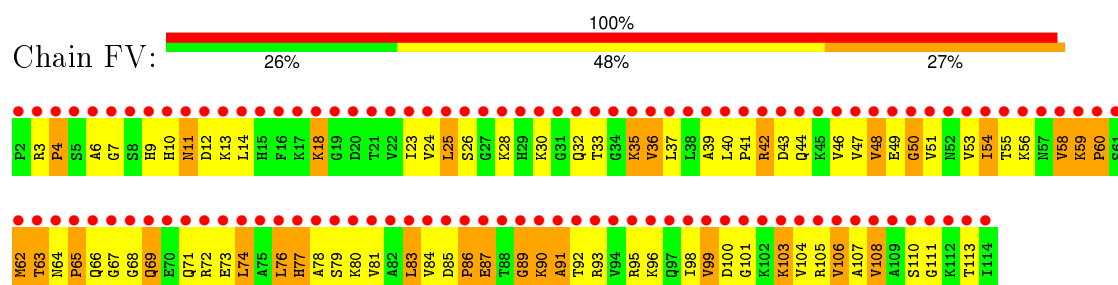
- Molecule 42: 50S ribosomal protein L24



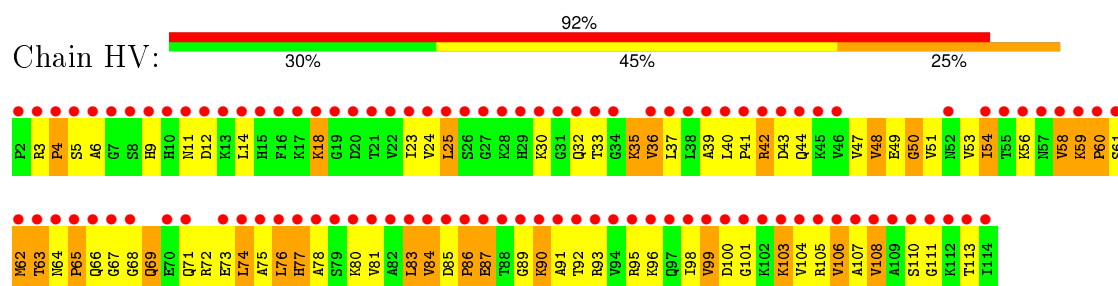
- Molecule 42: 50S ribosomal protein L24



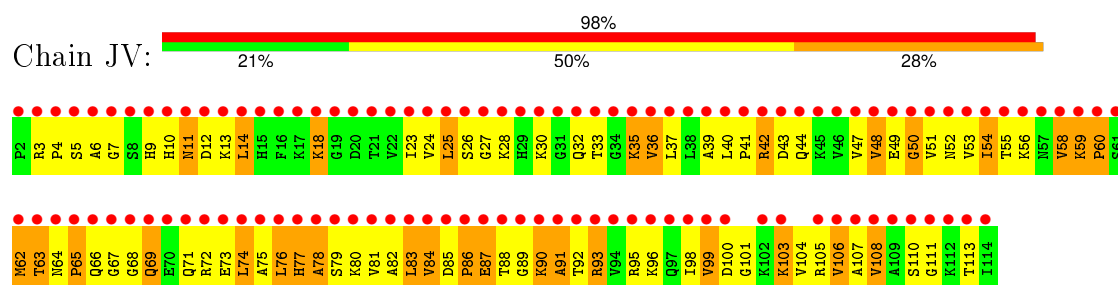
- Molecule 42: 50S ribosomal protein L24



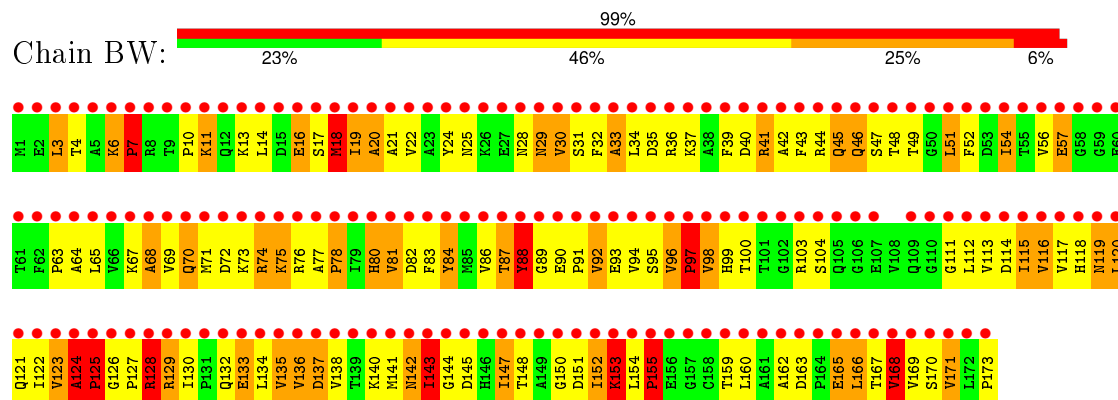
- Molecule 42: 50S ribosomal protein L24



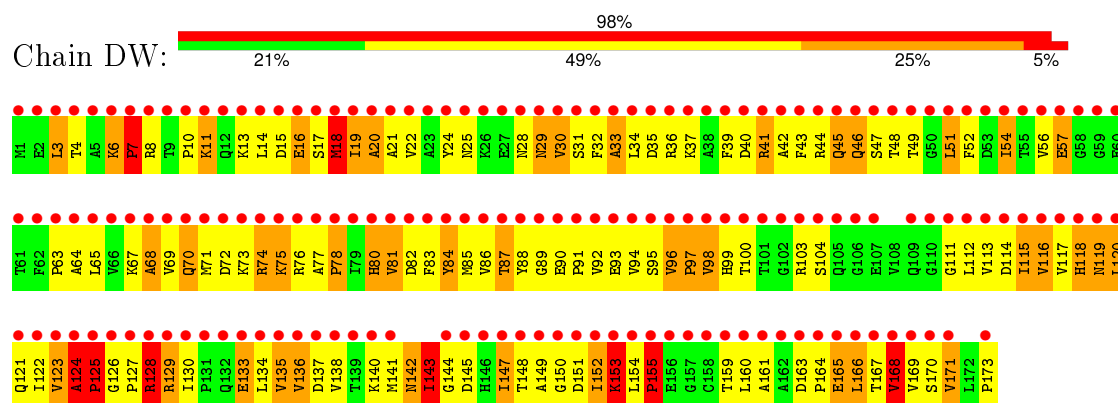
- Molecule 42: 50S ribosomal protein L24



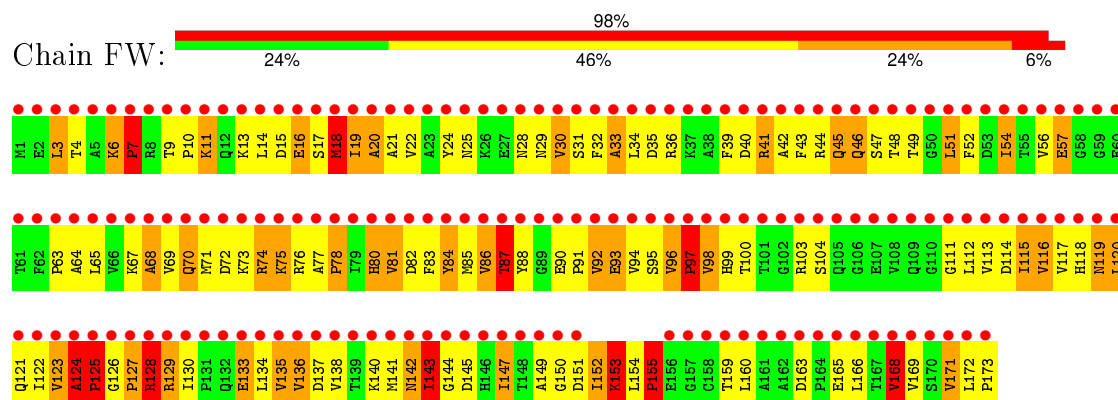
## • Molecule 43: general stress protein Ctc



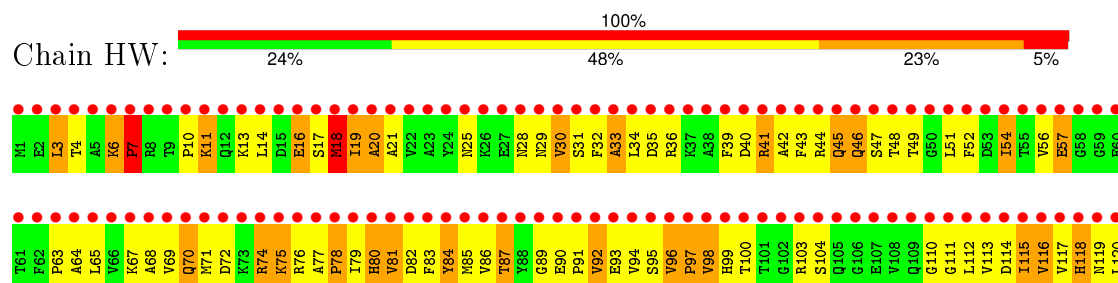
## • Molecule 43: general stress protein Ctc

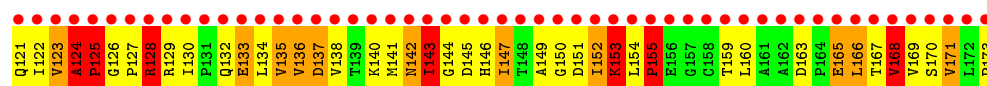


## • Molecule 43: general stress protein Ctc

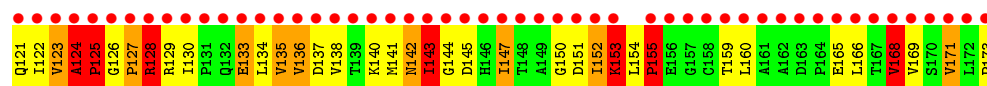
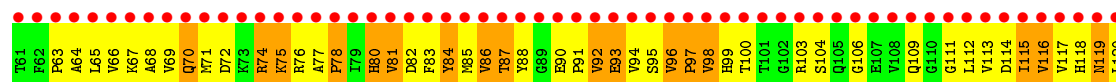
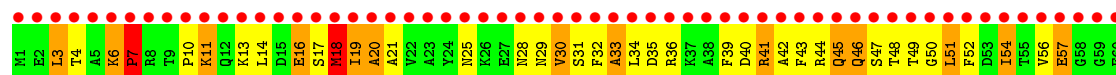


## • Molecule 43: general stress protein Ctc

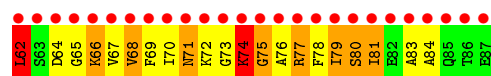
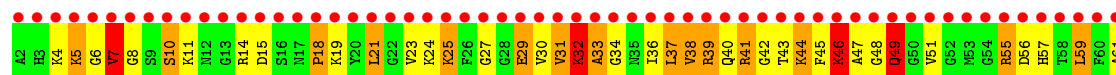




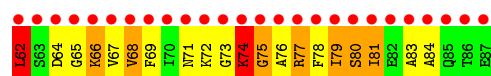
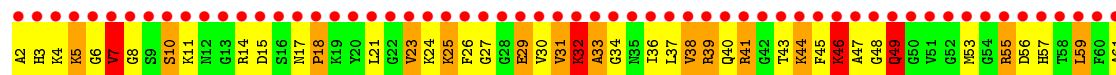
- Molecule 43: general stress protein Ctc



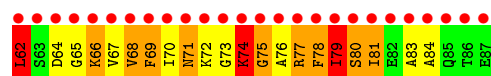
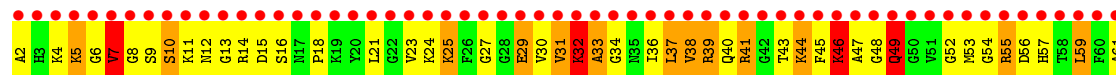
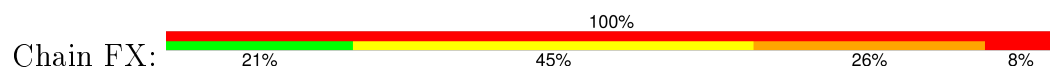
- Molecule 44: 50S ribosomal protein L27



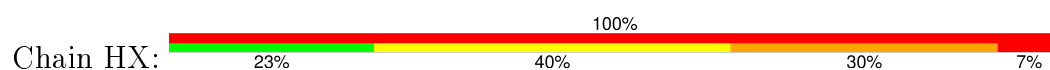
- Molecule 44: 50S ribosomal protein L27

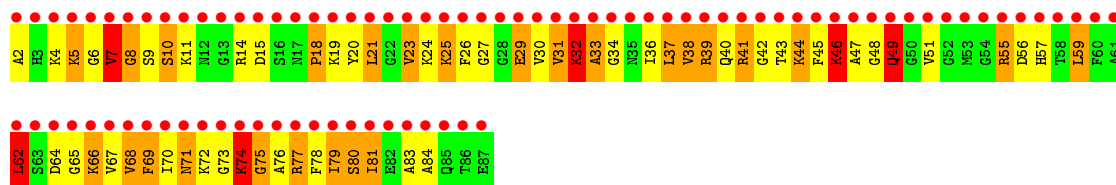


- Molecule 44: 50S ribosomal protein L27

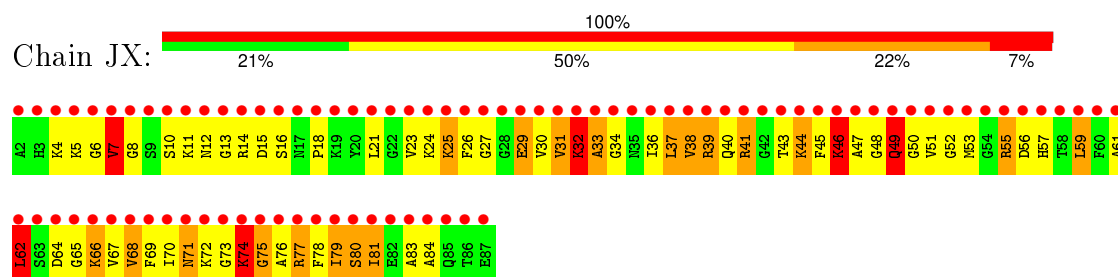


- Molecule 44: 50S ribosomal protein L27

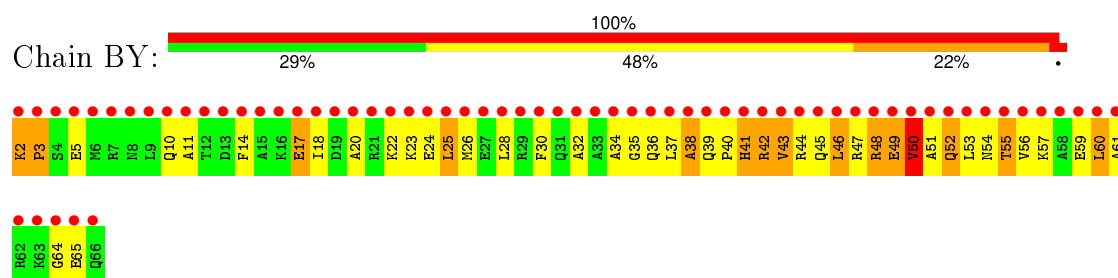




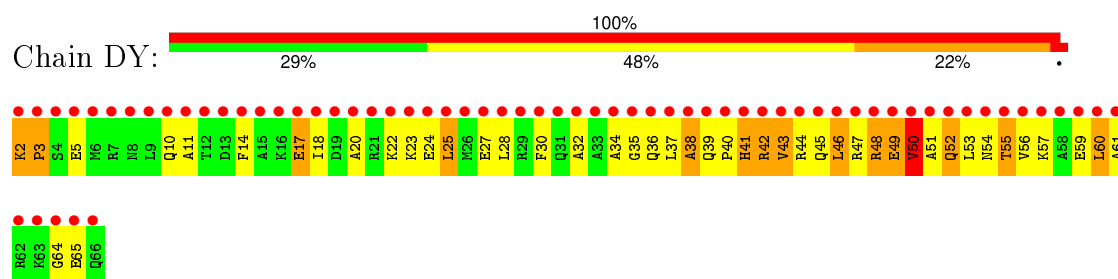
• Molecule 44: 50S ribosomal protein L27



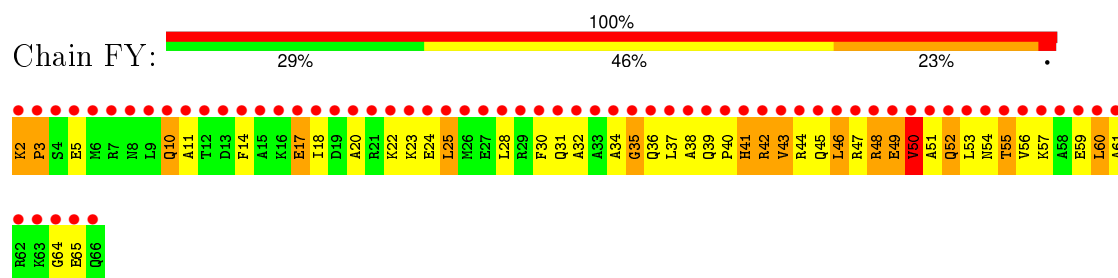
• Molecule 45: 50S ribosomal protein L29



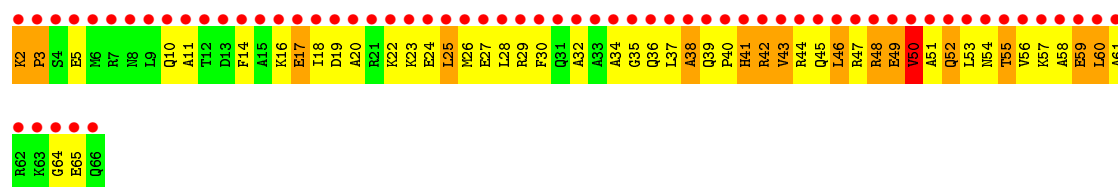
• Molecule 45: 50S ribosomal protein L29



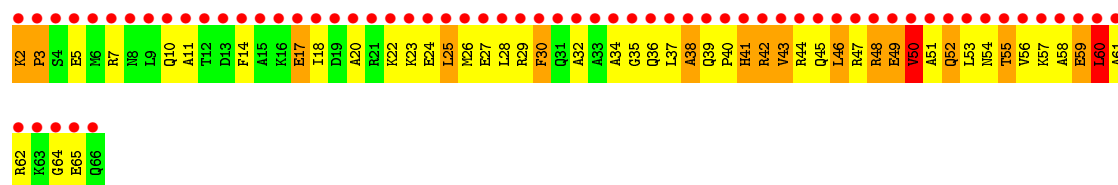
• Molecule 45: 50S ribosomal protein L29



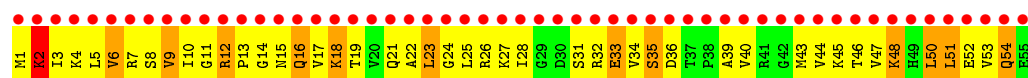
• Molecule 45: 50S ribosomal protein L29



• Molecule 45: 50S ribosomal protein L29



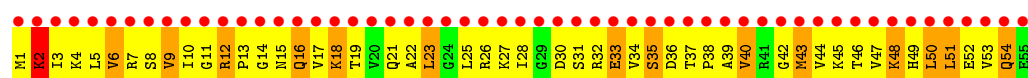
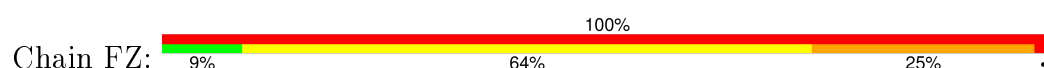
• Molecule 46: 50S ribosomal protein L30



• Molecule 46: 50S ribosomal protein L30



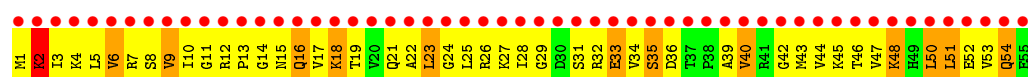
• Molecule 46: 50S ribosomal protein L30



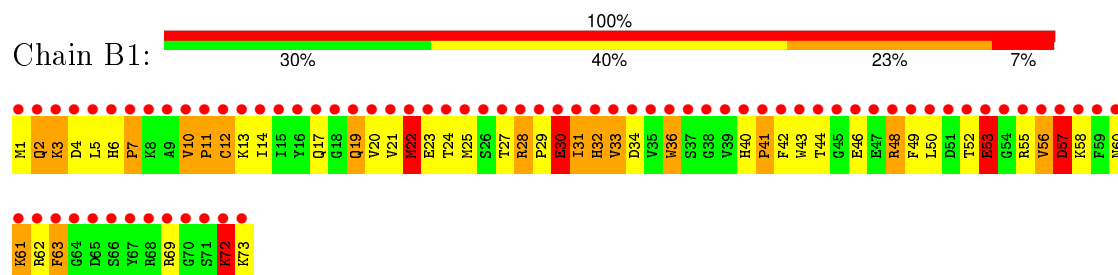
• Molecule 46: 50S ribosomal protein L30



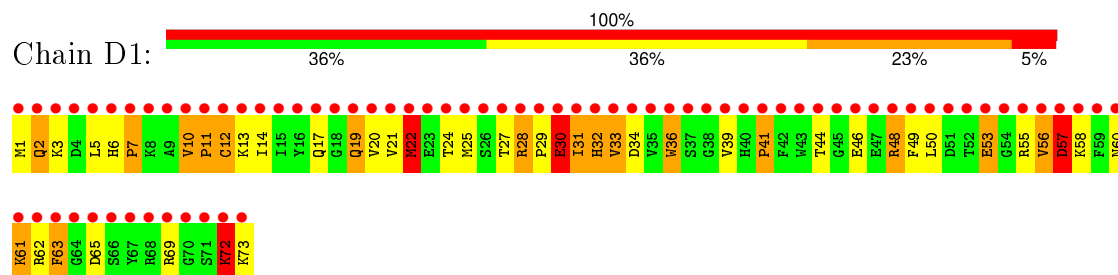
• Molecule 46: 50S ribosomal protein L30



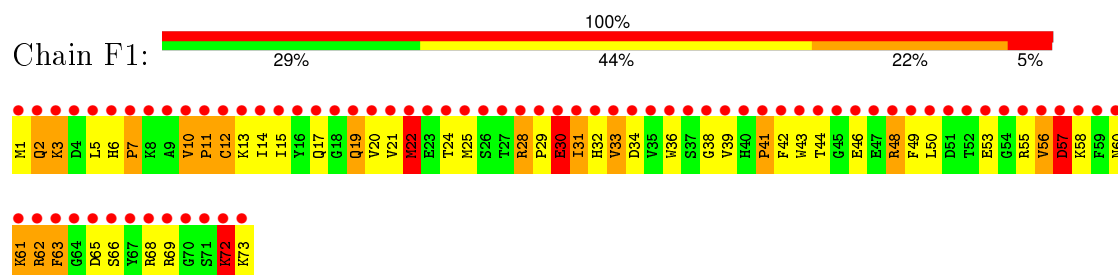
## • Molecule 47: 50S ribosomal protein L31



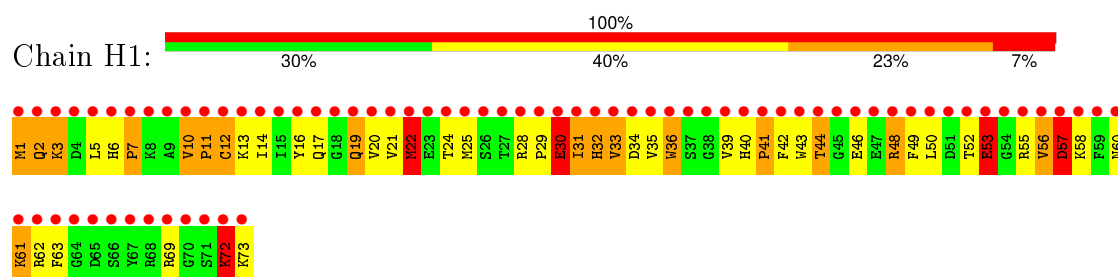
## • Molecule 47: 50S ribosomal protein L31



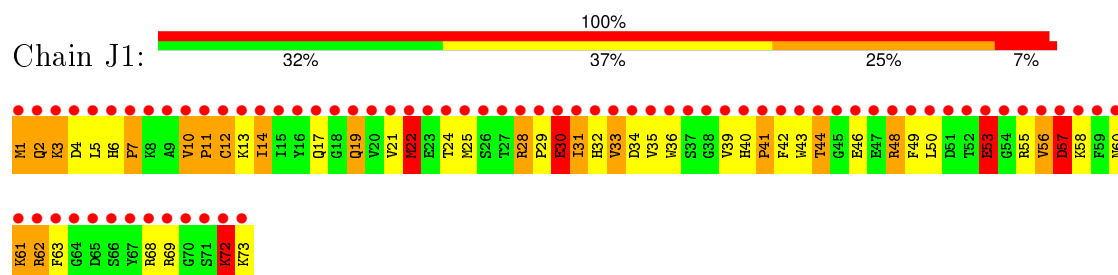
## • Molecule 47: 50S ribosomal protein L31



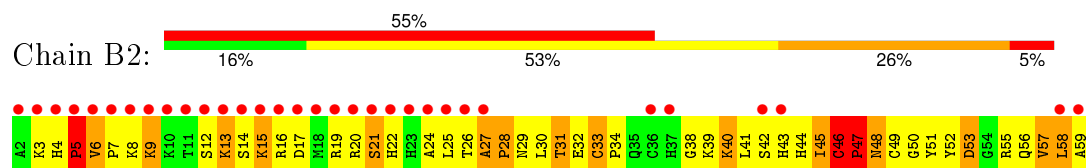
## • Molecule 47: 50S ribosomal protein L31



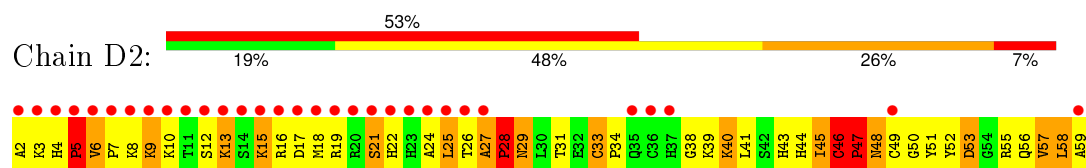
## • Molecule 47: 50S ribosomal protein L31



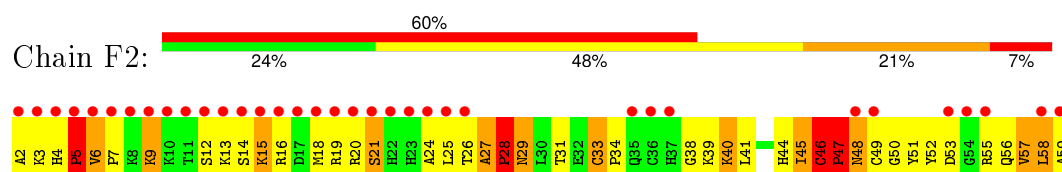
- Molecule 48: 50S ribosomal protein L32



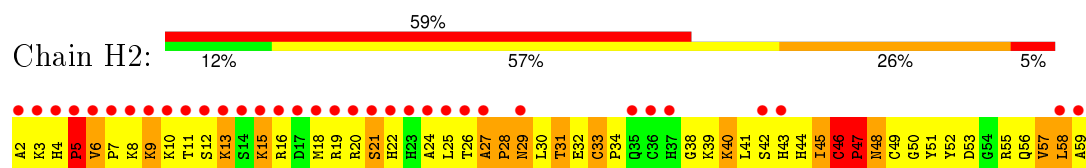
- Molecule 48: 50S ribosomal protein L32



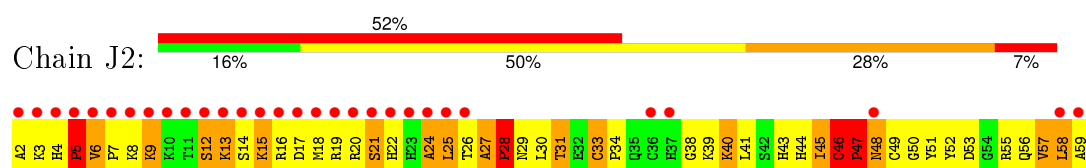
- Molecule 48: 50S ribosomal protein L32



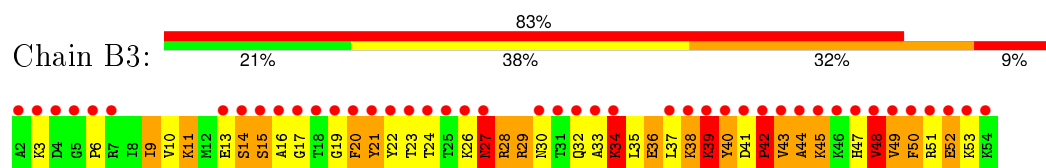
- Molecule 48: 50S ribosomal protein L32



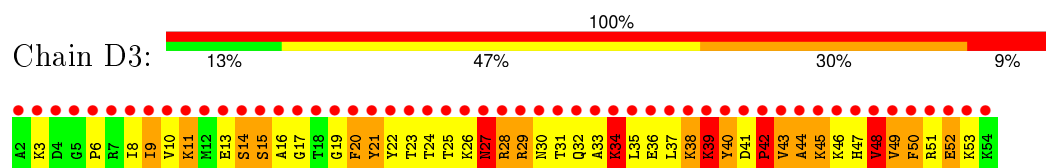
- Molecule 48: 50S ribosomal protein L32



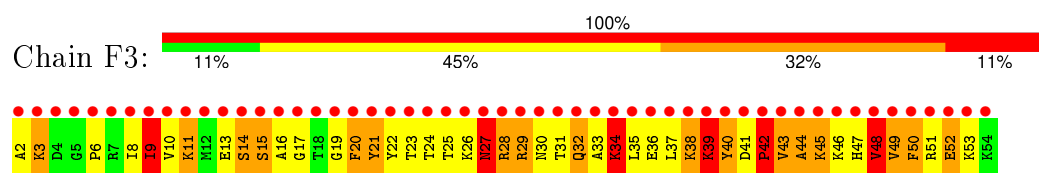
- Molecule 49: 50S ribosomal protein L33



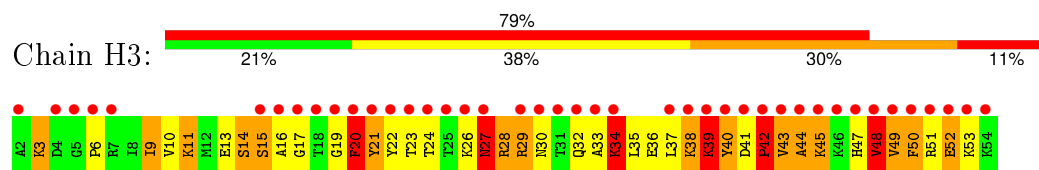
- Molecule 49: 50S ribosomal protein L33



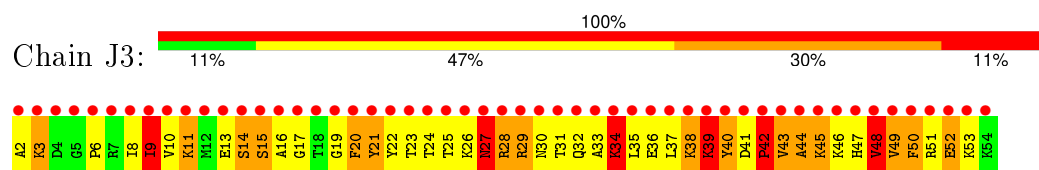
- Molecule 49: 50S ribosomal protein L33



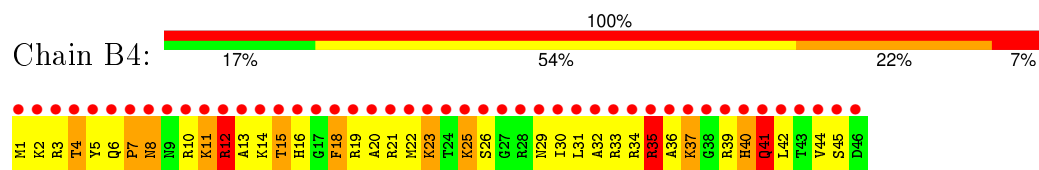
- Molecule 49: 50S ribosomal protein L33



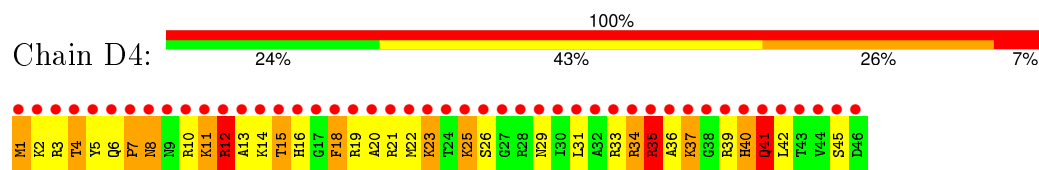
- Molecule 49: 50S ribosomal protein L33



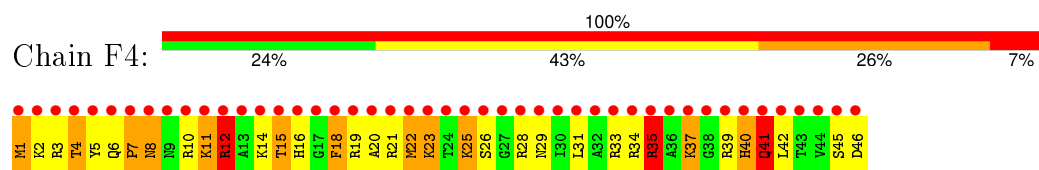
- Molecule 50: 50S ribosomal protein L34



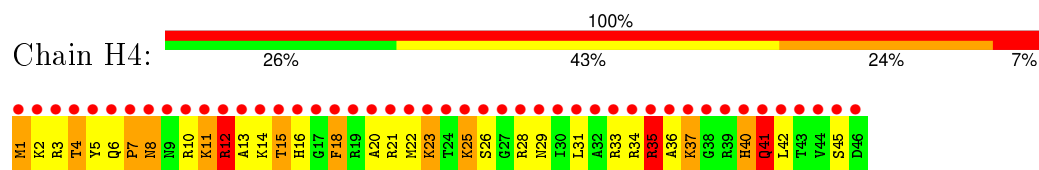
- Molecule 50: 50S ribosomal protein L34



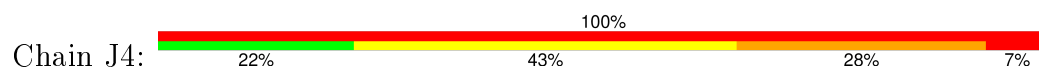
- Molecule 50: 50S ribosomal protein L34



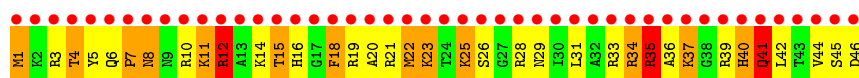
- Molecule 50: 50S ribosomal protein L34



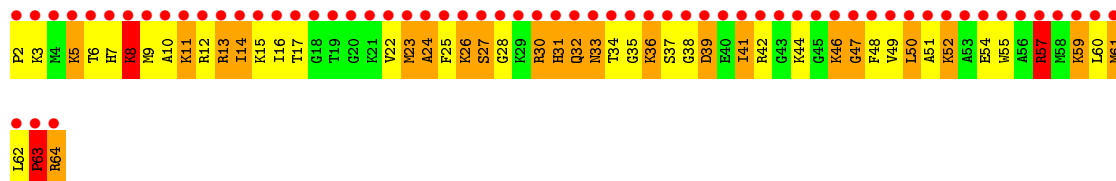
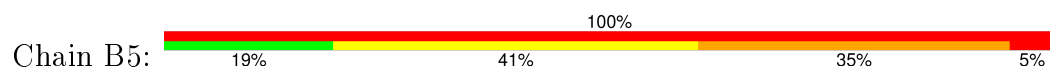
- Molecule 50: 50S ribosomal protein L34



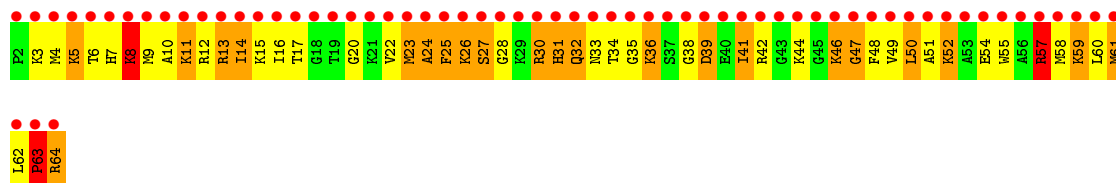
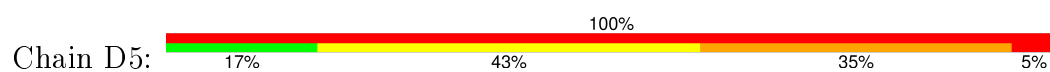




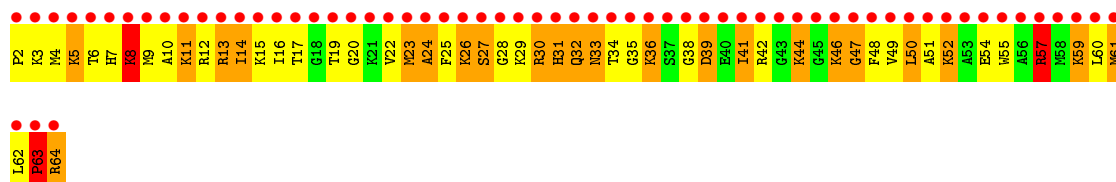
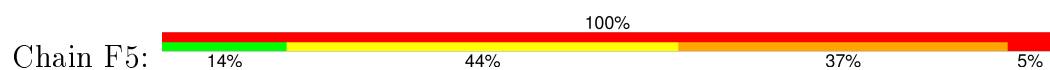
- Molecule 51: 50S ribosomal protein L35



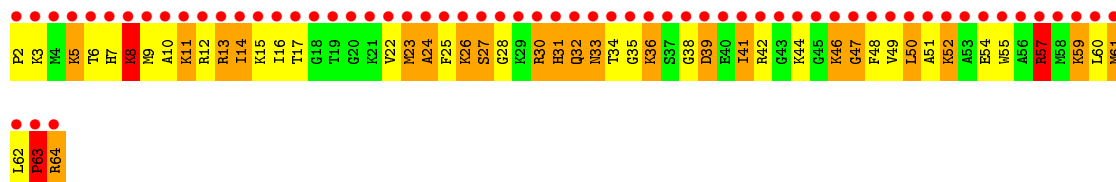
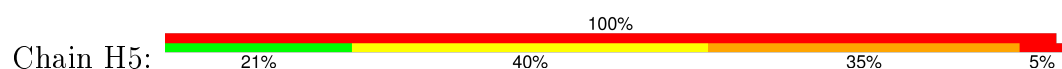
- Molecule 51: 50S ribosomal protein L35



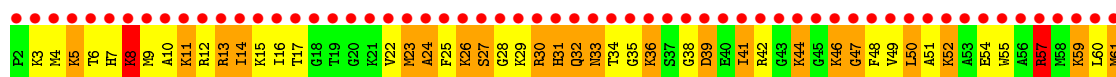
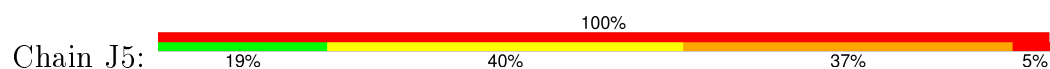
- Molecule 51: 50S ribosomal protein L35



- Molecule 51: 50S ribosomal protein L35

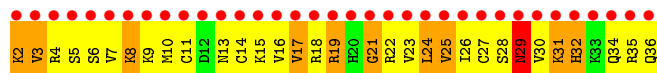
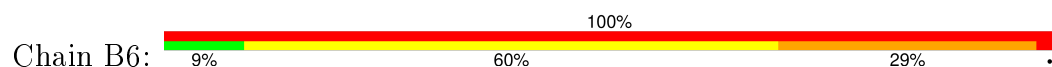


- Molecule 51: 50S ribosomal protein L35

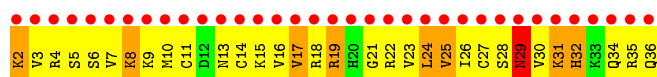
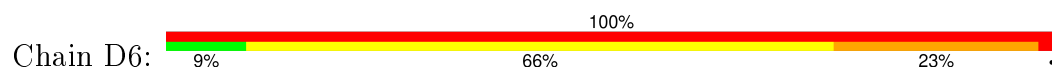




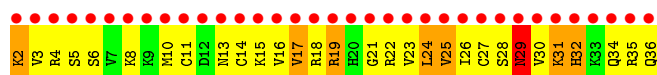
- Molecule 52: 50S ribosomal protein L36



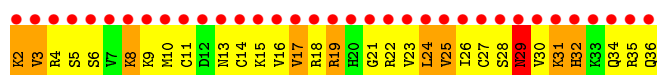
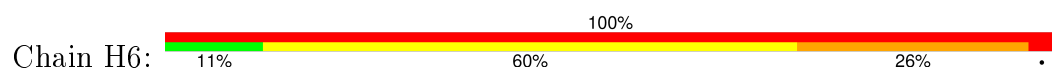
- Molecule 52: 50S ribosomal protein L36



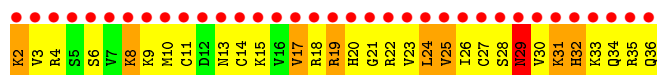
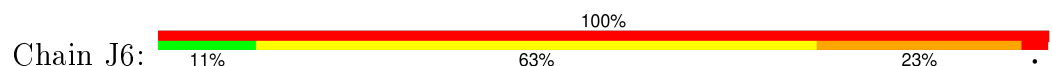
- Molecule 52: 50S ribosomal protein L36



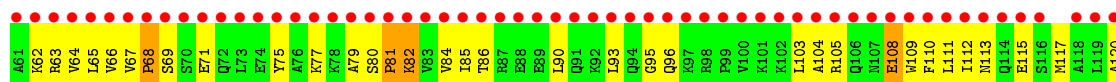
- Molecule 52: 50S ribosomal protein L36

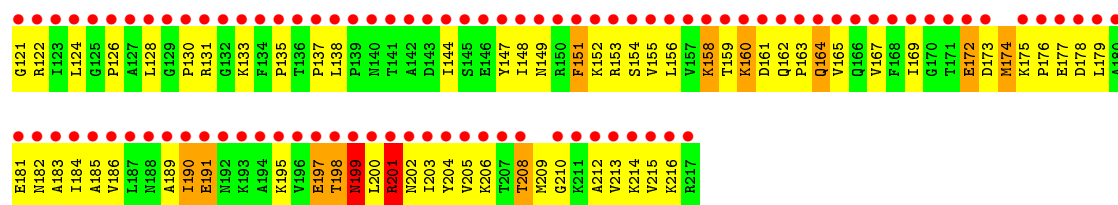


- Molecule 52: 50S ribosomal protein L36



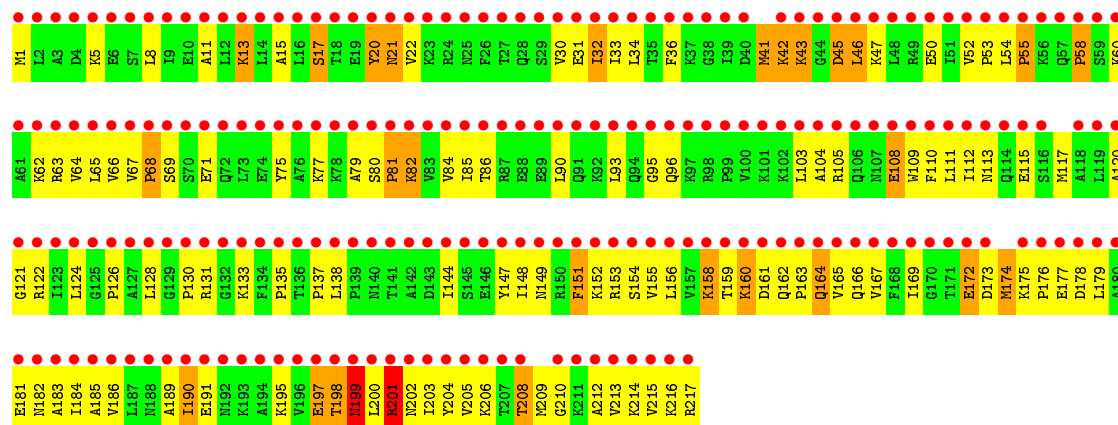
- Molecule 53: 50S ribosomal protein L1P





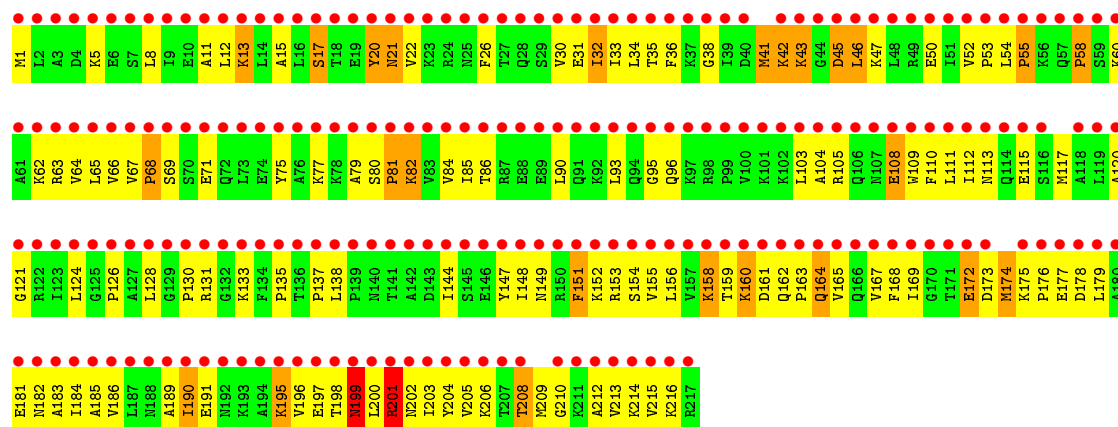
● Molecule 53: 50S ribosomal protein L1P

Chain D7: 98% 39% 48% 12%



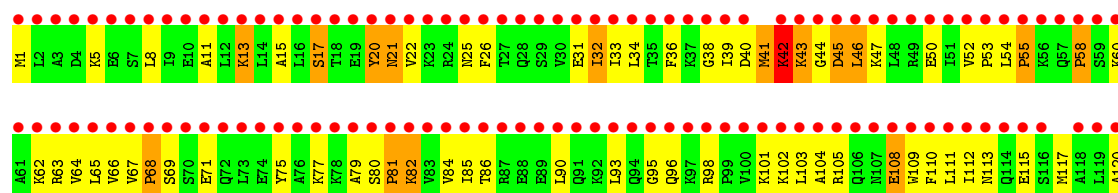
● Molecule 53: 50S ribosomal protein L1P

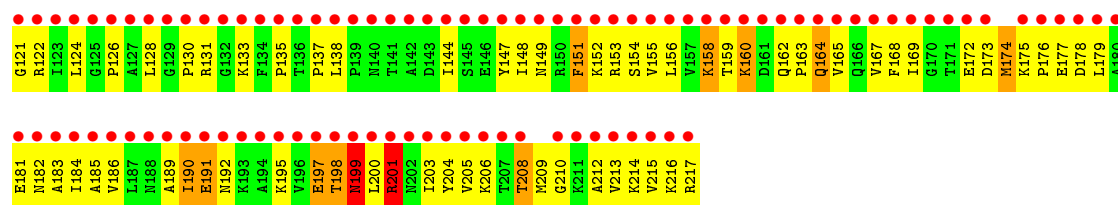
Chain F7: 98% 38% 50% 12%



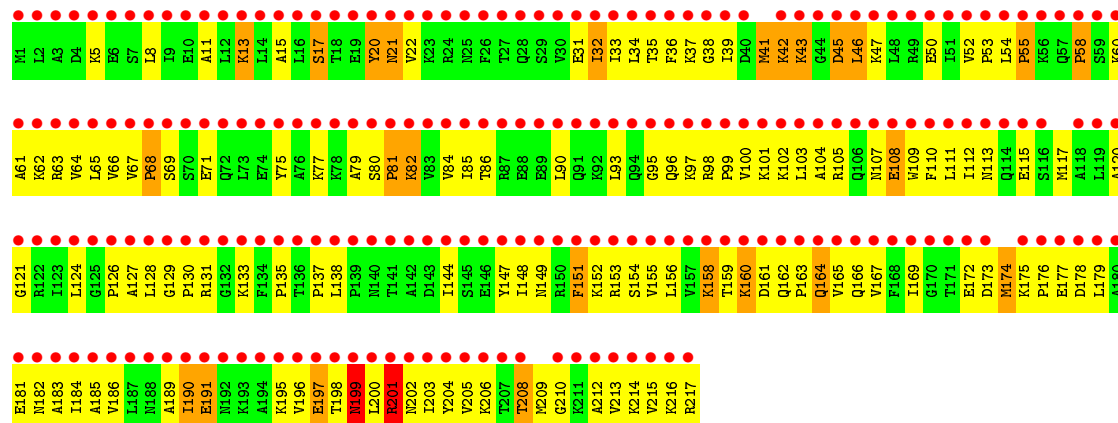
● Molecule 53: 50S ribosomal protein L1P

Chain H7: 98% 36% 51% 12%





• Molecule 53: 50S ribosomal protein L1P



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	687.90Å 687.90Å 1933.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	500.00 – 11.50 486.42 – 11.53	Depositor EDS
% Data completeness (in resolution range)	93.9 (500.00-11.50) 76.3 (486.42-11.53)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.18	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.395 , 0.401 0.411 , 0.420	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	(Not available)	Xtriage
Anisotropy	(Not available)	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.93 , -10.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>1</sup>	$\langle  L  \rangle =$ (Not available), $\langle L^2 \rangle =$ (Not available)	Xtriage
Outliers	(Not available)	Xtriage
$F_o, F_c$ correlation	0.84	EDS
Total number of atoms	717805	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	803.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *(Not available)*

<sup>1</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	AA	0.30	1/36713 (0.0%)	0.74	16/57289 (0.0%)
1	CA	0.30	1/36713 (0.0%)	0.74	15/57289 (0.0%)
1	EA	0.39	2/36714 (0.0%)	0.77	21/57293 (0.0%)
1	GA	0.39	2/36714 (0.0%)	0.75	19/57293 (0.0%)
1	IA	0.36	1/36714 (0.0%)	0.78	20/57293 (0.0%)
2	AB	0.26	0/1936	0.55	0/2609
2	CB	0.26	0/1936	0.55	0/2609
2	EB	0.26	0/1936	0.55	0/2609
2	GB	0.26	0/1936	0.55	0/2609
2	IB	0.26	0/1936	0.55	0/2609
3	AC	0.24	0/1637	0.53	0/2205
3	CC	0.24	0/1637	0.53	0/2205
3	EC	0.24	0/1637	0.53	0/2205
3	GC	0.24	0/1637	0.53	0/2205
3	IC	0.25	0/1637	0.53	0/2205
4	AD	0.24	0/1733	0.49	0/2318
4	CD	0.25	0/1733	0.49	0/2318
4	ED	0.25	0/1733	0.49	0/2318
4	GD	0.25	0/1733	0.49	0/2318
4	ID	0.25	0/1733	0.49	0/2318
5	AE	0.28	0/1163	0.59	0/1564
5	CE	0.28	0/1163	0.59	0/1564
5	EE	0.28	0/1163	0.59	0/1564
5	GE	0.28	0/1163	0.59	0/1564
5	IE	0.27	0/1163	0.59	0/1564
6	AF	0.24	0/856	0.52	0/1154
6	CF	0.24	0/856	0.52	0/1154
6	EF	0.24	0/856	0.52	0/1154
6	GF	0.24	0/856	0.52	0/1154
6	IF	0.24	0/856	0.52	0/1154
7	AG	0.24	0/1276	0.50	0/1709
7	CG	0.24	0/1276	0.50	0/1709
7	EG	0.25	0/1276	0.50	0/1709
7	GG	0.25	0/1276	0.50	0/1709

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
7	IG	0.25	0/1276	0.50	0/1709
8	AH	0.25	0/1136	0.56	0/1527
8	CH	0.25	0/1136	0.56	0/1527
8	EH	0.25	0/1136	0.56	0/1527
8	GH	0.25	0/1136	0.56	0/1527
8	IH	0.25	0/1136	0.56	0/1527
9	AI	0.26	0/1029	0.51	0/1378
9	CI	0.26	0/1029	0.51	0/1378
9	EI	0.25	0/1029	0.51	0/1378
9	GI	0.25	0/1029	0.51	0/1378
9	II	0.25	0/1029	0.51	0/1378
10	AJ	0.25	0/808	0.59	0/1085
10	CJ	0.25	0/808	0.59	0/1085
10	EJ	0.25	0/808	0.59	0/1085
10	GJ	0.25	0/808	0.58	0/1085
10	IJ	0.25	0/808	0.59	0/1085
11	AK	0.24	0/900	0.56	0/1213
11	CK	0.24	0/900	0.56	0/1213
11	EK	0.24	0/900	0.56	0/1213
11	GK	0.24	0/900	0.56	0/1213
11	IK	0.24	0/900	0.56	0/1213
12	AL	0.49	1/985 (0.1%)	0.68	1/1314 (0.1%)
12	CL	0.25	0/984	0.58	0/1311
12	EL	0.35	1/985 (0.1%)	0.83	3/1314 (0.2%)
12	GL	0.25	0/984	0.58	0/1311
12	IL	0.86	1/985 (0.1%)	0.70	2/1314 (0.2%)
13	AM	0.27	0/1007	0.87	3/1344 (0.2%)
13	CM	0.26	0/1006	0.59	1/1341 (0.1%)
13	EM	0.26	0/1006	0.58	1/1341 (0.1%)
13	GM	0.52	1/1007 (0.1%)	1.07	3/1344 (0.2%)
13	IM	0.27	0/1006	0.58	1/1341 (0.1%)
14	AN	0.27	0/501	0.59	0/664
14	CN	0.27	0/501	0.59	0/664
14	EN	0.27	0/501	0.59	0/664
14	GN	0.27	0/501	0.59	0/664
14	IN	0.28	0/501	0.59	0/664
15	AO	0.24	0/745	0.51	0/992
15	CO	0.24	0/745	0.51	0/992
15	EO	0.24	0/745	0.51	0/992
15	GO	0.24	0/745	0.51	0/992
15	IO	0.24	0/745	0.51	0/992
16	AP	0.26	0/717	0.58	0/963
16	CP	0.26	0/717	0.58	0/963

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
16	EP	0.26	0/717	0.58	0/963
16	GP	0.26	0/717	0.58	0/963
16	IP	0.26	0/717	0.59	0/963
17	AQ	0.26	0/870	0.59	0/1159
17	CQ	0.26	0/870	0.59	0/1159
17	EQ	0.26	0/870	0.59	0/1159
17	GQ	0.26	0/870	0.59	0/1159
17	IQ	0.26	0/870	0.59	0/1159
18	AR	0.26	0/603	0.52	0/799
18	CR	0.26	0/603	0.52	0/799
18	ER	0.26	0/603	0.52	0/799
18	GR	0.26	0/603	0.52	0/799
18	IR	0.26	0/603	0.52	0/799
19	AS	0.25	0/662	0.60	0/890
19	CS	0.25	0/662	0.60	0/890
19	ES	0.25	0/662	0.60	0/890
19	GS	0.25	0/662	0.60	0/890
19	IS	0.25	0/662	0.60	0/890
20	AT	0.30	0/764	0.68	1/1006 (0.1%)
20	CT	0.29	0/764	0.68	1/1006 (0.1%)
20	ET	0.30	0/764	0.68	1/1006 (0.1%)
20	GT	0.29	0/764	0.68	1/1006 (0.1%)
20	IT	0.29	0/764	0.68	1/1006 (0.1%)
21	Aa	0.23	0/731	0.36	0/987
21	Ca	0.23	0/731	0.36	0/987
21	Ea	0.23	0/731	0.36	0/987
21	Ga	0.23	0/731	0.36	0/987
21	Ia	0.23	0/731	0.36	0/987
22	BB	0.90	55/67883 (0.1%)	0.93	143/105846 (0.1%)
22	DB	0.87	62/67886 (0.1%)	0.89	142/105858 (0.1%)
22	FB	0.85	58/67883 (0.1%)	0.92	138/105846 (0.1%)
22	HB	0.80	57/67884 (0.1%)	0.92	146/105850 (0.1%)
22	JB	0.81	56/67885 (0.1%)	0.85	130/105854 (0.1%)
23	BA	0.35	0/2816	0.75	0/4388
23	DA	0.35	0/2816	0.75	0/4388
23	FA	0.35	0/2816	0.75	0/4388
23	HA	0.35	0/2816	0.75	0/4388
23	JA	0.34	0/2816	0.75	0/4388
24	BD	0.33	0/2121	0.90	2/2854 (0.1%)
24	DD	0.33	0/2121	0.90	2/2854 (0.1%)
24	FD	0.33	0/2121	0.90	2/2854 (0.1%)
24	HD	0.32	0/2121	0.90	2/2854 (0.1%)
24	JD	0.33	0/2121	0.90	2/2854 (0.1%)



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
25	BE	0.33	0/1568	0.92	8/2105 (0.4%)
25	DE	0.33	0/1568	0.92	8/2105 (0.4%)
25	FE	0.33	0/1568	0.92	8/2105 (0.4%)
25	HE	0.33	0/1568	0.92	8/2105 (0.4%)
25	JE	0.33	0/1568	0.92	8/2105 (0.4%)
26	BF	0.29	0/1530	0.75	0/2070
26	DF	0.29	0/1530	0.75	0/2070
26	FF	0.29	0/1530	0.75	0/2070
26	HF	0.30	0/1530	0.75	0/2070
26	JF	0.29	0/1530	0.75	0/2070
27	BG	0.32	0/1429	0.87	3/1915 (0.2%)
27	DG	0.32	0/1429	0.87	3/1915 (0.2%)
27	FG	0.32	0/1429	0.87	3/1915 (0.2%)
27	HG	0.31	0/1429	0.87	3/1915 (0.2%)
27	JG	0.32	0/1429	0.87	3/1915 (0.2%)
28	BH	0.29	0/1338	0.80	3/1810 (0.2%)
28	DH	0.29	0/1338	0.79	3/1810 (0.2%)
28	FH	0.29	0/1338	0.79	3/1810 (0.2%)
28	HH	0.29	0/1338	0.79	3/1810 (0.2%)
28	JH	0.29	0/1338	0.80	3/1810 (0.2%)
29	BI	0.36	0/405	0.96	3/545 (0.6%)
29	DI	0.35	0/405	0.97	3/545 (0.6%)
29	FI	0.35	0/405	0.97	3/545 (0.6%)
29	HI	0.35	0/405	0.97	3/545 (0.6%)
29	JI	0.36	0/405	0.97	3/545 (0.6%)
30	BJ	0.31	0/1058	0.88	2/1433 (0.1%)
30	DJ	0.31	0/1058	0.88	2/1433 (0.1%)
30	FJ	0.31	0/1058	0.88	2/1433 (0.1%)
30	HJ	0.31	0/1058	0.88	2/1433 (0.1%)
30	JJ	0.31	0/1058	0.88	2/1433 (0.1%)
31	BK	0.32	0/1146	0.87	3/1549 (0.2%)
31	DK	0.32	0/1146	0.87	3/1549 (0.2%)
31	FK	0.32	0/1146	0.87	3/1549 (0.2%)
31	HK	0.32	0/1146	0.87	3/1549 (0.2%)
31	JK	0.32	0/1146	0.87	3/1549 (0.2%)
32	BL	0.28	0/991	0.76	1/1331 (0.1%)
32	DL	0.28	0/991	0.76	1/1331 (0.1%)
32	FL	0.28	0/991	0.76	1/1331 (0.1%)
32	HL	0.28	0/991	0.76	1/1331 (0.1%)
32	JL	0.28	0/991	0.76	1/1331 (0.1%)
33	BM	0.32	0/1082	0.82	1/1448 (0.1%)
33	DM	0.32	0/1082	0.82	1/1448 (0.1%)
33	FM	0.32	0/1082	0.82	1/1448 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	HM	0.32	0/1082	0.82	1/1448 (0.1%)
33	JM	0.32	0/1082	0.82	1/1448 (0.1%)
34	BN	0.36	0/1008	1.07	4/1346 (0.3%)
34	DN	0.36	0/1008	1.07	4/1346 (0.3%)
34	FN	0.36	0/1008	1.07	4/1346 (0.3%)
34	HN	0.36	0/1008	1.07	4/1346 (0.3%)
34	JN	0.36	0/1008	1.07	4/1346 (0.3%)
35	BO	0.28	0/894	0.79	0/1198
35	DO	0.28	0/894	0.79	0/1198
35	FO	0.27	0/894	0.79	0/1198
35	HO	0.27	0/894	0.79	0/1198
35	JO	0.28	0/894	0.79	0/1198
36	BP	0.29	0/841	0.70	0/1124
36	DP	0.28	0/841	0.70	0/1124
36	FP	0.28	0/841	0.70	0/1124
36	HP	0.28	0/841	0.70	0/1124
36	JP	0.28	0/841	0.70	0/1124
37	BQ	0.32	0/1021	0.90	3/1363 (0.2%)
37	DQ	0.32	0/1021	0.90	3/1363 (0.2%)
37	FQ	0.32	0/1021	0.90	3/1363 (0.2%)
37	HQ	0.32	0/1021	0.90	3/1363 (0.2%)
37	JQ	0.33	0/1021	0.90	3/1363 (0.2%)
38	BR	0.34	0/994	0.82	0/1323
38	DR	0.33	0/994	0.82	0/1323
38	FR	0.33	0/994	0.82	0/1323
38	HR	0.33	0/994	0.82	0/1323
38	JR	0.33	0/994	0.82	0/1323
39	BS	0.36	0/797	0.96	3/1061 (0.3%)
39	DS	0.35	0/797	0.96	3/1061 (0.3%)
39	FS	0.36	0/797	0.96	3/1061 (0.3%)
39	HS	0.36	0/797	0.96	3/1061 (0.3%)
39	JS	0.35	0/797	0.96	3/1061 (0.3%)
40	BT	0.31	0/1052	0.93	4/1407 (0.3%)
40	DT	0.31	0/1052	0.93	4/1407 (0.3%)
40	FT	0.31	0/1052	0.93	4/1407 (0.3%)
40	HT	0.31	0/1052	0.93	4/1407 (0.3%)
40	JT	0.31	0/1052	0.93	4/1407 (0.3%)
41	BU	0.33	0/738	0.87	2/988 (0.2%)
41	DU	0.32	0/738	0.87	2/988 (0.2%)
41	FU	0.33	0/738	0.87	2/988 (0.2%)
41	HU	0.33	0/738	0.87	2/988 (0.2%)
41	JU	0.33	0/738	0.87	2/988 (0.2%)
42	BV	0.28	0/863	0.92	1/1158 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
42	DV	0.28	0/863	0.92	1/1158 (0.1%)
42	FV	0.29	0/863	0.92	1/1158 (0.1%)
42	HV	0.29	0/863	0.92	1/1158 (0.1%)
42	JV	0.29	0/863	0.92	1/1158 (0.1%)
43	BW	0.43	1/1351 (0.1%)	1.39	10/1833 (0.5%)
43	DW	0.32	0/1350	0.89	7/1830 (0.4%)
43	FW	0.33	0/1350	0.89	7/1830 (0.4%)
43	HW	0.32	0/1350	0.89	7/1830 (0.4%)
43	JW	0.32	0/1350	0.89	7/1830 (0.4%)
44	BX	0.35	0/650	1.09	5/860 (0.6%)
44	DX	0.36	0/650	1.09	5/860 (0.6%)
44	FX	0.36	0/650	1.09	5/860 (0.6%)
44	HX	0.36	0/650	1.08	5/860 (0.6%)
44	JX	0.36	0/650	1.09	5/860 (0.6%)
45	BY	0.32	0/530	1.08	5/704 (0.7%)
45	DY	0.32	0/530	1.08	5/704 (0.7%)
45	FY	0.32	0/530	1.08	5/704 (0.7%)
45	HY	0.32	0/530	1.08	5/704 (0.7%)
45	JY	0.32	0/530	1.08	5/704 (0.7%)
46	BZ	0.27	0/426	0.70	0/568
46	DZ	0.27	0/426	0.71	0/568
46	FZ	0.27	0/426	0.70	0/568
46	HZ	0.27	0/426	0.70	0/568
46	JZ	0.27	0/426	0.71	0/568
47	B1	0.40	0/620	0.87	2/831 (0.2%)
47	D1	0.40	0/620	0.87	2/831 (0.2%)
47	F1	0.40	0/620	0.87	1/831 (0.1%)
47	H1	0.40	0/620	0.88	2/831 (0.2%)
47	J1	0.40	0/620	0.87	1/831 (0.1%)
48	B2	0.33	0/470	1.37	5/629 (0.8%)
48	D2	0.33	0/470	1.37	6/629 (1.0%)
48	F2	0.33	0/470	1.37	5/629 (0.8%)
48	H2	0.33	0/470	1.37	5/629 (0.8%)
48	J2	0.33	0/470	1.37	6/629 (1.0%)
49	B3	0.45	0/439	0.89	0/583
49	D3	0.45	0/439	0.90	0/583
49	F3	0.45	0/439	0.89	0/583
49	H3	0.44	0/439	0.89	0/583
49	J3	0.45	0/439	0.89	0/583
50	B4	0.30	0/388	0.82	0/509
50	D4	0.30	0/388	0.82	0/509
50	F4	0.30	0/388	0.82	0/509
50	H4	0.30	0/388	0.82	0/509

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
50	J4	0.30	0/388	0.82	0/509
51	B5	0.32	0/503	0.81	2/657 (0.3%)
51	D5	0.32	0/503	0.81	2/657 (0.3%)
51	F5	0.32	0/503	0.81	2/657 (0.3%)
51	H5	0.33	0/503	0.81	2/657 (0.3%)
51	J5	0.32	0/503	0.82	2/657 (0.3%)
52	B6	0.28	0/286	0.76	0/375
52	D6	0.27	0/286	0.76	0/375
52	F6	0.27	0/286	0.76	0/375
52	H6	0.28	0/286	0.76	0/375
52	J6	0.28	0/286	0.76	0/375
53	B7	0.49	3/1740 (0.2%)	0.76	11/2333 (0.5%)
53	D7	0.49	3/1740 (0.2%)	0.76	11/2333 (0.5%)
53	F7	0.49	3/1740 (0.2%)	0.76	11/2333 (0.5%)
53	H7	0.49	3/1740 (0.2%)	0.76	11/2333 (0.5%)
53	J7	0.49	3/1740 (0.2%)	0.76	11/2333 (0.5%)
All	All	0.61	315/778750 (0.0%)	0.83	1213/1161574 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	5
1	CA	0	5
1	EA	0	5
1	GA	0	5
1	IA	0	6
12	AL	0	1
12	EL	0	1
13	AM	0	1
13	GM	0	1
22	BB	0	21
22	DB	0	21
22	FB	0	21
22	HB	0	21
22	JB	0	21
24	BD	0	1
24	DD	0	1
24	FD	0	1
24	HD	0	1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	#Chirality outliers	#Planarity outliers
24	JD	0	1
27	BG	0	1
27	DG	0	1
27	FG	0	1
27	HG	0	1
27	JG	0	1
43	BW	0	1
All	All	0	146

The worst 5 of 315 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	BB	1888	C	O3'-P	-87.06	0.56	1.61
22	DB	1411	C	O3'-P	-62.45	0.86	1.61
22	FB	1047	G	O3'-P	-62.19	0.86	1.61
22	DB	1437	A	O3'-P	-58.70	0.90	1.61
22	FB	1586	A	O3'-P	-55.84	0.94	1.61

The worst 5 of 1213 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	DB	1888	C	P-O3'-C3'	-81.68	21.69	119.70
22	HB	910	U	P-O3'-C3'	-72.53	32.66	119.70
22	BB	1888	C	P-O3'-C3'	-66.03	40.47	119.70
22	FB	3197	U	P-O3'-C3'	-60.64	46.93	119.70
22	FB	1411	C	O3'-P-O5'	-53.08	3.15	104.00

There are no chirality outliers.

5 of 146 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	187	G	Sidechain
1	AA	188	C	Sidechain
1	AA	190	A	Sidechain
1	AA	197	A	Sidechain
1	AA	916	G	Sidechain

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32799	0	16508	3508	4
1	CA	32799	0	16515	3468	3
1	EA	32799	0	16515	3290	2
1	GA	32799	0	16500	3234	3
1	IA	32799	0	16508	3429	10
2	AB	1901	0	1950	183	0
2	CB	1901	0	1951	212	0
2	EB	1901	0	1948	269	0
2	GB	1901	0	1951	188	0
2	IB	1901	0	1951	207	0
3	AC	1613	0	1677	235	0
3	CC	1613	0	1677	271	0
3	EC	1613	0	1674	311	0
3	GC	1613	0	1676	221	0
3	IC	1613	0	1676	319	0
4	AD	1703	0	1765	340	2
4	CD	1703	0	1765	475	24
4	ED	1703	0	1762	358	12
4	GD	1703	0	1767	242	1
4	ID	1703	0	1766	225	2
5	AE	1147	0	1195	303	0
5	CE	1147	0	1198	360	0
5	EE	1147	0	1205	202	0
5	GE	1147	0	1199	236	0
5	IE	1147	0	1202	169	0
6	AF	843	0	857	106	2
6	CF	843	0	857	123	12
6	EF	843	0	857	127	11
6	GF	843	0	857	99	1
6	IF	843	0	857	140	2
7	AG	1257	0	1284	306	0
7	CG	1257	0	1292	310	0
7	EG	1257	0	1296	252	1
7	GG	1257	0	1294	306	21
7	IG	1257	0	1290	237	10
8	AH	1116	0	1175	239	0
8	CH	1116	0	1169	296	0
8	EH	1116	0	1166	369	0
8	GH	1116	0	1176	198	0
8	IH	1116	0	1168	368	0
9	AI	1011	0	1036	313	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	CI	1011	0	1039	268	0
9	EI	1011	0	1017	278	0
9	GI	1011	0	1038	262	0
9	II	1011	0	1031	331	1
10	AJ	795	0	837	303	0
10	CJ	795	0	839	192	0
10	EJ	795	0	831	188	1
10	GJ	795	0	835	260	21
10	IJ	795	0	838	211	11
11	AK	885	0	904	112	0
11	CK	885	0	903	118	12
11	EK	885	0	904	163	1
11	GK	885	0	899	174	0
11	IK	885	0	900	239	0
12	AL	971	0	1046	198	0
12	CL	971	0	1041	188	0
12	EL	971	0	1049	248	3
12	GL	971	0	1044	190	0
12	IL	971	0	1052	198	21
13	AM	997	0	1052	373	0
13	CM	997	0	1047	387	0
13	EM	997	0	1061	198	0
13	GM	997	0	1051	335	0
13	IM	997	0	1057	274	0
14	AN	492	0	531	320	0
14	CN	492	0	532	190	0
14	EN	492	0	532	207	0
14	GN	492	0	533	224	0
14	IN	492	0	532	159	0
15	AO	734	0	771	244	0
15	CO	734	0	767	148	0
15	EO	734	0	769	110	0
15	GO	734	0	770	179	0
15	IO	734	0	768	153	0
16	AP	701	0	718	117	0
16	CP	701	0	719	125	0
16	EP	701	0	712	184	0
16	GP	701	0	716	107	0
16	IP	701	0	713	178	0
17	AQ	857	0	917	348	0
17	CQ	857	0	916	300	0
17	EQ	857	0	920	289	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	GQ	857	0	916	320	0
17	IQ	857	0	923	252	0
18	AR	597	0	667	114	0
18	CR	597	0	666	123	0
18	ER	597	0	668	96	0
18	GR	597	0	666	155	0
18	IR	597	0	668	126	0
19	AS	648	0	673	215	0
19	CS	648	0	673	177	0
19	ES	648	0	671	227	0
19	GS	648	0	673	168	0
19	IS	648	0	668	233	0
20	AT	762	0	856	194	0
20	CT	762	0	854	132	0
20	ET	762	0	848	142	0
20	GT	762	0	850	336	0
20	IT	762	0	848	154	0
21	Aa	719	0	735	0	0
21	Ca	719	0	734	0	0
21	Ea	719	0	737	0	0
21	Ga	719	0	738	0	0
21	Ia	719	0	735	0	0
22	BB	60635	0	30507	6789	5
22	DB	60635	0	30501	6512	4
22	FB	60635	0	30479	6851	6
22	HB	60635	0	30492	6628	2
22	JB	60635	0	30478	7310	31
23	BA	2519	0	1281	279	6
23	DA	2519	0	1279	352	3
23	FA	2519	0	1279	281	0
23	HA	2519	0	1283	137	4
23	JA	2519	0	1284	252	9
24	BD	2079	0	2144	622	0
24	DD	2079	0	2144	593	0
24	FD	2079	0	2152	466	0
24	HD	2079	0	2149	544	0
24	JD	2079	0	2146	636	0
25	BE	1540	0	1592	596	0
25	DE	1540	0	1579	737	0
25	FE	1540	0	1582	628	0
25	HE	1540	0	1597	338	0
25	JE	1540	0	1600	367	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	BF	1507	0	1521	251	0
26	DF	1507	0	1520	196	0
26	FF	1507	0	1523	253	0
26	HF	1507	0	1525	180	0
26	JF	1507	0	1518	322	0
27	BG	1410	0	1489	221	0
27	DG	1410	0	1485	267	0
27	FG	1410	0	1488	320	0
27	HG	1410	0	1487	187	0
27	JG	1410	0	1486	229	0
28	BH	1316	0	1362	246	0
28	DH	1316	0	1360	253	0
28	FH	1316	0	1361	210	0
28	HH	1316	0	1361	164	0
28	JH	1316	0	1361	212	0
29	BI	401	0	426	36	0
29	DI	401	0	424	78	0
29	FI	401	0	425	99	0
29	HI	401	0	426	48	1
29	JI	401	0	426	102	0
30	BJ	1039	0	1083	201	0
30	DJ	1039	0	1083	105	0
30	FJ	1039	0	1083	103	0
30	HJ	1039	0	1083	151	0
30	JJ	1039	0	1080	160	0
31	BK	1122	0	1141	432	0
31	DK	1122	0	1132	390	0
31	FK	1122	0	1146	312	0
31	HK	1122	0	1143	329	0
31	JK	1122	0	1153	200	0
32	BL	981	0	1020	247	0
32	DL	981	0	1020	313	0
32	FL	981	0	1017	246	0
32	HL	981	0	1018	276	0
32	JL	981	0	1019	179	0
33	BM	1068	0	1098	308	0
33	DM	1068	0	1099	305	0
33	FM	1068	0	1100	290	0
33	HM	1068	0	1103	358	0
33	JM	1068	0	1091	414	0
34	BN	986	0	1010	489	0
34	DN	986	0	1006	542	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	FN	986	0	1006	381	0
34	HN	986	0	1011	371	0
34	JN	986	0	1012	300	0
35	BO	886	0	939	236	0
35	DO	886	0	939	252	0
35	FO	886	0	934	286	0
35	HO	886	0	936	259	0
35	JO	886	0	936	247	0
36	BP	834	0	874	71	0
36	DP	834	0	874	147	0
36	FP	834	0	863	177	0
36	HP	834	0	872	114	0
36	JP	834	0	868	170	0
37	BQ	1008	0	1048	323	0
37	DQ	1008	0	1050	269	0
37	FQ	1008	0	1048	212	0
37	HQ	1008	0	1050	276	0
37	JQ	1008	0	1045	336	0
38	BR	978	0	1018	183	0
38	DR	978	0	1015	377	0
38	FR	978	0	1011	513	0
38	HR	978	0	1009	306	0
38	JR	978	0	999	354	0
39	BS	787	0	803	206	0
39	DS	787	0	804	257	0
39	FS	787	0	800	291	0
39	HS	787	0	804	152	0
39	JS	787	0	798	247	0
40	BT	1039	0	1111	284	0
40	DT	1039	0	1105	328	0
40	FT	1039	0	1107	323	0
40	HT	1039	0	1107	453	0
40	JT	1039	0	1110	312	0
41	BU	727	0	752	108	0
41	DU	727	0	749	117	0
41	FU	727	0	736	211	0
41	HU	727	0	751	157	0
41	JU	727	0	747	183	0
42	BV	852	0	909	121	0
42	DV	852	0	911	104	0
42	FV	852	0	908	201	0
42	HV	852	0	908	132	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	JV	852	0	905	292	0
43	BW	1328	0	1343	486	0
43	DW	1328	0	1338	594	0
43	FW	1328	0	1341	325	0
43	HW	1328	0	1350	306	0
43	JW	1328	0	1342	254	0
44	BX	642	0	664	280	0
44	DX	642	0	665	210	0
44	FX	642	0	658	257	0
44	HX	642	0	663	295	0
44	JX	642	0	661	246	0
45	BY	526	0	546	72	0
45	DY	526	0	543	49	0
45	FY	526	0	538	102	0
45	HY	526	0	535	211	0
45	JY	526	0	535	196	0
46	BZ	424	0	468	76	0
46	DZ	424	0	468	109	0
46	FZ	424	0	467	204	0
46	HZ	424	0	466	82	0
46	JZ	424	0	468	135	0
47	B1	604	0	594	201	0
47	D1	604	0	593	193	0
47	F1	604	0	592	177	0
47	H1	604	0	582	203	0
47	J1	604	0	592	232	0
48	B2	458	0	457	218	0
48	D2	458	0	461	188	0
48	F2	458	0	459	178	0
48	H2	458	0	456	286	0
48	J2	458	0	460	221	0
49	B3	432	0	456	53	0
49	D3	432	0	456	87	0
49	F3	432	0	453	181	0
49	H3	432	0	455	74	0
49	J3	432	0	452	154	0
50	B4	384	0	406	139	0
50	D4	384	0	403	166	0
50	F4	384	0	408	198	0
50	H4	384	0	409	115	0
50	J4	384	0	401	167	0
51	B5	496	0	547	162	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	D5	496	0	542	191	0
51	F5	496	0	542	251	0
51	H5	496	0	545	230	0
51	J5	496	0	536	298	0
52	B6	285	0	305	210	0
52	D6	285	0	313	119	0
52	F6	285	0	309	72	0
52	H6	285	0	310	88	0
52	J6	285	0	311	114	0
53	B7	1720	0	1842	221	6
53	D7	1720	0	1842	167	4
53	F7	1720	0	1847	223	9
53	H7	1720	0	1843	360	3
53	J7	1720	0	1826	472	0
All	All	717805	0	489246	75816	144

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 63.

The worst 5 of 75816 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)
34:DN:66:TYR:CE2	43:DW:118:HIS:CE1	1.77	1.72
22:HB:2733:A:C2	52:H6:15:LYS:HE2	1.22	1.72
22:BB:1437:A:H2'	22:BB:1438:G:C8	1.25	1.70
22:BB:1805:G:C2	24:BD:52:ARG:HD3	1.26	1.69
34:BN:66:TYR:CD1	43:BW:115:ILE:HG21	1.25	1.69

The worst 5 of 144 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:435:C:OP1	22:BB:3096:C:OP1[3_465]	0.46	1.74
12:IL:128:ALA:C	22:JB:3157:G:C4'[4_445]	0.52	1.68
7:GG:60:LYS:CD	10:GJ:90:LEU:CD1[3_465]	0.58	1.62
7:GG:60:LYS:CE	10:GJ:90:LEU:CG[3_465]	0.60	1.60
4:CD:173:TRP:N	6:CF:15:ASP:OD2[3_465]	0.63	1.57

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	
2	AB	232/234 (99%)	129 (56%)	74 (32%)	29 (12%)	0	8
2	CB	232/234 (99%)	128 (55%)	75 (32%)	29 (12%)	0	8
2	EB	232/234 (99%)	127 (55%)	76 (33%)	29 (12%)	0	8
2	GB	232/234 (99%)	129 (56%)	74 (32%)	29 (12%)	0	8
2	IB	232/234 (99%)	128 (55%)	75 (32%)	29 (12%)	0	8
3	AC	204/206 (99%)	125 (61%)	60 (29%)	19 (9%)	1	16
3	CC	204/206 (99%)	124 (61%)	61 (30%)	19 (9%)	1	16
3	EC	204/206 (99%)	125 (61%)	60 (29%)	19 (9%)	1	16
3	GC	204/206 (99%)	124 (61%)	61 (30%)	19 (9%)	1	16
3	IC	204/206 (99%)	124 (61%)	61 (30%)	19 (9%)	1	16
4	AD	206/208 (99%)	130 (63%)	56 (27%)	20 (10%)	1	14
4	CD	206/208 (99%)	129 (63%)	57 (28%)	20 (10%)	1	14
4	ED	206/208 (99%)	130 (63%)	56 (27%)	20 (10%)	1	14
4	GD	206/208 (99%)	128 (62%)	58 (28%)	20 (10%)	1	14
4	ID	206/208 (99%)	129 (63%)	57 (28%)	20 (10%)	1	14
5	AE	148/150 (99%)	93 (63%)	43 (29%)	12 (8%)	1	19
5	CE	148/150 (99%)	91 (62%)	45 (30%)	12 (8%)	1	19
5	EE	148/150 (99%)	92 (62%)	44 (30%)	12 (8%)	1	19
5	GE	148/150 (99%)	92 (62%)	44 (30%)	12 (8%)	1	19
5	IE	148/150 (99%)	92 (62%)	44 (30%)	12 (8%)	1	19
6	AF	99/101 (98%)	67 (68%)	25 (25%)	7 (7%)	1	22
6	CF	99/101 (98%)	67 (68%)	25 (25%)	7 (7%)	1	22
6	EF	99/101 (98%)	67 (68%)	25 (25%)	7 (7%)	1	22
6	GF	99/101 (98%)	67 (68%)	25 (25%)	7 (7%)	1	22
6	IF	99/101 (98%)	67 (68%)	25 (25%)	7 (7%)	1	22

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	AG	153/155 (99%)	94 (61%)	47 (31%)	12 (8%)	1	20
7	CG	153/155 (99%)	94 (61%)	47 (31%)	12 (8%)	1	20
7	EG	153/155 (99%)	93 (61%)	48 (31%)	12 (8%)	1	20
7	GG	153/155 (99%)	94 (61%)	47 (31%)	12 (8%)	1	20
7	IG	153/155 (99%)	94 (61%)	47 (31%)	12 (8%)	1	20
8	AH	136/138 (99%)	83 (61%)	38 (28%)	15 (11%)	0	11
8	CH	136/138 (99%)	83 (61%)	37 (27%)	16 (12%)	0	9
8	EH	136/138 (99%)	83 (61%)	37 (27%)	16 (12%)	0	9
8	GH	136/138 (99%)	83 (61%)	37 (27%)	16 (12%)	0	9
8	IH	136/138 (99%)	83 (61%)	37 (27%)	16 (12%)	0	9
9	AI	125/127 (98%)	68 (54%)	43 (34%)	14 (11%)	0	11
9	CI	125/127 (98%)	68 (54%)	43 (34%)	14 (11%)	0	11
9	EI	125/127 (98%)	68 (54%)	43 (34%)	14 (11%)	0	11
9	GI	125/127 (98%)	68 (54%)	43 (34%)	14 (11%)	0	11
9	II	125/127 (98%)	68 (54%)	43 (34%)	14 (11%)	0	11
10	AJ	96/98 (98%)	52 (54%)	22 (23%)	22 (23%)	0	2
10	CJ	96/98 (98%)	53 (55%)	21 (22%)	22 (23%)	0	2
10	EJ	96/98 (98%)	52 (54%)	22 (23%)	22 (23%)	0	2
10	GJ	96/98 (98%)	52 (54%)	22 (23%)	22 (23%)	0	2
10	IJ	96/98 (98%)	52 (54%)	22 (23%)	22 (23%)	0	2
11	AK	117/119 (98%)	72 (62%)	32 (27%)	13 (11%)	0	11
11	CK	117/119 (98%)	74 (63%)	30 (26%)	13 (11%)	0	11
11	EK	117/119 (98%)	73 (62%)	31 (26%)	13 (11%)	0	11
11	GK	117/119 (98%)	73 (62%)	31 (26%)	13 (11%)	0	11
11	IK	117/119 (98%)	73 (62%)	31 (26%)	13 (11%)	0	11
12	AL	118/124 (95%)	77 (65%)	34 (29%)	7 (6%)	2	27
12	CL	116/124 (94%)	76 (66%)	32 (28%)	8 (7%)	1	23
12	EL	118/124 (95%)	76 (64%)	34 (29%)	8 (7%)	1	23
12	GL	116/124 (94%)	77 (66%)	31 (27%)	8 (7%)	1	23
12	IL	118/124 (95%)	78 (66%)	33 (28%)	7 (6%)	2	27
13	AM	121/125 (97%)	77 (64%)	32 (26%)	12 (10%)	1	14

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	CM	119/125 (95%)	77 (65%)	32 (27%)	10 (8%)	1	18
13	EM	119/125 (95%)	77 (65%)	32 (27%)	10 (8%)	1	18
13	GM	121/125 (97%)	77 (64%)	32 (26%)	12 (10%)	1	14
13	IM	119/125 (95%)	78 (66%)	30 (25%)	11 (9%)	1	17
14	AN	58/60 (97%)	22 (38%)	27 (47%)	9 (16%)	0	5
14	CN	58/60 (97%)	23 (40%)	26 (45%)	9 (16%)	0	5
14	EN	58/60 (97%)	22 (38%)	27 (47%)	9 (16%)	0	5
14	GN	58/60 (97%)	22 (38%)	27 (47%)	9 (16%)	0	5
14	IN	58/60 (97%)	22 (38%)	27 (47%)	9 (16%)	0	5
15	AO	86/88 (98%)	59 (69%)	19 (22%)	8 (9%)	1	16
15	CO	86/88 (98%)	59 (69%)	20 (23%)	7 (8%)	1	19
15	EO	86/88 (98%)	59 (69%)	19 (22%)	8 (9%)	1	16
15	GO	86/88 (98%)	59 (69%)	20 (23%)	7 (8%)	1	19
15	IO	86/88 (98%)	59 (69%)	19 (22%)	8 (9%)	1	16
16	AP	81/83 (98%)	48 (59%)	29 (36%)	4 (5%)	3	31
16	CP	81/83 (98%)	48 (59%)	29 (36%)	4 (5%)	3	31
16	EP	81/83 (98%)	48 (59%)	29 (36%)	4 (5%)	3	31
16	GP	81/83 (98%)	48 (59%)	29 (36%)	4 (5%)	3	31
16	IP	81/83 (98%)	49 (60%)	28 (35%)	4 (5%)	3	31
17	AQ	102/104 (98%)	53 (52%)	34 (33%)	15 (15%)	0	6
17	CQ	102/104 (98%)	53 (52%)	34 (33%)	15 (15%)	0	6
17	EQ	102/104 (98%)	53 (52%)	34 (33%)	15 (15%)	0	6
17	GQ	102/104 (98%)	53 (52%)	34 (33%)	15 (15%)	0	6
17	IQ	102/104 (98%)	53 (52%)	34 (33%)	15 (15%)	0	6
18	AR	71/73 (97%)	43 (61%)	20 (28%)	8 (11%)	0	10
18	CR	71/73 (97%)	43 (61%)	20 (28%)	8 (11%)	0	10
18	ER	71/73 (97%)	43 (61%)	20 (28%)	8 (11%)	0	10
18	GR	71/73 (97%)	43 (61%)	20 (28%)	8 (11%)	0	10
18	IR	71/73 (97%)	43 (61%)	20 (28%)	8 (11%)	0	10
19	AS	78/80 (98%)	48 (62%)	22 (28%)	8 (10%)	1	12
19	CS	78/80 (98%)	49 (63%)	21 (27%)	8 (10%)	1	12

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	ES	78/80 (98%)	48 (62%)	22 (28%)	8 (10%)	1	12
19	GS	78/80 (98%)	49 (63%)	20 (26%)	9 (12%)	0	9
19	IS	78/80 (98%)	48 (62%)	21 (27%)	9 (12%)	0	9
20	AT	97/99 (98%)	65 (67%)	20 (21%)	12 (12%)	0	8
20	CT	97/99 (98%)	64 (66%)	21 (22%)	12 (12%)	0	8
20	ET	97/99 (98%)	64 (66%)	21 (22%)	12 (12%)	0	8
20	GT	97/99 (98%)	64 (66%)	21 (22%)	12 (12%)	0	8
20	IT	97/99 (98%)	64 (66%)	21 (22%)	12 (12%)	0	8
21	Aa	88/90 (98%)	77 (88%)	10 (11%)	1 (1%)	17	63
21	Ca	88/90 (98%)	77 (88%)	10 (11%)	1 (1%)	17	63
21	Ea	88/90 (98%)	77 (88%)	10 (11%)	1 (1%)	17	63
21	Ga	88/90 (98%)	77 (88%)	10 (11%)	1 (1%)	17	63
21	Ia	88/90 (98%)	77 (88%)	10 (11%)	1 (1%)	17	63
24	BD	268/270 (99%)	96 (36%)	93 (35%)	79 (30%)	0	0
24	DD	268/270 (99%)	98 (37%)	92 (34%)	78 (29%)	0	0
24	FD	268/270 (99%)	97 (36%)	93 (35%)	78 (29%)	0	0
24	HD	268/270 (99%)	97 (36%)	93 (35%)	78 (29%)	0	0
24	JD	268/270 (99%)	96 (36%)	95 (35%)	77 (29%)	0	0
25	BE	203/205 (99%)	85 (42%)	74 (36%)	44 (22%)	0	2
25	DE	203/205 (99%)	85 (42%)	74 (36%)	44 (22%)	0	2
25	FE	203/205 (99%)	85 (42%)	73 (36%)	45 (22%)	0	2
25	HE	203/205 (99%)	85 (42%)	73 (36%)	45 (22%)	0	2
25	JE	203/205 (99%)	86 (42%)	73 (36%)	44 (22%)	0	2
26	BF	195/198 (98%)	90 (46%)	59 (30%)	46 (24%)	0	2
26	DF	195/198 (98%)	90 (46%)	59 (30%)	46 (24%)	0	2
26	FF	195/198 (98%)	90 (46%)	59 (30%)	46 (24%)	0	2
26	HF	195/198 (98%)	90 (46%)	59 (30%)	46 (24%)	0	2
26	JF	195/198 (98%)	90 (46%)	59 (30%)	46 (24%)	0	2
27	BG	176/178 (99%)	75 (43%)	59 (34%)	42 (24%)	0	2
27	DG	176/178 (99%)	75 (43%)	59 (34%)	42 (24%)	0	2
27	FG	176/178 (99%)	74 (42%)	60 (34%)	42 (24%)	0	2

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	HG	176/178 (99%)	75 (43%)	59 (34%)	42 (24%)	0	2
27	JG	176/178 (99%)	75 (43%)	58 (33%)	43 (24%)	0	2
28	BH	175/177 (99%)	84 (48%)	55 (31%)	36 (21%)	0	3
28	DH	175/177 (99%)	83 (47%)	56 (32%)	36 (21%)	0	3
28	FH	175/177 (99%)	83 (47%)	56 (32%)	36 (21%)	0	3
28	HH	175/177 (99%)	84 (48%)	55 (31%)	36 (21%)	0	3
28	JH	175/177 (99%)	83 (47%)	56 (32%)	36 (21%)	0	3
29	BI	50/52 (96%)	16 (32%)	19 (38%)	15 (30%)	0	0
29	DI	50/52 (96%)	16 (32%)	19 (38%)	15 (30%)	0	0
29	FI	50/52 (96%)	16 (32%)	19 (38%)	15 (30%)	0	0
29	HI	50/52 (96%)	16 (32%)	19 (38%)	15 (30%)	0	0
29	JI	50/52 (96%)	16 (32%)	19 (38%)	15 (30%)	0	0
30	BJ	141/143 (99%)	56 (40%)	47 (33%)	38 (27%)	0	0
30	DJ	141/143 (99%)	56 (40%)	47 (33%)	38 (27%)	0	0
30	FJ	141/143 (99%)	56 (40%)	47 (33%)	38 (27%)	0	0
30	HJ	141/143 (99%)	56 (40%)	47 (33%)	38 (27%)	0	0
30	JJ	141/143 (99%)	56 (40%)	47 (33%)	38 (27%)	0	0
31	BK	141/143 (99%)	55 (39%)	58 (41%)	28 (20%)	0	3
31	DK	141/143 (99%)	55 (39%)	58 (41%)	28 (20%)	0	3
31	FK	141/143 (99%)	55 (39%)	58 (41%)	28 (20%)	0	3
31	HK	141/143 (99%)	55 (39%)	58 (41%)	28 (20%)	0	3
31	JK	141/143 (99%)	55 (39%)	58 (41%)	28 (20%)	0	3
32	BL	130/132 (98%)	56 (43%)	37 (28%)	37 (28%)	0	0
32	DL	130/132 (98%)	56 (43%)	37 (28%)	37 (28%)	0	0
32	FL	130/132 (98%)	56 (43%)	37 (28%)	37 (28%)	0	0
32	HL	130/132 (98%)	56 (43%)	37 (28%)	37 (28%)	0	0
32	JL	130/132 (98%)	56 (43%)	37 (28%)	37 (28%)	0	0
33	BM	139/141 (99%)	60 (43%)	43 (31%)	36 (26%)	0	1
33	DM	139/141 (99%)	60 (43%)	43 (31%)	36 (26%)	0	1
33	FM	139/141 (99%)	60 (43%)	43 (31%)	36 (26%)	0	1
33	HM	139/141 (99%)	60 (43%)	43 (31%)	36 (26%)	0	1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	JM	139/141 (99%)	60 (43%)	43 (31%)	36 (26%)	0	1
34	BN	122/124 (98%)	60 (49%)	35 (29%)	27 (22%)	0	2
34	DN	122/124 (98%)	61 (50%)	34 (28%)	27 (22%)	0	2
34	FN	122/124 (98%)	61 (50%)	34 (28%)	27 (22%)	0	2
34	HN	122/124 (98%)	61 (50%)	34 (28%)	27 (22%)	0	2
34	JN	122/124 (98%)	61 (50%)	34 (28%)	27 (22%)	0	2
35	BO	112/114 (98%)	52 (46%)	38 (34%)	22 (20%)	0	3
35	DO	112/114 (98%)	52 (46%)	38 (34%)	22 (20%)	0	3
35	FO	112/114 (98%)	52 (46%)	37 (33%)	23 (20%)	0	3
35	HO	112/114 (98%)	52 (46%)	38 (34%)	22 (20%)	0	3
35	JO	112/114 (98%)	51 (46%)	39 (35%)	22 (20%)	0	3
36	BP	109/111 (98%)	52 (48%)	37 (34%)	20 (18%)	0	4
36	DP	109/111 (98%)	52 (48%)	37 (34%)	20 (18%)	0	4
36	FP	109/111 (98%)	52 (48%)	37 (34%)	20 (18%)	0	4
36	HP	109/111 (98%)	52 (48%)	37 (34%)	20 (18%)	0	4
36	JP	109/111 (98%)	52 (48%)	37 (34%)	20 (18%)	0	4
37	BQ	123/125 (98%)	50 (41%)	47 (38%)	26 (21%)	0	3
37	DQ	123/125 (98%)	50 (41%)	48 (39%)	25 (20%)	0	3
37	FQ	123/125 (98%)	50 (41%)	47 (38%)	26 (21%)	0	3
37	HQ	123/125 (98%)	50 (41%)	48 (39%)	25 (20%)	0	3
37	JQ	123/125 (98%)	50 (41%)	47 (38%)	26 (21%)	0	3
38	BR	115/117 (98%)	55 (48%)	41 (36%)	19 (16%)	0	5
38	DR	115/117 (98%)	55 (48%)	41 (36%)	19 (16%)	0	5
38	FR	115/117 (98%)	55 (48%)	41 (36%)	19 (16%)	0	5
38	HR	115/117 (98%)	55 (48%)	40 (35%)	20 (17%)	0	4
38	JR	115/117 (98%)	55 (48%)	41 (36%)	19 (16%)	0	5
39	BS	98/100 (98%)	39 (40%)	37 (38%)	22 (22%)	0	2
39	DS	98/100 (98%)	38 (39%)	38 (39%)	22 (22%)	0	2
39	FS	98/100 (98%)	39 (40%)	37 (38%)	22 (22%)	0	2
39	HS	98/100 (98%)	39 (40%)	37 (38%)	22 (22%)	0	2
39	JS	98/100 (98%)	39 (40%)	37 (38%)	22 (22%)	0	2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	BT	128/130 (98%)	52 (41%)	51 (40%)	25 (20%)	0	3
40	DT	128/130 (98%)	52 (41%)	51 (40%)	25 (20%)	0	3
40	FT	128/130 (98%)	52 (41%)	51 (40%)	25 (20%)	0	3
40	HT	128/130 (98%)	52 (41%)	51 (40%)	25 (20%)	0	3
40	JT	128/130 (98%)	53 (41%)	50 (39%)	25 (20%)	0	3
41	BU	91/93 (98%)	29 (32%)	30 (33%)	32 (35%)	0	0
41	DU	91/93 (98%)	29 (32%)	30 (33%)	32 (35%)	0	0
41	FU	91/93 (98%)	28 (31%)	31 (34%)	32 (35%)	0	0
41	HU	91/93 (98%)	29 (32%)	30 (33%)	32 (35%)	0	0
41	JU	91/93 (98%)	28 (31%)	31 (34%)	32 (35%)	0	0
42	BV	111/113 (98%)	43 (39%)	35 (32%)	33 (30%)	0	0
42	DV	111/113 (98%)	43 (39%)	36 (32%)	32 (29%)	0	0
42	FV	111/113 (98%)	43 (39%)	36 (32%)	32 (29%)	0	0
42	HV	111/113 (98%)	43 (39%)	35 (32%)	33 (30%)	0	0
42	JV	111/113 (98%)	43 (39%)	36 (32%)	32 (29%)	0	0
43	BW	169/173 (98%)	45 (27%)	69 (41%)	55 (32%)	0	0
43	DW	168/173 (97%)	44 (26%)	70 (42%)	54 (32%)	0	0
43	FW	168/173 (97%)	44 (26%)	69 (41%)	55 (33%)	0	0
43	HW	168/173 (97%)	44 (26%)	70 (42%)	54 (32%)	0	0
43	JW	168/173 (97%)	44 (26%)	70 (42%)	54 (32%)	0	0
44	BX	84/86 (98%)	31 (37%)	29 (34%)	24 (29%)	0	0
44	DX	84/86 (98%)	31 (37%)	29 (34%)	24 (29%)	0	0
44	FX	84/86 (98%)	31 (37%)	29 (34%)	24 (29%)	0	0
44	HX	84/86 (98%)	31 (37%)	29 (34%)	24 (29%)	0	0
44	JX	84/86 (98%)	31 (37%)	29 (34%)	24 (29%)	0	0
45	BY	63/65 (97%)	35 (56%)	16 (25%)	12 (19%)	0	3
45	DY	63/65 (97%)	35 (56%)	16 (25%)	12 (19%)	0	3
45	FY	63/65 (97%)	35 (56%)	16 (25%)	12 (19%)	0	3
45	HY	63/65 (97%)	35 (56%)	16 (25%)	12 (19%)	0	3
45	JY	63/65 (97%)	35 (56%)	16 (25%)	12 (19%)	0	3
46	BZ	53/55 (96%)	25 (47%)	19 (36%)	9 (17%)	0	5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	DZ	53/55 (96%)	25 (47%)	19 (36%)	9 (17%)	0	5
46	FZ	53/55 (96%)	25 (47%)	19 (36%)	9 (17%)	0	5
46	HZ	53/55 (96%)	25 (47%)	19 (36%)	9 (17%)	0	5
46	JZ	53/55 (96%)	25 (47%)	19 (36%)	9 (17%)	0	5
47	B1	71/73 (97%)	26 (37%)	24 (34%)	21 (30%)	0	0
47	D1	71/73 (97%)	26 (37%)	24 (34%)	21 (30%)	0	0
47	F1	71/73 (97%)	26 (37%)	25 (35%)	20 (28%)	0	0
47	H1	71/73 (97%)	26 (37%)	24 (34%)	21 (30%)	0	0
47	J1	71/73 (97%)	26 (37%)	24 (34%)	21 (30%)	0	0
48	B2	56/58 (97%)	19 (34%)	23 (41%)	14 (25%)	0	2
48	D2	56/58 (97%)	19 (34%)	23 (41%)	14 (25%)	0	2
48	F2	56/58 (97%)	19 (34%)	23 (41%)	14 (25%)	0	2
48	H2	56/58 (97%)	19 (34%)	23 (41%)	14 (25%)	0	2
48	J2	56/58 (97%)	19 (34%)	23 (41%)	14 (25%)	0	2
49	B3	51/53 (96%)	13 (26%)	18 (35%)	20 (39%)	0	0
49	D3	51/53 (96%)	13 (26%)	18 (35%)	20 (39%)	0	0
49	F3	51/53 (96%)	13 (26%)	18 (35%)	20 (39%)	0	0
49	H3	51/53 (96%)	13 (26%)	18 (35%)	20 (39%)	0	0
49	J3	51/53 (96%)	13 (26%)	18 (35%)	20 (39%)	0	0
50	B4	44/46 (96%)	20 (46%)	15 (34%)	9 (20%)	0	3
50	D4	44/46 (96%)	20 (46%)	15 (34%)	9 (20%)	0	3
50	F4	44/46 (96%)	20 (46%)	15 (34%)	9 (20%)	0	3
50	H4	44/46 (96%)	20 (46%)	15 (34%)	9 (20%)	0	3
50	J4	44/46 (96%)	20 (46%)	15 (34%)	9 (20%)	0	3
51	B5	61/63 (97%)	26 (43%)	19 (31%)	16 (26%)	0	1
51	D5	61/63 (97%)	27 (44%)	19 (31%)	15 (25%)	0	2
51	F5	61/63 (97%)	26 (43%)	20 (33%)	15 (25%)	0	2
51	H5	61/63 (97%)	26 (43%)	20 (33%)	15 (25%)	0	2
51	J5	61/63 (97%)	26 (43%)	20 (33%)	15 (25%)	0	2
52	B6	33/35 (94%)	12 (36%)	10 (30%)	11 (33%)	0	0
52	D6	33/35 (94%)	12 (36%)	10 (30%)	11 (33%)	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	F6	33/35 (94%)	12 (36%)	10 (30%)	11 (33%)	0	0
52	H6	33/35 (94%)	12 (36%)	10 (30%)	11 (33%)	0	0
52	J6	33/35 (94%)	12 (36%)	10 (30%)	11 (33%)	0	0
53	B7	215/217 (99%)	112 (52%)	79 (37%)	24 (11%)	0	11
53	D7	215/217 (99%)	113 (53%)	78 (36%)	24 (11%)	0	11
53	F7	215/217 (99%)	114 (53%)	77 (36%)	24 (11%)	0	11
53	H7	215/217 (99%)	113 (53%)	78 (36%)	24 (11%)	0	11
53	J7	215/217 (99%)	112 (52%)	79 (37%)	24 (11%)	0	11
All	All	29701/30260 (98%)	14747 (50%)	9520 (32%)	5434 (18%)	0	4

5 of 5434 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	19	HIS
2	AB	24	TRP
2	AB	165	VAL
2	AB	195	ASP
3	AC	4	LYS

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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	
2	AB	202/202 (100%)	179 (89%)	23 (11%)	7	33
2	CB	202/202 (100%)	179 (89%)	23 (11%)	7	33
2	EB	202/202 (100%)	179 (89%)	23 (11%)	7	33
2	GB	202/202 (100%)	179 (89%)	23 (11%)	7	33
2	IB	202/202 (100%)	179 (89%)	23 (11%)	7	33
3	AC	160/160 (100%)	150 (94%)	10 (6%)	22	59
3	CC	160/160 (100%)	150 (94%)	10 (6%)	22	59
3	EC	160/160 (100%)	150 (94%)	10 (6%)	22	59

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	GC	160/160 (100%)	150 (94%)	10 (6%)	22	59
3	IC	160/160 (100%)	150 (94%)	10 (6%)	22	59
4	AD	180/180 (100%)	157 (87%)	23 (13%)	5	29
4	CD	180/180 (100%)	157 (87%)	23 (13%)	5	29
4	ED	180/180 (100%)	157 (87%)	23 (13%)	5	29
4	GD	180/180 (100%)	157 (87%)	23 (13%)	5	29
4	ID	180/180 (100%)	157 (87%)	23 (13%)	5	29
5	AE	115/115 (100%)	106 (92%)	9 (8%)	16	51
5	CE	115/115 (100%)	106 (92%)	9 (8%)	16	51
5	EE	115/115 (100%)	106 (92%)	9 (8%)	16	51
5	GE	115/115 (100%)	106 (92%)	9 (8%)	16	51
5	IE	115/115 (100%)	106 (92%)	9 (8%)	16	51
6	AF	90/90 (100%)	82 (91%)	8 (9%)	12	44
6	CF	90/90 (100%)	81 (90%)	9 (10%)	9	38
6	EF	90/90 (100%)	82 (91%)	8 (9%)	12	44
6	GF	90/90 (100%)	82 (91%)	8 (9%)	12	44
6	IF	90/90 (100%)	81 (90%)	9 (10%)	9	38
7	AG	126/126 (100%)	115 (91%)	11 (9%)	13	45
7	CG	126/126 (100%)	115 (91%)	11 (9%)	13	45
7	EG	126/126 (100%)	115 (91%)	11 (9%)	13	45
7	GG	126/126 (100%)	115 (91%)	11 (9%)	13	45
7	IG	126/126 (100%)	115 (91%)	11 (9%)	13	45
8	AH	119/119 (100%)	113 (95%)	6 (5%)	30	66
8	CH	119/119 (100%)	113 (95%)	6 (5%)	30	66
8	EH	119/119 (100%)	113 (95%)	6 (5%)	30	66
8	GH	119/119 (100%)	113 (95%)	6 (5%)	30	66
8	IH	119/119 (100%)	113 (95%)	6 (5%)	30	66
9	AI	98/98 (100%)	87 (89%)	11 (11%)	7	33
9	CI	98/98 (100%)	87 (89%)	11 (11%)	7	33
9	EI	98/98 (100%)	88 (90%)	10 (10%)	9	37
9	GI	98/98 (100%)	87 (89%)	11 (11%)	7	33

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	II	98/98 (100%)	87 (89%)	11 (11%)	7	33
10	AJ	88/88 (100%)	81 (92%)	7 (8%)	15	50
10	CJ	88/88 (100%)	81 (92%)	7 (8%)	15	50
10	EJ	88/88 (100%)	81 (92%)	7 (8%)	15	50
10	GJ	88/88 (100%)	81 (92%)	7 (8%)	15	50
10	IJ	88/88 (100%)	81 (92%)	7 (8%)	15	50
11	AK	90/90 (100%)	80 (89%)	10 (11%)	8	34
11	CK	90/90 (100%)	80 (89%)	10 (11%)	8	34
11	EK	90/90 (100%)	80 (89%)	10 (11%)	8	34
11	GK	90/90 (100%)	80 (89%)	10 (11%)	8	34
11	IK	90/90 (100%)	80 (89%)	10 (11%)	8	34
12	AL	104/104 (100%)	98 (94%)	6 (6%)	25	61
12	CL	104/104 (100%)	98 (94%)	6 (6%)	25	61
12	EL	104/104 (100%)	98 (94%)	6 (6%)	25	61
12	GL	104/104 (100%)	98 (94%)	6 (6%)	25	61
12	IL	104/104 (100%)	98 (94%)	6 (6%)	25	61
13	AM	100/100 (100%)	86 (86%)	14 (14%)	4	26
13	CM	100/100 (100%)	86 (86%)	14 (14%)	4	26
13	EM	100/100 (100%)	86 (86%)	14 (14%)	4	26
13	GM	100/100 (100%)	86 (86%)	14 (14%)	4	26
13	IM	100/100 (100%)	86 (86%)	14 (14%)	4	26
14	AN	49/49 (100%)	44 (90%)	5 (10%)	9	37
14	CN	49/49 (100%)	44 (90%)	5 (10%)	9	37
14	EN	49/49 (100%)	44 (90%)	5 (10%)	9	37
14	GN	49/49 (100%)	44 (90%)	5 (10%)	9	37
14	IN	49/49 (100%)	44 (90%)	5 (10%)	9	37
15	AO	79/79 (100%)	75 (95%)	4 (5%)	29	66
15	CO	79/79 (100%)	75 (95%)	4 (5%)	29	66
15	EO	79/79 (100%)	75 (95%)	4 (5%)	29	66
15	GO	79/79 (100%)	75 (95%)	4 (5%)	29	66
15	IO	79/79 (100%)	75 (95%)	4 (5%)	29	66

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	AP	72/72 (100%)	68 (94%)	4 (6%)	26	62
16	CP	72/72 (100%)	68 (94%)	4 (6%)	26	62
16	EP	72/72 (100%)	68 (94%)	4 (6%)	26	62
16	GP	72/72 (100%)	68 (94%)	4 (6%)	26	62
16	IP	72/72 (100%)	68 (94%)	4 (6%)	26	62
17	AQ	96/96 (100%)	88 (92%)	8 (8%)	14	49
17	CQ	96/96 (100%)	88 (92%)	8 (8%)	14	49
17	EQ	96/96 (100%)	88 (92%)	8 (8%)	14	49
17	GQ	96/96 (100%)	88 (92%)	8 (8%)	14	49
17	IQ	96/96 (100%)	88 (92%)	8 (8%)	14	49
18	AR	64/64 (100%)	57 (89%)	7 (11%)	8	35
18	CR	64/64 (100%)	57 (89%)	7 (11%)	8	35
18	ER	64/64 (100%)	57 (89%)	7 (11%)	8	35
18	GR	64/64 (100%)	57 (89%)	7 (11%)	8	35
18	IR	64/64 (100%)	57 (89%)	7 (11%)	8	35
19	AS	71/71 (100%)	62 (87%)	9 (13%)	5	29
19	CS	71/71 (100%)	62 (87%)	9 (13%)	5	29
19	ES	71/71 (100%)	62 (87%)	9 (13%)	5	29
19	GS	71/71 (100%)	62 (87%)	9 (13%)	5	29
19	IS	71/71 (100%)	62 (87%)	9 (13%)	5	29
20	AT	76/76 (100%)	73 (96%)	3 (4%)	39	72
20	CT	76/76 (100%)	73 (96%)	3 (4%)	39	72
20	ET	76/76 (100%)	73 (96%)	3 (4%)	39	72
20	GT	76/76 (100%)	73 (96%)	3 (4%)	39	72
20	IT	76/76 (100%)	73 (96%)	3 (4%)	39	72
21	Aa	80/80 (100%)	62 (78%)	18 (22%)	1	8
21	Ca	80/80 (100%)	62 (78%)	18 (22%)	1	8
21	Ea	80/80 (100%)	62 (78%)	18 (22%)	1	8
21	Ga	80/80 (100%)	62 (78%)	18 (22%)	1	8
21	Ia	80/80 (100%)	62 (78%)	18 (22%)	1	8
24	BD	212/212 (100%)	168 (79%)	44 (21%)	1	10

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	DD	212/212 (100%)	168 (79%)	44 (21%)	1	10
24	FD	212/212 (100%)	168 (79%)	44 (21%)	1	10
24	HD	212/212 (100%)	168 (79%)	44 (21%)	1	10
24	JD	212/212 (100%)	168 (79%)	44 (21%)	1	10
25	BE	155/155 (100%)	130 (84%)	25 (16%)	3	20
25	DE	155/155 (100%)	130 (84%)	25 (16%)	3	20
25	FE	155/155 (100%)	131 (84%)	24 (16%)	3	22
25	HE	155/155 (100%)	131 (84%)	24 (16%)	3	22
25	JE	155/155 (100%)	130 (84%)	25 (16%)	3	20
26	BF	157/158 (99%)	139 (88%)	18 (12%)	7	32
26	DF	157/158 (99%)	139 (88%)	18 (12%)	7	32
26	FF	157/158 (99%)	139 (88%)	18 (12%)	7	32
26	HF	157/158 (99%)	139 (88%)	18 (12%)	7	32
26	JF	157/158 (99%)	139 (88%)	18 (12%)	7	32
27	BG	154/154 (100%)	122 (79%)	32 (21%)	1	10
27	DG	154/154 (100%)	122 (79%)	32 (21%)	1	10
27	FG	154/154 (100%)	122 (79%)	32 (21%)	1	10
27	HG	154/154 (100%)	122 (79%)	32 (21%)	1	10
27	JG	154/154 (100%)	122 (79%)	32 (21%)	1	10
28	BH	137/137 (100%)	116 (85%)	21 (15%)	3	22
28	DH	137/137 (100%)	116 (85%)	21 (15%)	3	22
28	FH	137/137 (100%)	116 (85%)	21 (15%)	3	22
28	HH	137/137 (100%)	116 (85%)	21 (15%)	3	22
28	JH	137/137 (100%)	116 (85%)	21 (15%)	3	22
29	BI	44/44 (100%)	39 (89%)	5 (11%)	7	33
29	DI	44/44 (100%)	39 (89%)	5 (11%)	7	33
29	FI	44/44 (100%)	39 (89%)	5 (11%)	7	33
29	HI	44/44 (100%)	39 (89%)	5 (11%)	7	33
29	JI	44/44 (100%)	39 (89%)	5 (11%)	7	33
30	BJ	107/107 (100%)	95 (89%)	12 (11%)	7	33
30	DJ	107/107 (100%)	95 (89%)	12 (11%)	7	33

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	FJ	107/107 (100%)	95 (89%)	12 (11%)	7	33
30	HJ	107/107 (100%)	95 (89%)	12 (11%)	7	33
30	JJ	107/107 (100%)	95 (89%)	12 (11%)	7	33
31	BK	119/119 (100%)	102 (86%)	17 (14%)	4	25
31	DK	119/119 (100%)	102 (86%)	17 (14%)	4	25
31	FK	119/119 (100%)	102 (86%)	17 (14%)	4	25
31	HK	119/119 (100%)	102 (86%)	17 (14%)	4	25
31	JK	119/119 (100%)	102 (86%)	17 (14%)	4	25
32	BL	101/101 (100%)	88 (87%)	13 (13%)	5	28
32	DL	101/101 (100%)	88 (87%)	13 (13%)	5	28
32	FL	101/101 (100%)	88 (87%)	13 (13%)	5	28
32	HL	101/101 (100%)	88 (87%)	13 (13%)	5	28
32	JL	101/101 (100%)	88 (87%)	13 (13%)	5	28
33	BM	108/108 (100%)	88 (82%)	20 (18%)	2	14
33	DM	108/108 (100%)	88 (82%)	20 (18%)	2	14
33	FM	108/108 (100%)	88 (82%)	20 (18%)	2	14
33	HM	108/108 (100%)	88 (82%)	20 (18%)	2	14
33	JM	108/108 (100%)	88 (82%)	20 (18%)	2	14
34	BN	99/99 (100%)	75 (76%)	24 (24%)	1	6
34	DN	99/99 (100%)	75 (76%)	24 (24%)	1	6
34	FN	99/99 (100%)	75 (76%)	24 (24%)	1	6
34	HN	99/99 (100%)	75 (76%)	24 (24%)	1	6
34	JN	99/99 (100%)	75 (76%)	24 (24%)	1	6
35	BO	91/91 (100%)	78 (86%)	13 (14%)	4	25
35	DO	91/91 (100%)	78 (86%)	13 (14%)	4	25
35	FO	91/91 (100%)	78 (86%)	13 (14%)	4	25
35	HO	91/91 (100%)	78 (86%)	13 (14%)	4	25
35	JO	91/91 (100%)	78 (86%)	13 (14%)	4	25
36	BP	80/80 (100%)	71 (89%)	9 (11%)	7	33
36	DP	80/80 (100%)	71 (89%)	9 (11%)	7	33
36	FP	80/80 (100%)	71 (89%)	9 (11%)	7	33

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	HP	80/80 (100%)	71 (89%)	9 (11%)	7	33
36	JP	80/80 (100%)	71 (89%)	9 (11%)	7	33
37	BQ	108/108 (100%)	92 (85%)	16 (15%)	4	24
37	DQ	108/108 (100%)	92 (85%)	16 (15%)	4	24
37	FQ	108/108 (100%)	92 (85%)	16 (15%)	4	24
37	HQ	108/108 (100%)	92 (85%)	16 (15%)	4	24
37	JQ	108/108 (100%)	92 (85%)	16 (15%)	4	24
38	BR	96/96 (100%)	82 (85%)	14 (15%)	4	24
38	DR	96/96 (100%)	82 (85%)	14 (15%)	4	24
38	FR	96/96 (100%)	82 (85%)	14 (15%)	4	24
38	HR	96/96 (100%)	82 (85%)	14 (15%)	4	24
38	JR	96/96 (100%)	82 (85%)	14 (15%)	4	24
39	BS	79/79 (100%)	70 (89%)	9 (11%)	7	33
39	DS	79/79 (100%)	70 (89%)	9 (11%)	7	33
39	FS	79/79 (100%)	70 (89%)	9 (11%)	7	33
39	HS	79/79 (100%)	70 (89%)	9 (11%)	7	33
39	JS	79/79 (100%)	70 (89%)	9 (11%)	7	33
40	BT	112/112 (100%)	99 (88%)	13 (12%)	7	32
40	DT	112/112 (100%)	99 (88%)	13 (12%)	7	32
40	FT	112/112 (100%)	99 (88%)	13 (12%)	7	32
40	HT	112/112 (100%)	99 (88%)	13 (12%)	7	32
40	JT	112/112 (100%)	99 (88%)	13 (12%)	7	32
41	BU	75/75 (100%)	69 (92%)	6 (8%)	15	50
41	DU	75/75 (100%)	69 (92%)	6 (8%)	15	50
41	FU	75/75 (100%)	69 (92%)	6 (8%)	15	50
41	HU	75/75 (100%)	68 (91%)	7 (9%)	11	42
41	JU	75/75 (100%)	68 (91%)	7 (9%)	11	42
42	BV	94/94 (100%)	86 (92%)	8 (8%)	13	48
42	DV	94/94 (100%)	86 (92%)	8 (8%)	13	48
42	FV	94/94 (100%)	86 (92%)	8 (8%)	13	48
42	HV	94/94 (100%)	86 (92%)	8 (8%)	13	48

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	JV	94/94 (100%)	86 (92%)	8 (8%)	13	48
43	BW	147/147 (100%)	125 (85%)	22 (15%)	3	23
43	DW	147/147 (100%)	125 (85%)	22 (15%)	3	23
43	FW	147/147 (100%)	125 (85%)	22 (15%)	3	23
43	HW	147/147 (100%)	125 (85%)	22 (15%)	3	23
43	JW	147/147 (100%)	125 (85%)	22 (15%)	3	23
44	BX	64/64 (100%)	49 (77%)	15 (23%)	1	7
44	DX	64/64 (100%)	49 (77%)	15 (23%)	1	7
44	FX	64/64 (100%)	48 (75%)	16 (25%)	1	6
44	HX	64/64 (100%)	48 (75%)	16 (25%)	1	6
44	JX	64/64 (100%)	49 (77%)	15 (23%)	1	7
45	BY	53/53 (100%)	44 (83%)	9 (17%)	2	18
45	DY	53/53 (100%)	44 (83%)	9 (17%)	2	18
45	FY	53/53 (100%)	44 (83%)	9 (17%)	2	18
45	HY	53/53 (100%)	44 (83%)	9 (17%)	2	18
45	JY	53/53 (100%)	44 (83%)	9 (17%)	2	18
46	BZ	48/48 (100%)	38 (79%)	10 (21%)	1	10
46	DZ	48/48 (100%)	38 (79%)	10 (21%)	1	10
46	FZ	48/48 (100%)	38 (79%)	10 (21%)	1	10
46	HZ	48/48 (100%)	38 (79%)	10 (21%)	1	10
46	JZ	48/48 (100%)	38 (79%)	10 (21%)	1	10
47	B1	66/66 (100%)	53 (80%)	13 (20%)	1	12
47	D1	66/66 (100%)	53 (80%)	13 (20%)	1	12
47	F1	66/66 (100%)	53 (80%)	13 (20%)	1	12
47	H1	66/66 (100%)	53 (80%)	13 (20%)	1	12
47	J1	66/66 (100%)	53 (80%)	13 (20%)	1	12
48	B2	51/51 (100%)	39 (76%)	12 (24%)	1	7
48	D2	51/51 (100%)	39 (76%)	12 (24%)	1	7
48	F2	51/51 (100%)	39 (76%)	12 (24%)	1	7
48	H2	51/51 (100%)	39 (76%)	12 (24%)	1	7
48	J2	51/51 (100%)	39 (76%)	12 (24%)	1	7

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	B3	46/46 (100%)	33 (72%)	13 (28%)	0	3
49	D3	46/46 (100%)	33 (72%)	13 (28%)	0	3
49	F3	46/46 (100%)	33 (72%)	13 (28%)	0	3
49	H3	46/46 (100%)	33 (72%)	13 (28%)	0	3
49	J3	46/46 (100%)	33 (72%)	13 (28%)	0	3
50	B4	39/39 (100%)	28 (72%)	11 (28%)	0	3
50	D4	39/39 (100%)	28 (72%)	11 (28%)	0	3
50	F4	39/39 (100%)	28 (72%)	11 (28%)	0	3
50	H4	39/39 (100%)	28 (72%)	11 (28%)	0	3
50	J4	39/39 (100%)	28 (72%)	11 (28%)	0	3
51	B5	50/50 (100%)	35 (70%)	15 (30%)	0	3
51	D5	50/50 (100%)	35 (70%)	15 (30%)	0	3
51	F5	50/50 (100%)	35 (70%)	15 (30%)	0	3
51	H5	50/50 (100%)	35 (70%)	15 (30%)	0	3
51	J5	50/50 (100%)	35 (70%)	15 (30%)	0	3
52	B6	34/34 (100%)	30 (88%)	4 (12%)	6	32
52	D6	34/34 (100%)	30 (88%)	4 (12%)	6	32
52	F6	34/34 (100%)	30 (88%)	4 (12%)	6	32
52	H6	34/34 (100%)	30 (88%)	4 (12%)	6	32
52	J6	34/34 (100%)	30 (88%)	4 (12%)	6	32
53	B7	191/187 (102%)	179 (94%)	12 (6%)	22	59
53	D7	191/187 (102%)	179 (94%)	12 (6%)	22	59
53	F7	191/187 (102%)	179 (94%)	12 (6%)	22	59
53	H7	191/187 (102%)	179 (94%)	12 (6%)	22	59
53	J7	191/187 (102%)	179 (94%)	12 (6%)	22	59
All	All	24880/24865 (100%)	21622 (87%)	3258 (13%)	5	28

5 of 3258 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	ES	36	ARG
43	FW	51	LEU
34	JN	12	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
24	FD	118	ASN
31	FK	30	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 944 such sidechains are listed below:

Mol	Chain	Res	Type
15	EO	13	GLN
42	FV	32	GLN
32	JL	26	ASN
19	ES	56	GLN
28	FH	74	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1521/1526 (99%)	348 (22%)	56 (3%)
1	CA	1521/1526 (99%)	348 (22%)	57 (3%)
1	EA	1522/1526 (99%)	349 (22%)	57 (3%)
1	GA	1522/1526 (99%)	349 (22%)	56 (3%)
1	IA	1522/1526 (99%)	348 (22%)	57 (3%)
22	BB	2801/2825 (99%)	768 (27%)	35 (1%)
22	DB	2804/2825 (99%)	771 (27%)	36 (1%)
22	FB	2801/2825 (99%)	768 (27%)	38 (1%)
22	HB	2803/2825 (99%)	768 (27%)	36 (1%)
22	JB	2804/2825 (99%)	765 (27%)	37 (1%)
23	BA	117/119 (98%)	30 (25%)	1 (0%)
23	DA	117/119 (98%)	30 (25%)	1 (0%)
23	FA	117/119 (98%)	31 (26%)	1 (0%)
23	HA	117/119 (98%)	30 (25%)	1 (0%)
23	JA	117/119 (98%)	30 (25%)	1 (0%)
All	All	22206/22350 (99%)	5733 (25%)	470 (2%)

5 of 5733 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	7	G
1	AA	8	A
1	AA	9	G
1	AA	31	G
1	AA	32	A

5 of 470 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	EA	687	A
22	FB	1710	U
22	JB	181	A
1	EA	975	A
1	EA	1397	C

## 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
22	FB	43
22	BB	42
22	JB	41
22	HB	39
22	DB	37
1	CA	4
1	GA	4
1	EA	4
1	AA	4
1	IA	4
12	GL	3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Number of breaks
12	IL	3
12	CL	3
43	HW	2
13	EM	2
13	GM	2
43	FW	2
12	EL	2
13	IM	2
43	DW	2
12	AL	2
13	CM	2
43	JW	2
13	AM	1
43	BW	1

The worst 5 of 253 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	JB	373:A	O3'	387:A	P	28.29
1	HB	373:A	O3'	387:A	P	28.03
1	FB	373:A	O3'	387:A	P	28.01
1	DB	373:A	O3'	387:A	P	27.91
1	FB	248:A	O3'	292:A	P	27.80



## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	AA	1526/1526 (100%)	68.84	1526 (100%) 0 0	521, 521, 521, 521	0
1	CA	1526/1526 (100%)	73.75	1526 (100%) 0 0	607, 607, 607, 607	0
1	EA	1526/1526 (100%)	70.70	1526 (100%) 0 0	628, 628, 628, 628	0
1	GA	1526/1526 (100%)	71.76	1526 (100%) 0 0	669, 669, 669, 669	0
1	IA	1526/1526 (100%)	75.64	1526 (100%) 0 0	743, 743, 743, 743	0
2	AB	234/234 (100%)	20.15	232 (99%) 0 0	521, 521, 521, 521	0
2	CB	234/234 (100%)	22.19	227 (97%) 0 1	607, 607, 607, 607	0
2	EB	234/234 (100%)	17.16	224 (95%) 0 1	628, 628, 628, 628	0
2	GB	234/234 (100%)	20.21	229 (97%) 0 1	669, 669, 669, 669	0
2	IB	234/234 (100%)	19.81	225 (96%) 0 1	743, 743, 743, 743	0
3	AC	206/206 (100%)	19.34	206 (100%) 0 0	521, 521, 521, 521	0
3	CC	206/206 (100%)	19.17	206 (100%) 0 0	607, 607, 607, 607	0
3	EC	206/206 (100%)	19.66	206 (100%) 0 0	628, 628, 628, 628	0
3	GC	206/206 (100%)	19.82	206 (100%) 0 0	669, 669, 669, 669	0
3	IC	206/206 (100%)	22.23	206 (100%) 0 0	743, 743, 743, 743	0
4	AD	208/208 (100%)	24.79	208 (100%) 0 0	521, 521, 521, 521	0
4	CD	208/208 (100%)	26.48	208 (100%) 0 0	607, 607, 607, 607	0
4	ED	208/208 (100%)	33.48	208 (100%) 0 0	628, 628, 628, 628	0
4	GD	208/208 (100%)	33.66	208 (100%) 0 0	669, 669, 669, 669	0
4	ID	208/208 (100%)	37.66	208 (100%) 0 0	743, 743, 743, 743	0
5	AE	150/150 (100%)	31.19	150 (100%) 0 0	521, 521, 521, 521	0
5	CE	150/150 (100%)	32.92	150 (100%) 0 0	607, 607, 607, 607	0
5	EE	150/150 (100%)	32.06	150 (100%) 0 0	628, 628, 628, 628	0
5	GE	150/150 (100%)	36.73	150 (100%) 0 0	669, 669, 669, 669	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
5	IE	150/150 (100%)	40.70	150 (100%)	0	0	743, 743, 743, 743	0
6	AF	101/101 (100%)	6.05	85 (84%)	0	2	521, 521, 521, 521	0
6	CF	101/101 (100%)	9.28	96 (95%)	0	1	607, 607, 607, 607	0
6	EF	101/101 (100%)	11.77	100 (99%)	0	0	628, 628, 628, 628	0
6	GF	101/101 (100%)	6.20	84 (83%)	0	2	669, 669, 669, 669	0
6	IF	101/101 (100%)	11.81	100 (99%)	0	0	743, 743, 743, 743	0
7	AG	155/155 (100%)	26.48	155 (100%)	0	0	521, 521, 521, 521	0
7	CG	155/155 (100%)	28.54	155 (100%)	0	0	607, 607, 607, 607	0
7	EG	155/155 (100%)	28.85	155 (100%)	0	0	628, 628, 628, 628	0
7	GG	155/155 (100%)	30.88	155 (100%)	0	0	669, 669, 669, 669	0
7	IG	155/155 (100%)	32.15	155 (100%)	0	0	743, 743, 743, 743	0
8	AH	138/138 (100%)	33.18	138 (100%)	0	0	521, 521, 521, 521	0
8	CH	138/138 (100%)	32.64	138 (100%)	0	0	607, 607, 607, 607	0
8	EH	138/138 (100%)	29.26	138 (100%)	0	0	628, 628, 628, 628	0
8	GH	138/138 (100%)	35.66	138 (100%)	0	0	669, 669, 669, 669	0
8	IH	138/138 (100%)	37.02	138 (100%)	0	0	743, 743, 743, 743	0
9	AI	127/127 (100%)	43.87	127 (100%)	0	0	521, 521, 521, 521	0
9	CI	127/127 (100%)	49.21	127 (100%)	0	0	607, 607, 607, 607	0
9	EI	127/127 (100%)	42.06	127 (100%)	0	0	628, 628, 628, 628	0
9	GI	127/127 (100%)	39.84	127 (100%)	0	0	669, 669, 669, 669	0
9	II	127/127 (100%)	36.95	127 (100%)	0	0	743, 743, 743, 743	0
10	AJ	98/98 (100%)	28.96	98 (100%)	0	0	521, 521, 521, 521	0
10	CJ	98/98 (100%)	35.06	98 (100%)	0	0	607, 607, 607, 607	0
10	EJ	98/98 (100%)	36.30	98 (100%)	0	0	628, 628, 628, 628	0
10	GJ	98/98 (100%)	33.57	98 (100%)	0	0	669, 669, 669, 669	0
10	IJ	98/98 (100%)	42.70	98 (100%)	0	0	743, 743, 743, 743	0
11	AK	119/119 (100%)	13.20	118 (99%)	0	0	521, 521, 521, 521	0
11	CK	119/119 (100%)	12.94	116 (97%)	0	1	607, 607, 607, 607	0
11	EK	119/119 (100%)	10.05	110 (92%)	0	1	628, 628, 628, 628	0
11	GK	119/119 (100%)	13.94	118 (99%)	0	0	669, 669, 669, 669	0
11	IK	119/119 (100%)	9.55	107 (89%)	0	1	743, 743, 743, 743	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
12	AL	124/124 (100%)	22.87	124 (100%)	0	0	521, 521, 521, 521	0
12	CL	124/124 (100%)	27.46	124 (100%)	0	0	607, 607, 607, 607	0
12	EL	124/124 (100%)	17.93	124 (100%)	0	0	628, 628, 628, 628	0
12	GL	124/124 (100%)	20.79	124 (100%)	0	0	669, 669, 669, 669	0
12	IL	124/124 (100%)	16.75	124 (100%)	0	0	743, 743, 743, 743	0
13	AM	125/125 (100%)	17.00	123 (98%)	0	0	521, 521, 521, 521	0
13	CM	125/125 (100%)	16.98	123 (98%)	0	0	607, 607, 607, 607	0
13	EM	125/125 (100%)	13.43	125 (100%)	0	0	628, 628, 628, 628	0
13	GM	125/125 (100%)	17.31	125 (100%)	0	0	669, 669, 669, 669	0
13	IM	125/125 (100%)	16.73	125 (100%)	0	0	743, 743, 743, 743	0
14	AN	60/60 (100%)	23.00	60 (100%)	0	0	521, 521, 521, 521	0
14	CN	60/60 (100%)	26.41	60 (100%)	0	0	607, 607, 607, 607	0
14	EN	60/60 (100%)	34.36	60 (100%)	0	0	628, 628, 628, 628	0
14	GN	60/60 (100%)	23.21	60 (100%)	0	0	669, 669, 669, 669	0
14	IN	60/60 (100%)	24.82	60 (100%)	0	0	743, 743, 743, 743	0
15	AO	88/88 (100%)	33.91	88 (100%)	0	0	521, 521, 521, 521	0
15	CO	88/88 (100%)	39.95	88 (100%)	0	0	607, 607, 607, 607	0
15	EO	88/88 (100%)	35.09	88 (100%)	0	0	628, 628, 628, 628	0
15	GO	88/88 (100%)	33.24	88 (100%)	0	0	669, 669, 669, 669	0
15	IO	88/88 (100%)	36.05	88 (100%)	0	0	743, 743, 743, 743	0
16	AP	83/83 (100%)	33.61	83 (100%)	0	0	521, 521, 521, 521	0
16	CP	83/83 (100%)	29.19	83 (100%)	0	0	607, 607, 607, 607	0
16	EP	83/83 (100%)	24.76	83 (100%)	0	0	628, 628, 628, 628	0
16	GP	83/83 (100%)	32.93	83 (100%)	0	0	669, 669, 669, 669	0
16	IP	83/83 (100%)	23.13	83 (100%)	0	0	743, 743, 743, 743	0
17	AQ	104/104 (100%)	27.85	104 (100%)	0	0	521, 521, 521, 521	0
17	CQ	104/104 (100%)	41.22	104 (100%)	0	0	607, 607, 607, 607	0
17	EQ	104/104 (100%)	32.72	104 (100%)	0	0	628, 628, 628, 628	0
17	GQ	104/104 (100%)	26.29	104 (100%)	0	0	669, 669, 669, 669	0
17	IQ	104/104 (100%)	34.27	104 (100%)	0	0	743, 743, 743, 743	0
18	AR	73/73 (100%)	19.67	73 (100%)	0	0	521, 521, 521, 521	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
18	CR	73/73 (100%)	23.62	73 (100%)	0	0	607, 607, 607, 607	0
18	ER	73/73 (100%)	19.59	73 (100%)	0	0	628, 628, 628, 628	0
18	GR	73/73 (100%)	21.27	73 (100%)	0	0	669, 669, 669, 669	0
18	IR	73/73 (100%)	25.80	73 (100%)	0	0	743, 743, 743, 743	0
19	AS	80/80 (100%)	15.92	80 (100%)	0	0	521, 521, 521, 521	0
19	CS	80/80 (100%)	13.92	78 (97%)	0	1	607, 607, 607, 607	0
19	ES	80/80 (100%)	10.59	75 (93%)	0	1	628, 628, 628, 628	0
19	GS	80/80 (100%)	12.35	74 (92%)	0	1	669, 669, 669, 669	0
19	IS	80/80 (100%)	10.71	73 (91%)	0	1	743, 743, 743, 743	0
20	AT	99/99 (100%)	23.27	99 (100%)	0	0	521, 521, 521, 521	0
20	CT	99/99 (100%)	30.36	99 (100%)	0	0	607, 607, 607, 607	0
20	ET	99/99 (100%)	27.84	99 (100%)	0	0	628, 628, 628, 628	0
20	GT	99/99 (100%)	25.26	99 (100%)	0	0	669, 669, 669, 669	0
20	IT	99/99 (100%)	28.74	99 (100%)	0	0	743, 743, 743, 743	0
21	Aa	90/90 (100%)	2.90	41 (45%)	0	4	4, 4, 4, 4	90 (100%)
21	Ca	90/90 (100%)	3.60	46 (51%)	0	4	4, 4, 4, 4	90 (100%)
21	Ea	90/90 (100%)	4.76	63 (70%)	0	3	4, 4, 4, 4	90 (100%)
21	Ga	90/90 (100%)	3.75	46 (51%)	0	4	4, 4, 4, 4	90 (100%)
21	Ia	90/90 (100%)	5.37	66 (73%)	0	3	4, 4, 4, 4	90 (100%)
22	BB	2825/2825 (100%)	51.22	2824 (99%)	0	0	849, 855, 857, 859	0
22	DB	2825/2825 (100%)	52.48	2824 (99%)	0	0	895, 902, 903, 904	0
22	FB	2825/2825 (100%)	51.34	2823 (99%)	0	0	896, 902, 905, 905	0
22	HB	2825/2825 (100%)	52.42	2823 (99%)	0	0	894, 902, 903, 903	0
22	JB	2825/2825 (100%)	53.56	2821 (99%)	0	0	897, 902, 906, 908	0
23	BA	118/119 (99%)	55.46	118 (100%)	0	0	846, 846, 846, 846	0
23	DA	118/119 (99%)	71.75	118 (100%)	0	0	893, 893, 893, 893	0
23	FA	118/119 (99%)	72.34	118 (100%)	0	0	896, 896, 896, 896	0
23	HA	118/119 (99%)	53.51	118 (100%)	0	0	894, 894, 894, 894	0
23	JA	118/119 (99%)	60.91	118 (100%)	0	0	894, 894, 894, 894	0
24	BD	270/270 (100%)	18.35	251 (92%)	0	1	904, 904, 904, 904	0
24	DD	270/270 (100%)	22.54	265 (98%)	0	1	950, 950, 950, 950	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
24	FD	270/270 (100%)	26.14	269 (99%)	0	0	950, 950, 950, 950	0
24	HD	270/270 (100%)	18.76	249 (92%)	0	1	950, 950, 950, 950	0
24	JD	270/270 (100%)	23.15	270 (100%)	0	0	950, 950, 950, 950	0
25	BE	205/205 (100%)	10.43	183 (89%)	0	2	904, 904, 904, 904	0
25	DE	205/205 (100%)	8.37	177 (86%)	0	2	950, 950, 950, 950	0
25	FE	205/205 (100%)	8.03	171 (83%)	0	2	950, 950, 950, 950	0
25	HE	205/205 (100%)	10.92	186 (90%)	0	1	950, 950, 950, 950	0
25	JE	205/205 (100%)	10.07	178 (86%)	0	2	950, 950, 950, 950	0
26	BF	197/198 (99%)	19.43	197 (100%)	0	0	904, 904, 904, 904	0
26	DF	197/198 (99%)	19.22	196 (99%)	0	0	950, 950, 950, 950	0
26	FF	197/198 (99%)	16.10	187 (94%)	0	1	950, 950, 950, 950	0
26	HF	197/198 (99%)	19.85	197 (100%)	0	0	950, 950, 950, 950	0
26	JF	197/198 (99%)	15.79	183 (92%)	0	1	950, 950, 950, 950	0
27	BG	178/178 (100%)	22.11	178 (100%)	0	0	904, 904, 904, 904	0
27	DG	178/178 (100%)	24.80	178 (100%)	0	0	950, 950, 950, 950	0
27	FG	178/178 (100%)	26.49	178 (100%)	0	0	950, 950, 950, 950	0
27	HG	178/178 (100%)	18.39	178 (100%)	0	0	950, 950, 950, 950	0
27	JG	178/178 (100%)	27.49	178 (100%)	0	0	950, 950, 950, 950	0
28	BH	177/177 (100%)	8.27	150 (84%)	0	2	904, 904, 904, 904	0
28	DH	177/177 (100%)	8.13	149 (84%)	0	2	950, 950, 950, 950	0
28	FH	177/177 (100%)	8.00	152 (85%)	0	2	950, 950, 950, 950	0
28	HH	177/177 (100%)	7.58	141 (79%)	0	2	950, 950, 950, 950	0
28	JH	177/177 (100%)	7.17	139 (78%)	0	2	950, 950, 950, 950	0
29	BI	52/52 (100%)	15.34	51 (98%)	0	1	904, 904, 904, 904	0
29	DI	52/52 (100%)	19.82	52 (100%)	0	0	950, 950, 950, 950	0
29	FI	52/52 (100%)	20.29	51 (98%)	0	1	950, 950, 950, 950	0
29	HI	52/52 (100%)	14.17	51 (98%)	0	1	950, 950, 950, 950	0
29	JI	52/52 (100%)	17.78	51 (98%)	0	1	950, 950, 950, 950	0
30	BJ	143/143 (100%)	18.46	141 (98%)	0	0	904, 904, 904, 904	0
30	DJ	143/143 (100%)	24.71	143 (100%)	0	0	950, 950, 950, 950	0
30	FJ	143/143 (100%)	33.08	143 (100%)	0	0	950, 950, 950, 950	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
30	HJ	143/143 (100%)	25.60	142 (99%)	0	0	950, 950, 950, 950	0
30	JJ	143/143 (100%)	33.26	143 (100%)	0	0	950, 950, 950, 950	0
31	BK	143/143 (100%)	8.24	138 (96%)	0	1	904, 904, 904, 904	0
31	DK	143/143 (100%)	7.48	118 (82%)	0	2	950, 950, 950, 950	0
31	FK	143/143 (100%)	8.23	109 (76%)	0	2	950, 950, 950, 950	0
31	HK	143/143 (100%)	9.26	139 (97%)	0	1	950, 950, 950, 950	0
31	JK	143/143 (100%)	8.64	109 (76%)	0	2	950, 950, 950, 950	0
32	BL	132/132 (100%)	12.55	132 (100%)	0	0	904, 904, 904, 904	0
32	DL	132/132 (100%)	11.25	132 (100%)	0	0	950, 950, 950, 950	0
32	FL	132/132 (100%)	11.56	131 (99%)	0	0	950, 950, 950, 950	0
32	HL	132/132 (100%)	13.98	132 (100%)	0	0	950, 950, 950, 950	0
32	JL	132/132 (100%)	16.15	132 (100%)	0	0	950, 950, 950, 950	0
33	BM	141/141 (100%)	23.39	141 (100%)	0	0	904, 904, 904, 904	0
33	DM	141/141 (100%)	20.74	141 (100%)	0	0	950, 950, 950, 950	0
33	FM	141/141 (100%)	24.03	138 (97%)	0	1	950, 950, 950, 950	0
33	HM	141/141 (100%)	26.82	141 (100%)	0	0	950, 950, 950, 950	0
33	JM	141/141 (100%)	28.70	138 (97%)	0	1	950, 950, 950, 950	0
34	BN	124/124 (100%)	14.76	124 (100%)	0	0	904, 904, 904, 904	0
34	DN	124/124 (100%)	20.32	124 (100%)	0	0	950, 950, 950, 950	0
34	FN	124/124 (100%)	27.48	124 (100%)	0	0	950, 950, 950, 950	0
34	HN	124/124 (100%)	17.49	124 (100%)	0	0	950, 950, 950, 950	0
34	JN	124/124 (100%)	31.04	124 (100%)	0	0	950, 950, 950, 950	0
35	BO	114/114 (100%)	17.04	106 (92%)	0	1	904, 904, 904, 904	0
35	DO	114/114 (100%)	18.86	106 (92%)	0	1	950, 950, 950, 950	0
35	FO	114/114 (100%)	15.40	107 (93%)	0	1	950, 950, 950, 950	0
35	HO	114/114 (100%)	19.90	107 (93%)	0	1	950, 950, 950, 950	0
35	JO	114/114 (100%)	16.08	107 (93%)	0	1	950, 950, 950, 950	0
36	BP	111/111 (100%)	36.47	111 (100%)	0	0	904, 904, 904, 904	7 (6%)
36	DP	111/111 (100%)	37.24	111 (100%)	0	0	950, 950, 950, 950	7 (6%)
36	FP	111/111 (100%)	37.28	111 (100%)	0	0	950, 950, 950, 950	7 (6%)
36	HP	111/111 (100%)	28.23	111 (100%)	0	0	950, 950, 950, 950	7 (6%)

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
36	JP	111/111 (100%)	38.70	111 (100%)	0	0	950, 950, 950, 950	7 (6%)
37	BQ	125/125 (100%)	19.45	125 (100%)	0	0	904, 904, 904, 904	0
37	DQ	125/125 (100%)	21.09	125 (100%)	0	0	950, 950, 950, 950	0
37	FQ	125/125 (100%)	18.92	124 (99%)	0	0	950, 950, 950, 950	0
37	HQ	125/125 (100%)	24.19	125 (100%)	0	0	950, 950, 950, 950	0
37	JQ	125/125 (100%)	25.43	125 (100%)	0	0	950, 950, 950, 950	0
38	BR	117/117 (100%)	10.54	110 (94%)	0	1	904, 904, 904, 904	9 (7%)
38	DR	117/117 (100%)	9.27	109 (93%)	0	1	950, 950, 950, 950	9 (7%)
38	FR	117/117 (100%)	8.39	104 (88%)	0	2	950, 950, 950, 950	9 (7%)
38	HR	117/117 (100%)	9.94	104 (88%)	0	2	950, 950, 950, 950	9 (7%)
38	JR	117/117 (100%)	8.71	101 (86%)	0	2	950, 950, 950, 950	9 (7%)
39	BS	100/100 (100%)	5.82	68 (68%)	0	3	904, 904, 904, 904	0
39	DS	100/100 (100%)	5.81	69 (69%)	0	3	950, 950, 950, 950	0
39	FS	100/100 (100%)	4.78	60 (60%)	0	3	950, 950, 950, 950	0
39	HS	100/100 (100%)	4.79	56 (56%)	0	3	950, 950, 950, 950	0
39	JS	100/100 (100%)	4.43	50 (50%)	0	4	950, 950, 950, 950	0
40	BT	130/130 (100%)	2.94	73 (56%)	0	3	904, 904, 904, 904	0
40	DT	130/130 (100%)	2.59	63 (48%)	0	4	950, 950, 950, 950	0
40	FT	130/130 (100%)	2.73	65 (50%)	0	4	950, 950, 950, 950	0
40	HT	130/130 (100%)	2.98	74 (56%)	0	3	950, 950, 950, 950	0
40	JT	130/130 (100%)	2.41	58 (44%)	0	4	950, 950, 950, 950	0
41	BU	93/93 (100%)	8.95	85 (91%)	0	1	904, 904, 904, 904	0
41	DU	93/93 (100%)	10.84	93 (100%)	0	0	950, 950, 950, 950	0
41	FU	93/93 (100%)	11.37	93 (100%)	0	0	950, 950, 950, 950	0
41	HU	93/93 (100%)	8.45	92 (98%)	0	0	950, 950, 950, 950	0
41	JU	93/93 (100%)	10.60	93 (100%)	0	0	950, 950, 950, 950	0
42	BV	113/113 (100%)	8.16	107 (94%)	0	1	904, 904, 904, 904	0
42	DV	113/113 (100%)	9.37	112 (99%)	0	0	950, 950, 950, 950	0
42	FV	113/113 (100%)	10.92	113 (100%)	0	0	950, 950, 950, 950	0
42	HV	113/113 (100%)	7.99	104 (92%)	0	1	950, 950, 950, 950	0
42	JV	113/113 (100%)	10.05	111 (98%)	0	0	950, 950, 950, 950	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
43	BW	173/173 (100%)	21.59	172 (99%)	0	0	904, 904, 904, 904	0
43	DW	173/173 (100%)	20.14	169 (97%)	0	1	950, 950, 950, 950	0
43	FW	173/173 (100%)	17.77	169 (97%)	0	1	950, 950, 950, 950	0
43	HW	173/173 (100%)	21.21	173 (100%)	0	0	950, 950, 950, 950	0
43	JW	173/173 (100%)	17.07	172 (99%)	0	0	950, 950, 950, 950	0
44	BX	86/86 (100%)	38.61	86 (100%)	0	0	904, 904, 904, 904	0
44	DX	86/86 (100%)	38.20	86 (100%)	0	0	950, 950, 950, 950	0
44	FX	86/86 (100%)	41.16	86 (100%)	0	0	950, 950, 950, 950	0
44	HX	86/86 (100%)	36.52	86 (100%)	0	0	950, 950, 950, 950	0
44	JX	86/86 (100%)	39.80	86 (100%)	0	0	950, 950, 950, 950	0
45	BY	65/65 (100%)	8.60	65 (100%)	0	0	904, 904, 904, 904	0
45	DY	65/65 (100%)	13.59	65 (100%)	0	0	950, 950, 950, 950	0
45	FY	65/65 (100%)	18.88	65 (100%)	0	0	950, 950, 950, 950	0
45	HY	65/65 (100%)	8.30	65 (100%)	0	0	950, 950, 950, 950	0
45	JY	65/65 (100%)	15.08	65 (100%)	0	0	950, 950, 950, 950	0
46	BZ	55/55 (100%)	28.51	55 (100%)	0	0	904, 904, 904, 904	3 (5%)
46	DZ	55/55 (100%)	40.30	55 (100%)	0	0	950, 950, 950, 950	3 (5%)
46	FZ	55/55 (100%)	23.53	55 (100%)	0	0	950, 950, 950, 950	3 (5%)
46	HZ	55/55 (100%)	18.48	55 (100%)	0	0	950, 950, 950, 950	3 (5%)
46	JZ	55/55 (100%)	18.03	55 (100%)	0	0	950, 950, 950, 950	3 (5%)
47	B1	73/73 (100%)	33.01	73 (100%)	0	0	904, 904, 904, 904	0
47	D1	73/73 (100%)	35.65	73 (100%)	0	0	950, 950, 950, 950	0
47	F1	73/73 (100%)	48.10	73 (100%)	0	0	950, 950, 950, 950	0
47	H1	73/73 (100%)	31.11	73 (100%)	0	0	950, 950, 950, 950	0
47	J1	73/73 (100%)	39.41	73 (100%)	0	0	950, 950, 950, 950	0
48	B2	58/58 (100%)	4.70	32 (55%)	0	3	904, 904, 904, 904	0
48	D2	58/58 (100%)	5.48	31 (53%)	0	4	950, 950, 950, 950	0
48	F2	58/58 (100%)	5.51	35 (60%)	0	3	950, 950, 950, 950	0
48	H2	58/58 (100%)	4.46	34 (58%)	0	3	950, 950, 950, 950	0
48	J2	58/58 (100%)	4.51	30 (51%)	0	4	950, 950, 950, 950	0
49	B3	53/53 (100%)	7.28	44 (83%)	0	2	904, 904, 904, 904	0

*Continued on next page...*



Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
49	D3	53/53 (100%)	17.31	53 (100%)	0	0	950, 950, 950, 950	0
49	F3	53/53 (100%)	21.07	53 (100%)	0	0	950, 950, 950, 950	0
49	H3	53/53 (100%)	6.44	42 (79%)	0	2	950, 950, 950, 950	0
49	J3	53/53 (100%)	14.96	53 (100%)	0	0	950, 950, 950, 950	0
50	B4	46/46 (100%)	20.52	46 (100%)	0	0	904, 904, 904, 904	0
50	D4	46/46 (100%)	20.48	46 (100%)	0	0	950, 950, 950, 950	0
50	F4	46/46 (100%)	19.93	46 (100%)	0	0	950, 950, 950, 950	0
50	H4	46/46 (100%)	20.51	46 (100%)	0	0	950, 950, 950, 950	0
50	J4	46/46 (100%)	20.81	46 (100%)	0	0	950, 950, 950, 950	0
51	B5	63/63 (100%)	41.58	63 (100%)	0	0	904, 904, 904, 904	0
51	D5	63/63 (100%)	56.38	63 (100%)	0	0	950, 950, 950, 950	0
51	F5	63/63 (100%)	58.50	63 (100%)	0	0	950, 950, 950, 950	0
51	H5	63/63 (100%)	36.46	63 (100%)	0	0	950, 950, 950, 950	0
51	J5	63/63 (100%)	56.57	63 (100%)	0	0	950, 950, 950, 950	0
52	B6	35/35 (100%)	19.34	35 (100%)	0	0	904, 904, 904, 904	0
52	D6	35/35 (100%)	31.11	35 (100%)	0	0	950, 950, 950, 950	0
52	F6	35/35 (100%)	34.28	35 (100%)	0	0	950, 950, 950, 950	0
52	H6	35/35 (100%)	22.75	35 (100%)	0	0	950, 950, 950, 950	0
52	J6	35/35 (100%)	27.43	35 (100%)	0	0	950, 950, 950, 950	0
53	B7	213/217 (98%)	21.59	213 (100%)	0	0	904, 904, 904, 904	0
53	D7	213/217 (98%)	30.05	213 (100%)	0	0	950, 950, 950, 950	0
53	F7	213/217 (98%)	31.73	213 (100%)	0	0	950, 950, 950, 950	0
53	H7	213/217 (98%)	26.45	213 (100%)	0	0	950, 950, 950, 950	0
53	J7	213/217 (98%)	28.75	213 (100%)	0	0	950, 950, 950, 950	0
All	All	52580/52610 (99%)	37.45	50994 (96%)	0	1	4, 900, 950, 950	545 (1%)

The worst 5 of 50994 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	EA	976	G	272.8
1	GA	1349	A	266.7
1	IA	725	G	263.8
1	IA	1063	C	259.4
1	GA	1063	C	255.9

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.