wwPDB EM Map/Model Validation Report (i)

Sep 29, 2016 – 03:52 PM EDT

PDB ID	:	5JUS
EMDB ID:	:	EMD-6645
Title	:	Saccharomyces cerevisiae 80S ribosome bound with elongation factor eEF2-GDP-sordarin and Taura Syndrome Virus IRES, Structure III (mid-rotated 40S subunit)
Authors	:	Abeyrathne, P.; Koh, C.S.; Grant, T.; Grigorieff, N.; Korostelev, A.A.
Deposited on	:	2016-05-10
Resolution	:	4.20 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

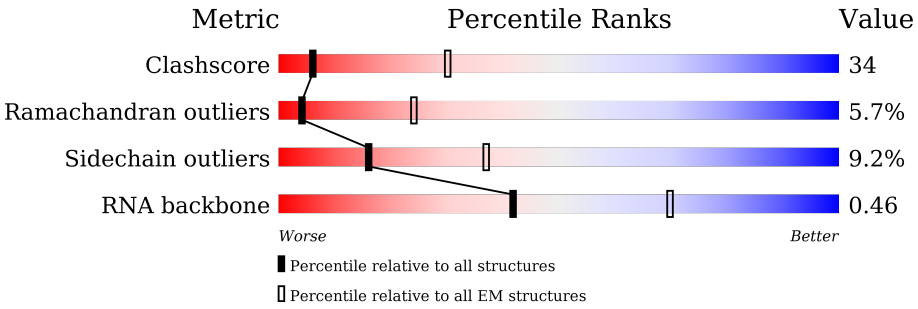
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027939

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for >=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 <=5%

Mol	Chain	Length	Quality of chain
1	A	1798	30% 57% 12% •
2	B	3396	21% 56% 19% • •
3	C	158	20% 62% 18% •
4	D	121	26% 63% 11% •
5	E	217	30% 40% 8% 21%
6	F	254	26% 62% 10% ••
7	G	387	29% 61% 9%
8	H	362	34% 56% 9% •

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Mol	Chain	Length	Quality of chain
9	I	297	42% 46% 12%
10	J	176	35% 57% 8%
11	K	244	30% 51% 9% 9%
12	L	256	33% 46% 11% 9%
13	M	191	31% 61% 8%
14	N	221	33% 54% 8% 5%
15	O	174	41% 48% 7%
16	P	165	17% 31% 8% 43%
17	Q	199	36% 50% 11%
18	R	138	29% 58% 12%
19	S	204	23% 65% 12%
20	T	199	27% 62% 9%
21	U	184	36% 51% 11%
22	V	186	29% 60% 11%
23	W	189	41% 53% 5%
24	X	172	26% 65% 9%
25	Y	160	38% 48% 13%
26	Z	121	45% 36% 17%
27	AA	137	47% 45% 6%
28	BA	155	6% 26% 6% 61%
29	CA	142	36% 42% 8% 15%
30	DA	127	32% 55% 10%
31	EA	136	33% 58% 8%
32	FA	149	27% 61% 11%
33	GA	59	49% 46%

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Mol	Chain	Length	Quality of chain
34	HA	105	29% 60% 8%
35	IA	113	39% 51% 6%
36	JA	130	28% 58% 12%
37	KA	107	33% 59% 7%
38	LA	121	34% 51% 7% 7%
39	MA	120	36% 58% 5%
40	NA	100	33% 58% 8%
41	OA	88	36% 48% 13%
42	PA	78	65% 28%
43	QA	51	39% 47% 12%
44	RA	128	15% 21% 59%
45	SA	25	68% 20% 12%
46	TA	106	21% 70% 8%
47	UA	92	36% 52% 10%
48	VA	312	20% 34% 7% 39%
49	WA	319	45% 51%
50	XA	252	29% 43% 8% 18%
51	YA	255	76% 7% 16%
52	ZA	254	38% 44% 15%
53	AB	240	45% 42% 5% 7%
54	BB	261	32% 60% 7%
55	CB	225	31% 52% 8% 8%
56	DB	236	44% 48%
57	EB	190	41% 46% 11%
58	FB	200	40% 47% 7% 6%

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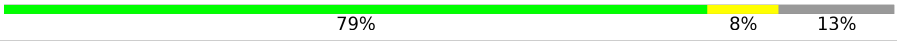
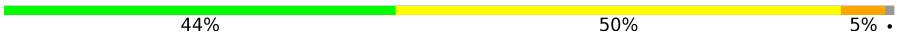
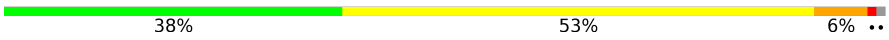
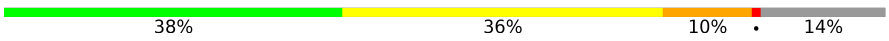
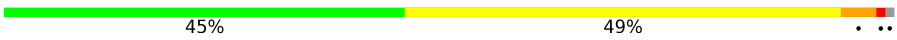
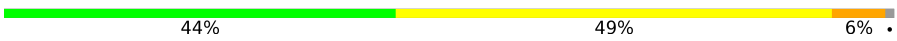
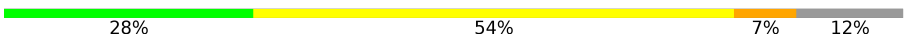
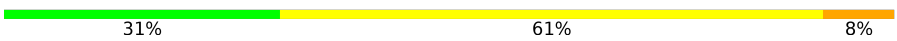
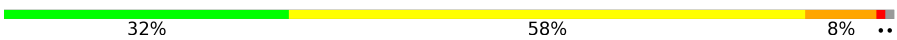
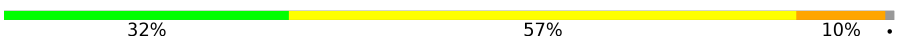
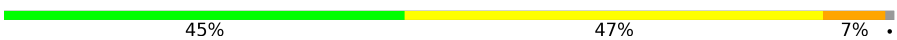
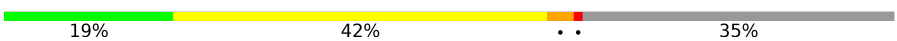
Mol	Chain	Length	Quality of chain
59	GB	197	
60	HB	105	
61	IB	156	
62	JB	143	
63	KB	151	
64	LB	137	
65	MB	142	
66	NB	143	
67	OB	136	
68	PB	146	
69	QB	144	
70	RB	121	
71	SB	87	
72	TB	130	
73	UB	145	
74	VB	135	
75	WB	108	
76	XB	119	
77	YB	82	
78	ZB	67	
79	AC	56	
80	BC	63	
81	CC	152	
82	DC	842	
83	EC	201	

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 212680 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1781	36760	16335	6359	12285	1781	0	0

- Molecule 2 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	3309	70288	31354	12595	23030	3309	0	0

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C	158	3354	1500	586	1110	158	0	0

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	D	121	2580	1152	461	846	121	0	0

- Molecule 5 is a protein called uL1 (yeast L1).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	171	1359	869	232	251	7	0	0

- Molecule 6 is a protein called uL2 (yeast L2).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	252	1918	1193	389	335	1	0	0

- Molecule 7 is a protein called uL3 (yeast L3).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	386	Total	C	N	O	S	0	0
			3082	1956	584	534	8		

- Molecule 8 is a protein called uL4 (yeast L4).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	361	Total	C	N	O	S	0	0
			2750	1730	522	495	3		

- Molecule 9 is a protein called uL18 (yeast L5).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	296	Total	C	N	O	S	0	0
			2376	1501	414	459	2		

- Molecule 10 is a protein called eL6 (yeast L6).

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	175	Total	C	N	O	S	0	0
			1401	902	251	247	1		

- Molecule 11 is a protein called uL30 (yeast L7).

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	222	Total	C	N	O	S	0	0
			1785	1151	324	309	1		

- Molecule 12 is a protein called eL8 (yeast L8).

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	233	Total	C	N	O	S	0	0
			1818	1159	326	330	3		

- Molecule 13 is a protein called uL6 (yeast L9).

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	191	Total	C	N	O	S	0	0
			1519	963	274	278	4		

- Molecule 14 is a protein called uL16 (yeast L10).

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	211	Total	C	N	O	S	0	0
			1718	1089	325	298	6		

- Molecule 15 is a protein called uL5 (yeast L11).

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	169	Total	C	N	O	S	0	0
			1354	847	253	250	4		

- Molecule 16 is a protein called uL11 (yeast L12).

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	94	Total	C	N	O	S	0	0
			723	448	138	135	2		

- Molecule 17 is a protein called eL13 (yeast L13).

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 18 is a protein called eL14 (yeast L14).

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	136	Total	C	N	O	S	0	0
			1054	675	199	178	2		

- Molecule 19 is a protein called eL15 (yeast L15).

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	203	Total	C	N	O	S	0	0
			1721	1077	361	282	1		

- Molecule 20 is a protein called uL13 (yeast L16).

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	197	Total	C	N	O	S	0	0
			1556	1003	289	263	1		

- Molecule 21 is a protein called uL22 (yeast L17).

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	183	Total	C	N	O	0	0
			1443	896	287	260		

- Molecule 22 is a protein called eL18 (yeast L18).

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	185	Total	C	N	O	S	0	0
			1442	908	290	242	2		

- Molecule 23 is a protein called eL19 (yeast L19).

Mol	Chain	Residues	Atoms				AltConf	Trace
23	W	188	Total	C	N	O	0	0
			1522	935	326	261		

- Molecule 24 is a protein called eL20 (yeast L20).

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	172	Total	C	N	O	S	0	0
			1446	930	267	245	4		

- Molecule 25 is a protein called eL21 (yeast L21).

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	159	Total	C	N	O	S	0	0
			1277	805	246	222	4		

- Molecule 26 is a protein called eL22 (yeast L22).

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Z	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 27 is a protein called uL14 (yeast L23).

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AA	136	Total	C	N	O	S	0	0
			1004	628	189	180	7		

- Molecule 28 is a protein called eL24 (yeast L24).

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BA	61	Total	C	N	O	S	0	0
			509	328	100	80	1		

- Molecule 29 is a protein called uL23 (yeast L25).

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CA	121	Total	C	N	O	S	0	0
			969	623	170	174	2		

- Molecule 30 is a protein called uL24 (yeast L26).

Mol	Chain	Residues	Atoms				AltConf	Trace
30	DA	126	Total	C	N	O	0	0
			994	625	192	177		

- Molecule 31 is a protein called eL27 (yeast L27).

Mol	Chain	Residues	Atoms				AltConf	Trace
31	EA	135	Total	C	N	O	0	0
			1093	710	202	181		

- Molecule 32 is a protein called uL15 (yeast L28).

Mol	Chain	Residues	Atoms					AltConf	Trace
32	FA	148	Total	C	N	O	S	0	0
			1174	749	231	191	3		

- Molecule 33 is a protein called eL29 (yeast L29).

Mol	Chain	Residues	Atoms				AltConf	Trace
33	GA	58	Total	C	N	O	0	0
			463	289	100	74		

- Molecule 34 is a protein called eL30 (yeast L30).

Mol	Chain	Residues	Atoms					AltConf	Trace
34	HA	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 35 is a protein called eL31 (yeast L31).

Mol	Chain	Residues	Atoms					AltConf	Trace
35	IA	109	Total	C	N	O	S	0	0
			890	565	168	156	1		

- Molecule 36 is a protein called eL32 (yeast L32).

Mol	Chain	Residues	Atoms					AltConf	Trace
36	JA	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 37 is a protein called eL33 (yeast L33).

Mol	Chain	Residues	Atoms					AltConf	Trace
37	KA	106	Total	C	N	O	S	0	0
			851	540	165	145	1		

- Molecule 38 is a protein called eL34 (yeast L34).

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LA	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 39 is a protein called uL29 (yeast L35).

Mol	Chain	Residues	Atoms					AltConf	Trace
39	MA	119	Total	C	N	O	S	0	0
			970	615	186	168	1		

- Molecule 40 is a protein called eL36 (yeast L36).

Mol	Chain	Residues	Atoms					AltConf	Trace
40	NA	99	Total	C	N	O	S	0	0
			772	481	156	133	2		

- Molecule 41 is a protein called eL37 (yeast L37).

Mol	Chain	Residues	Atoms					AltConf	Trace
41	OA	87	Total	C	N	O	S	0	0
			682	414	148	115	5		

- Molecule 42 is a protein called eL38 (yeast L38).

Mol	Chain	Residues	Atoms				AltConf	Trace
42	PA	77	Total	C	N	O	0	0
			613	391	115	107		

- Molecule 43 is a protein called eL39 (yeast L39).

Mol	Chain	Residues	Atoms					AltConf	Trace
43	QA	50	Total	C	N	O	S	0	0
			437	272	97	66	2		

- Molecule 44 is a protein called eL40 (yeast L40).

Mol	Chain	Residues	Atoms					AltConf	Trace
44	RA	52	Total	C	N	O	S	0	0
			418	259	86	68	5		

- Molecule 45 is a protein called eL41 (yeast L41).

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

- Molecule 46 is a protein called eL42 (yeast L42).

Mol	Chain	Residues	Atoms					AltConf	Trace
46	TA	105	Total	C	N	O	S	0	0
			848	534	170	139	5		

- Molecule 47 is a protein called eL43 (yeast L43).

Mol	Chain	Residues	Atoms					AltConf	Trace
47	UA	91	Total	C	N	O	S	0	0
			695	429	138	122	6		

- Molecule 48 is a protein called uL10 (yeast P0).

Mol	Chain	Residues	Atoms					AltConf	Trace
48	VA	189	Total	C	N	O	S	0	0
			1473	942	257	270	4		

- Molecule 49 is a protein called RACK1 (yeast Asc1).

Mol	Chain	Residues	Atoms					AltConf	Trace
49	WA	318	Total	C	N	O	S	0	0
			2445	1546	419	472	8		

- Molecule 50 is a protein called uS2 (yeast S0).

Mol	Chain	Residues	Atoms					AltConf	Trace
50	XA	206	Total	C	N	O	S	0	0
			1612	1034	285	291	2		

- Molecule 51 is a protein called eS1 (yeast S1).

Mol	Chain	Residues	Atoms				AltConf	Trace
51	YA	214	Total	C	N	O	0	0
			856	428	214	214		

- Molecule 52 is a protein called uS5 (yeast S2).

Mol	Chain	Residues	Atoms					AltConf	Trace
52	ZA	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 53 is a protein called uS3 (yeast S3).

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AB	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 54 is a protein called eS4 (yeast S4).

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BB	260	Total	C	N	O	S	0	0
			2069	1316	389	361	3		

- Molecule 55 is a protein called uS7 (yeast S5).

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CB	206	Total	C	N	O	S	0	0
			1610	1007	300	300	3		

- Molecule 56 is a protein called eS6 (yeast S6).

Mol	Chain	Residues	Atoms					AltConf	Trace
56	DB	226	Total	C	N	O	S	0	0
			1820	1142	350	325	3		

- Molecule 57 is a protein called eS7 (yeast S7).

Mol	Chain	Residues	Atoms				AltConf	Trace
57	EB	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 58 is a protein called eS8 (yeast S8).

Mol	Chain	Residues	Atoms					AltConf	Trace
58	FB	188	Total	C	N	O	S	0	0
			1490	925	298	265	2		

- Molecule 59 is a protein called uS4 (yeast S9).

Mol	Chain	Residues	Atoms					AltConf	Trace
59	GB	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 60 is a protein called eS10 (yeast S10).

Mol	Chain	Residues	Atoms					AltConf	Trace
60	HB	96	Total	C	N	O	S	0	0
			817	529	133	153	2		

- Molecule 61 is a protein called uS17 (yeast S11).

Mol	Chain	Residues	Atoms					AltConf	Trace
61	IB	155	Total	C	N	O	S	0	0
			1245	798	235	209	3		

- Molecule 62 is a protein called eS12 (yeast S12).

Mol	Chain	Residues	Atoms				AltConf	Trace
62	JB	124	Total	C	N	O	0	0
			496	248	124	124		

- Molecule 63 is a protein called uS15 (yeast S13).

Mol	Chain	Residues	Atoms					AltConf	Trace
63	KB	150	Total	C	N	O	S	0	0
			1193	759	224	208	2		

- Molecule 64 is a protein called uS11 (yeast S14).

Mol	Chain	Residues	Atoms				AltConf	Trace
64	LB	127	Total	C	N	O	0	0
			508	254	127	127		

- Molecule 65 is a protein called uS19 (yeast S15).

Mol	Chain	Residues	Atoms					AltConf	Trace
65	MB	122	Total	C	N	O	S	0	0
			975	622	182	164	7		

- Molecule 66 is a protein called uS9 (yeast S16).

Mol	Chain	Residues	Atoms				AltConf	Trace
66	NB	141	Total	C	N	O	0	0
			1106	708	203	195		

- Molecule 67 is a protein called eS17 (yeast S17).

Mol	Chain	Residues	Atoms					AltConf	Trace
67	OB	117	Total	C	N	O	S	0	0
			836	515	166	153	2		

- Molecule 68 is a protein called uS13 (yeast S18).

Mol	Chain	Residues	Atoms					AltConf	Trace
68	PB	145	Total	C	N	O	S	0	0
			1193	743	237	211	2		

- Molecule 69 is a protein called eS19 (yeast S19).

Mol	Chain	Residues	Atoms					AltConf	Trace
69	QB	143	Total	C	N	O	S	0	0
			1113	694	208	209	2		

- Molecule 70 is a protein called uS10 (yeast S20).

Mol	Chain	Residues	Atoms					AltConf	Trace
70	RB	107	Total	C	N	O	S	0	0
			856	539	156	160	1		

- Molecule 71 is a protein called eS21 (yeast S21).

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

- Molecule 72 is a protein called uS8 (yeast S22).

Mol	Chain	Residues	Atoms					AltConf	Trace
72	TB	129	Total	C	N	O	S	0	0
			1022	650	188	181	3		

- Molecule 73 is a protein called uS12 (yeast S23).

Mol	Chain	Residues	Atoms					AltConf	Trace
73	UB	144	Total	C	N	O	S	0	0
			1122	708	220	192	2		

- Molecule 74 is a protein called eS24 (yeast S24).

Mol	Chain	Residues	Atoms				AltConf	Trace
74	VB	134	Total	C	N	O	0	0
			1074	676	208	190		

- Molecule 75 is a protein called eS25 (yeast S25).

Mol	Chain	Residues	Atoms				AltConf	Trace
75	WB	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 76 is a protein called eS26 (yeast S26).

Mol	Chain	Residues	Atoms				AltConf	Trace
76	XB	97	Total	C	N	O	0	0
			388	194	97	97		

- Molecule 77 is a protein called eS27 (yeast S27).

Mol	Chain	Residues	Atoms					AltConf	Trace
77	YB	81	Total	C	N	O	S	0	0
			611	382	110	114	5		

- Molecule 78 is a protein called eS28 (yeast S28).

Mol	Chain	Residues	Atoms					AltConf	Trace
78	ZB	63	Total	C	N	O	S	0	0
			498	306	99	92	1		

- Molecule 79 is a protein called uS14 (yeast S29).

Mol	Chain	Residues	Atoms					AltConf	Trace
79	AC	53	Total	C	N	O	S	0	0
			444	275	92	73	4		

- Molecule 80 is a protein called eS30 (yeast S30).

Mol	Chain	Residues	Atoms					AltConf	Trace
80	BC	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 81 is a protein called eS31 (yeast S31).

Mol	Chain	Residues	Atoms				AltConf	Trace
81	CC	71	Total	C	N	O	0	0
			284	142	71	71		

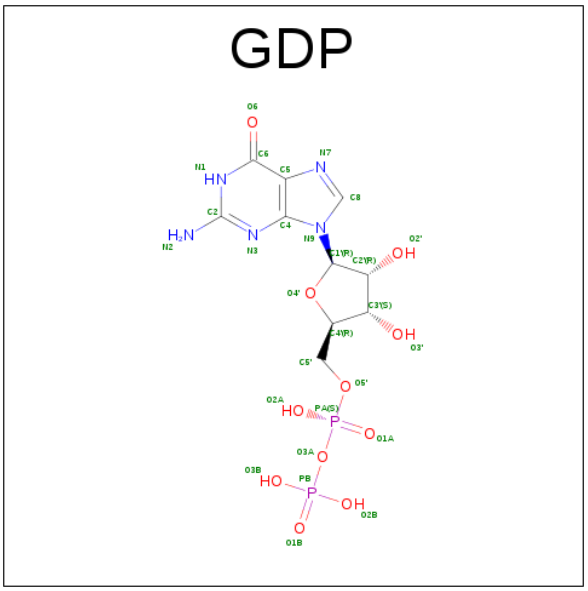
- Molecule 82 is a protein called yeast eEF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	DC	824	Total	C	N	O	S	0	0
			6419	4085	1096	1208	30		

- Molecule 83 is a RNA chain called IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	EC	198	Total	C	N	O	P	0	0
			4129	1839	725	1367	198		

- Molecule 84 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

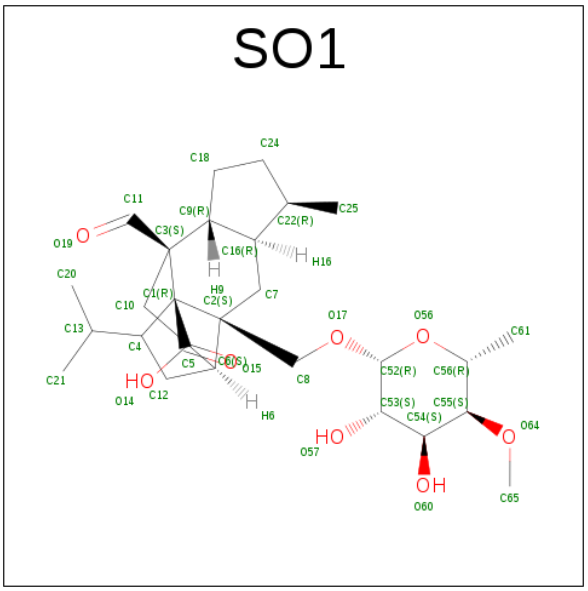


Mol	Chain	Residues	Atoms					AltConf
84	DC	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 85 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	DC	1	Total	Mg	0
			1	1	

- Molecule 86 is [1R-(1.ALPHA.,3A.BETA.,4.BETA.,4A.BETA.,7.BETA.,7A.ALPHA.,8A.BETA.)]8A-[(6-DEOXY-4-O-METHYL-BETA-D-ALTROPYRANOSYLOXY)METHYL]-4-FORMYL-4,4A,5,6,7,7A,8,8A-OCTAHYDRO-7-METHYL-3-(1-METHYLETHYL)-1,4-METHANO-S-INDACENE-3A(1H)-CARBOXYLIC ACID (three-letter code: SO1) (formula: $C_{27}H_{42}O_8$).



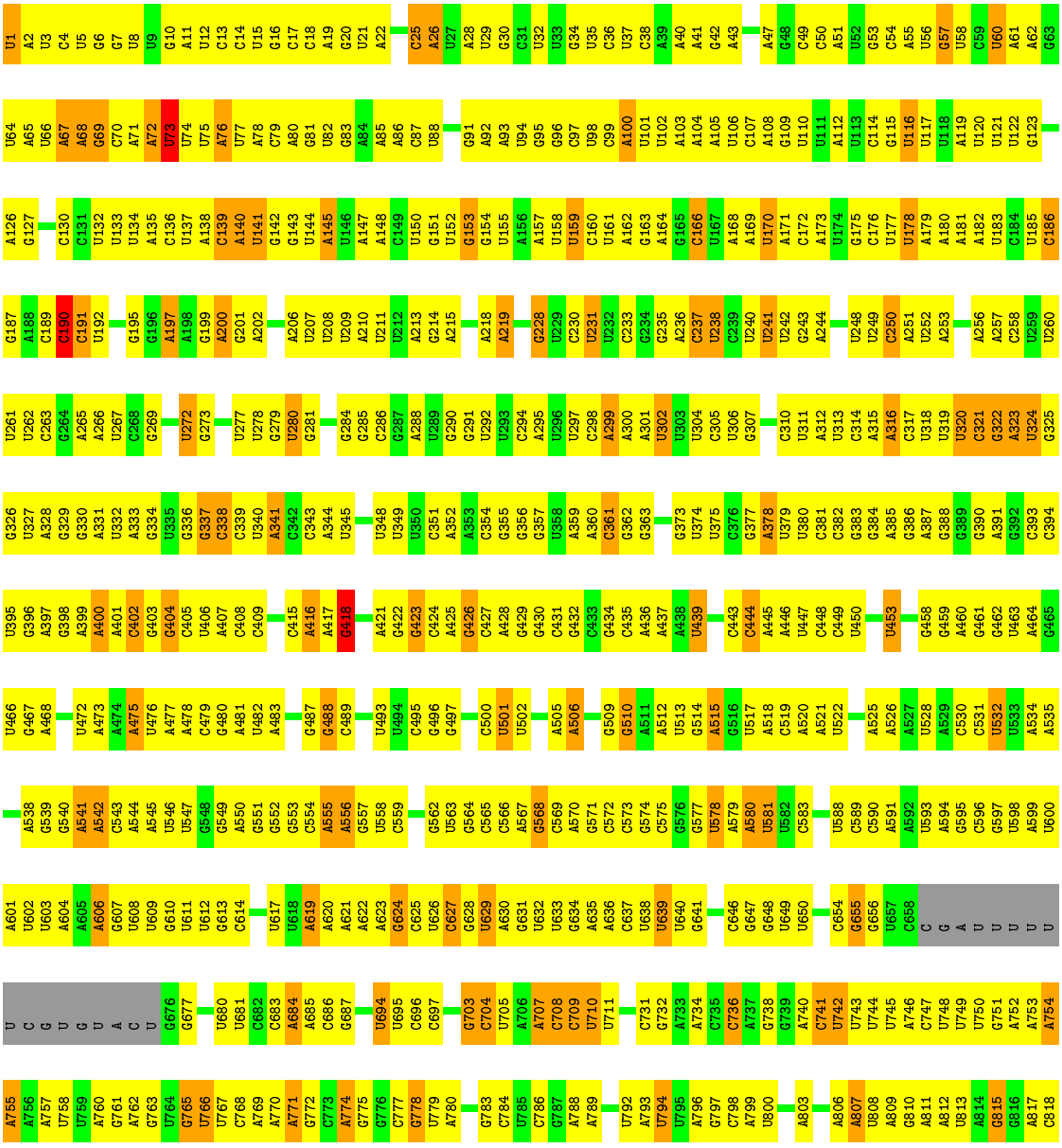
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
86	DC	1	35	27	8	0

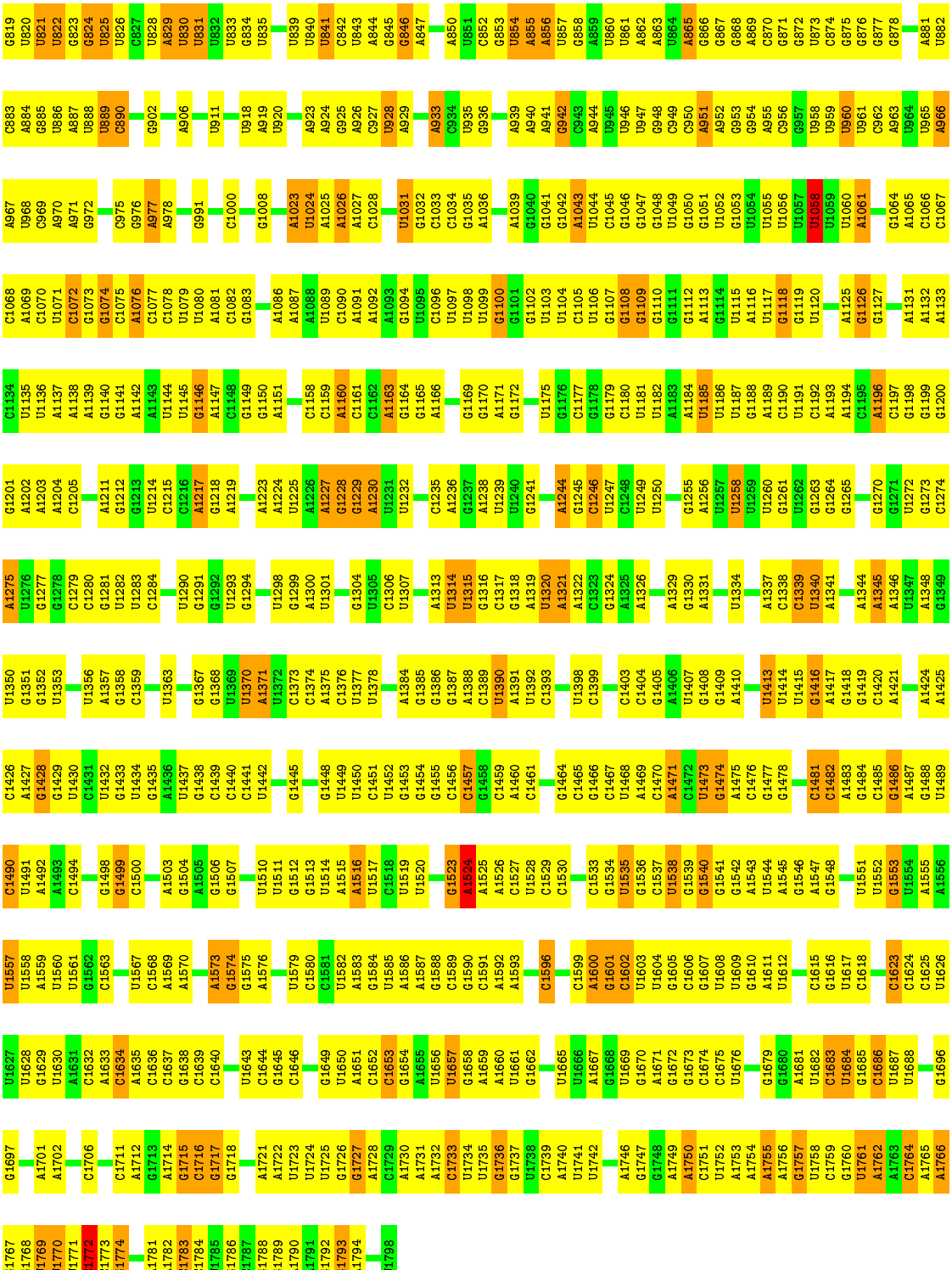
3 Residue-property plots (i)

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. 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. 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: 18S ribosomal RNA

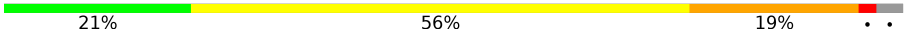
Chain A: 30% 57% 12%

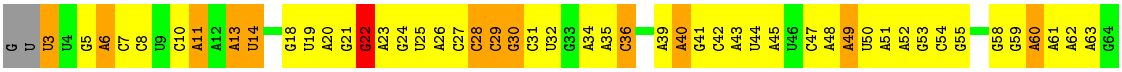


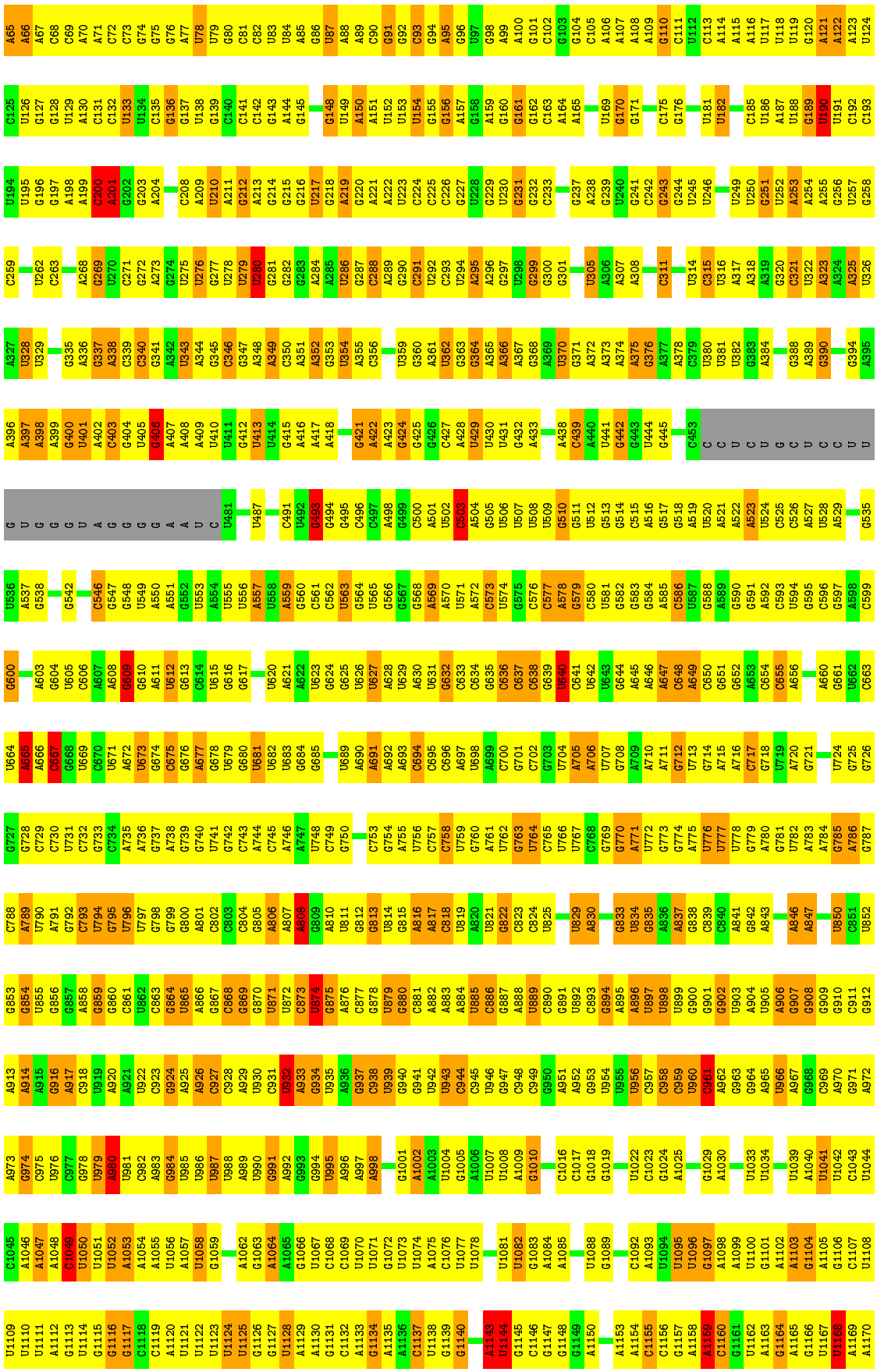


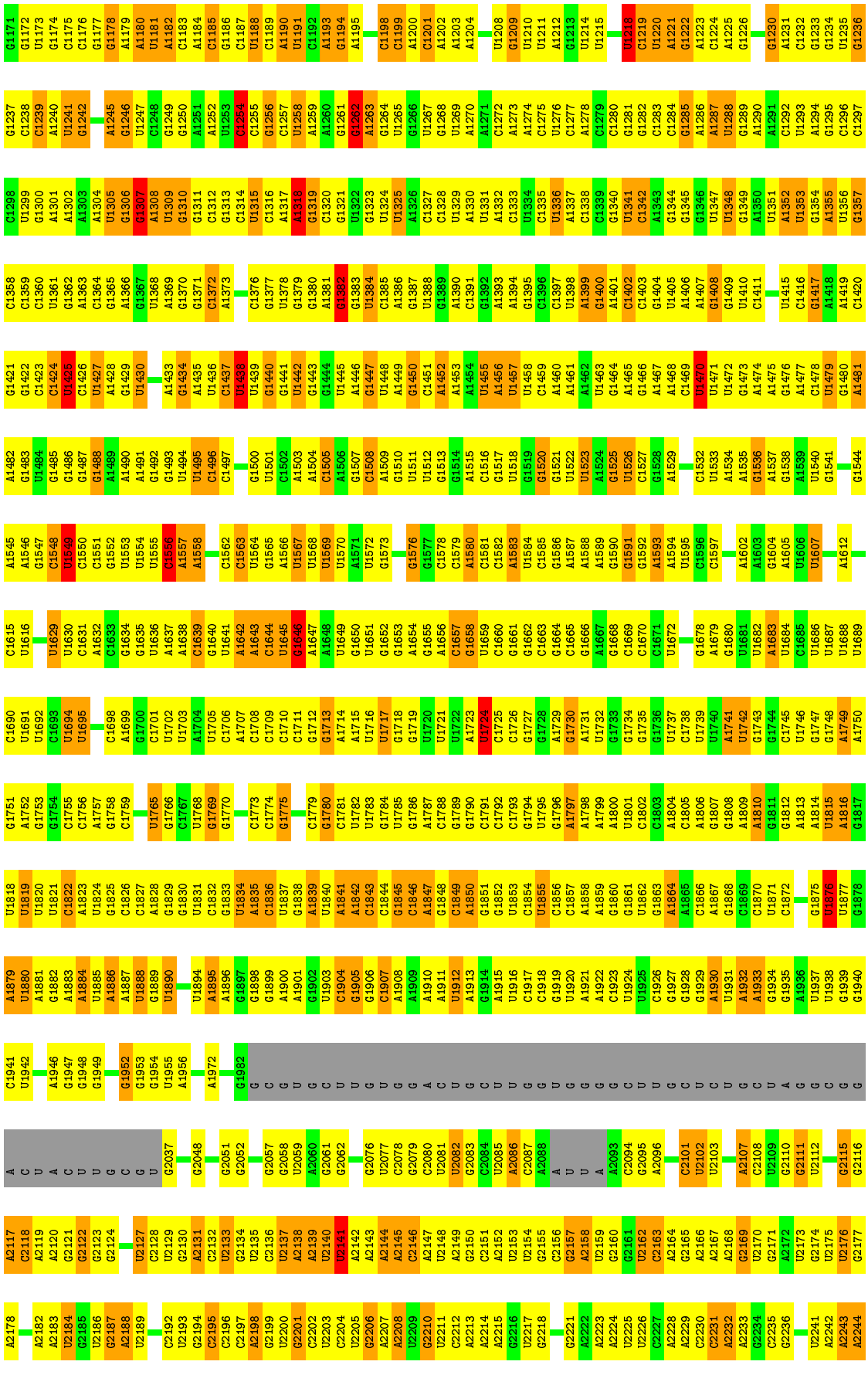
• Molecule 2: 25S ribosomal RNA

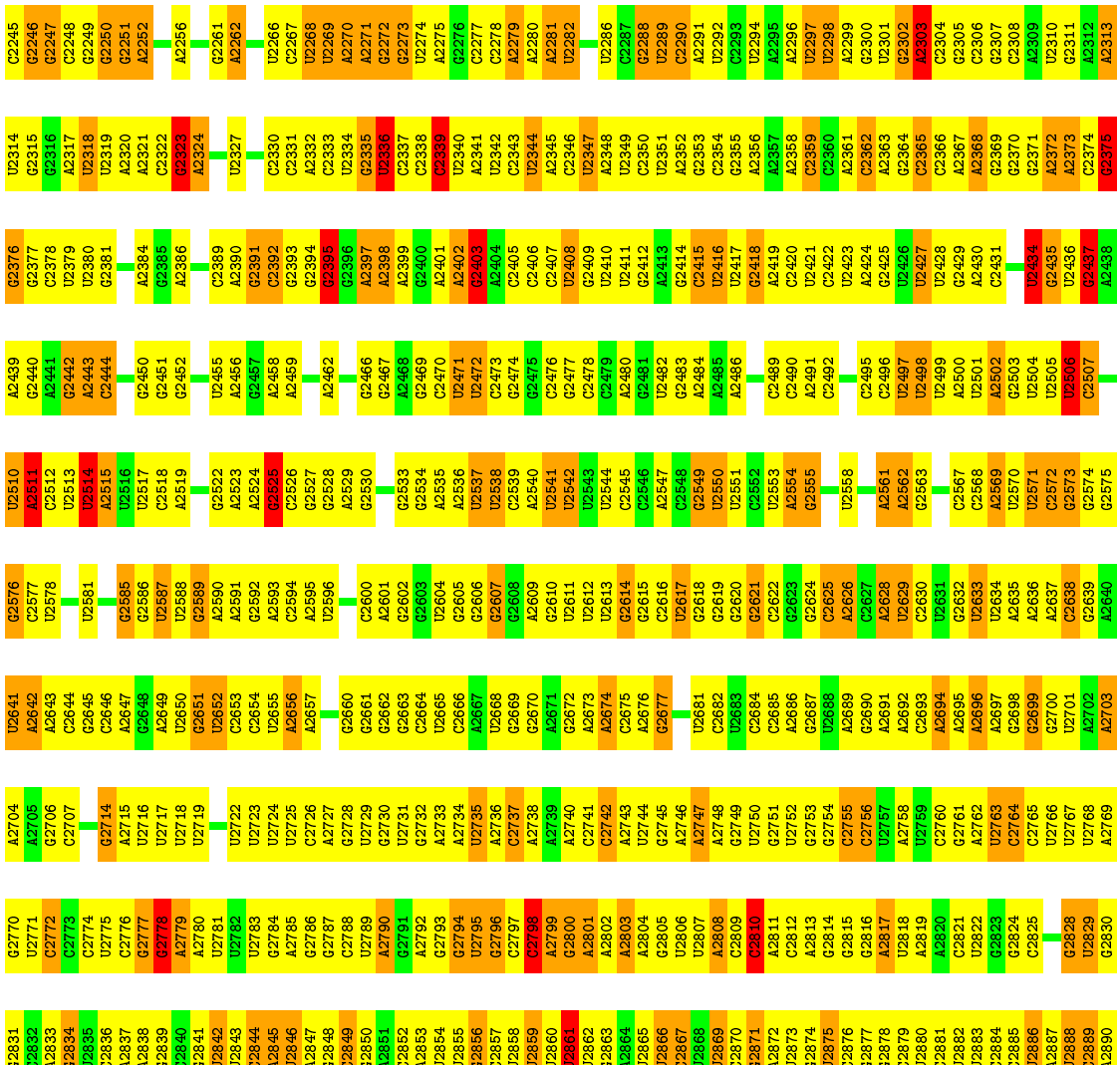
Chain B:

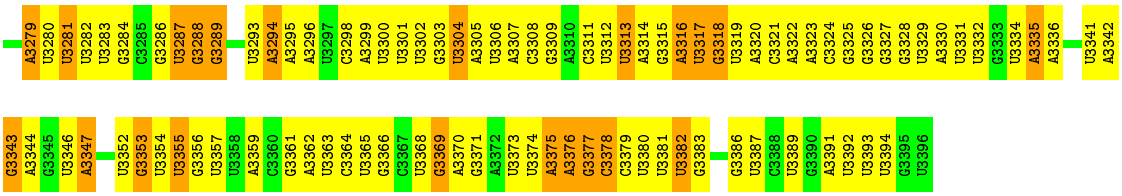






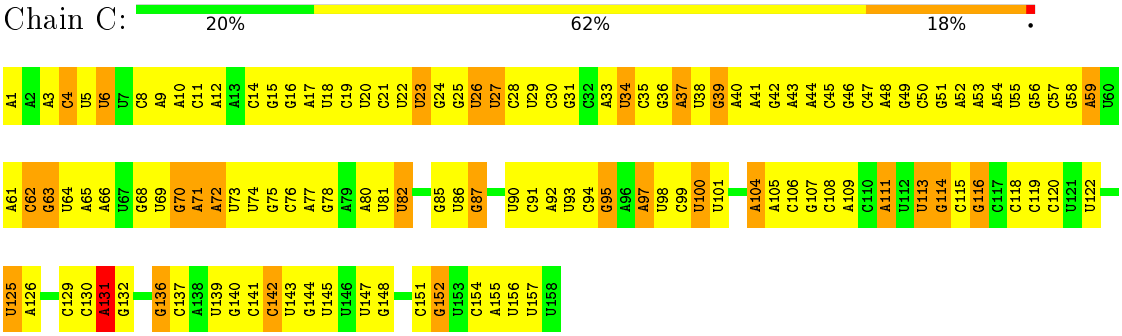






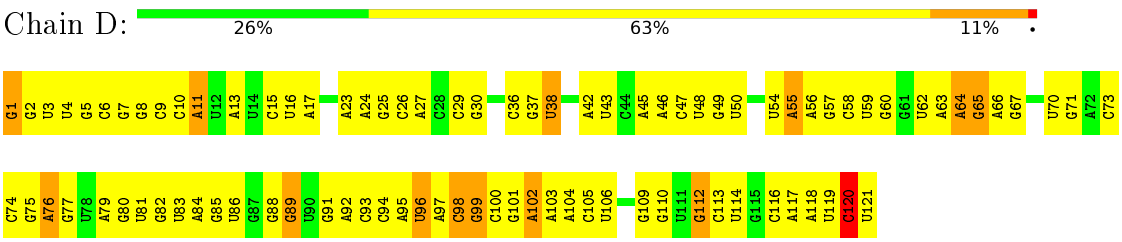
• Molecule 3: 5.8S ribosomal RNA

Chain C:



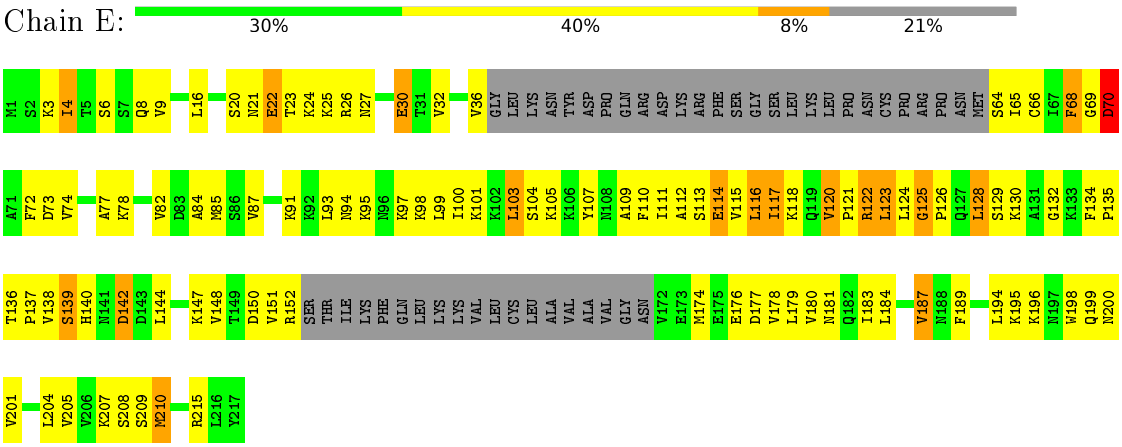
• Molecule 4: 5S ribosomal RNA

Chain D:



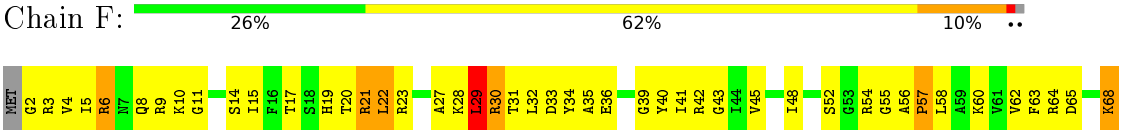
• Molecule 5: uL1 (yeast L1)

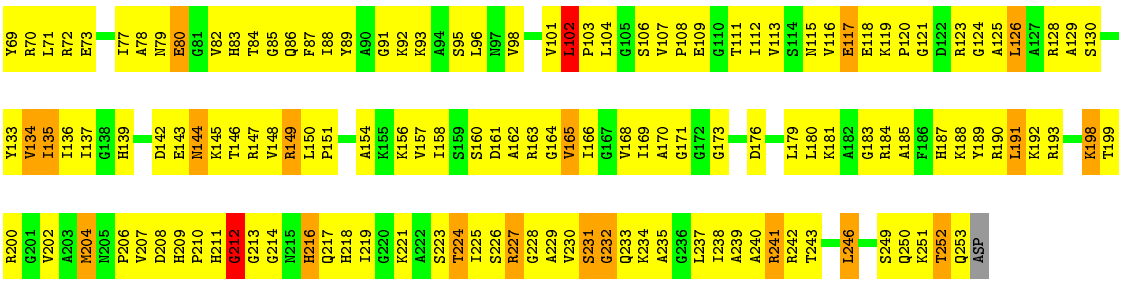
Chain E:



• Molecule 6: uL2 (yeast L2)

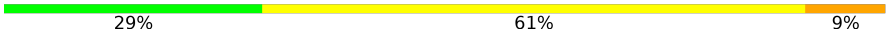
Chain F:

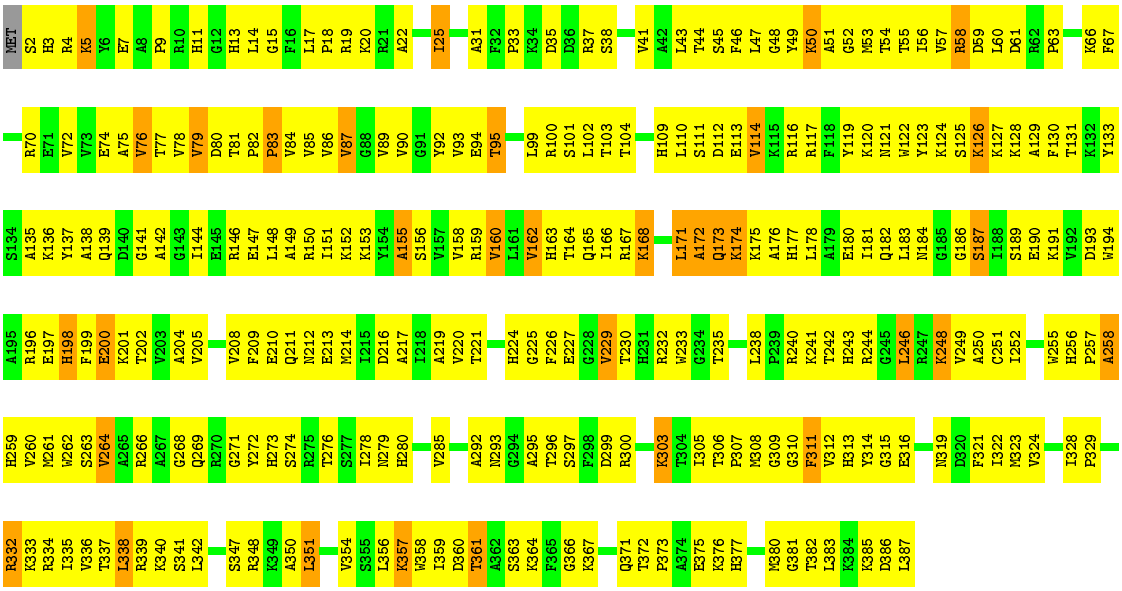




• Molecule 7: uL3 (yeast L3)

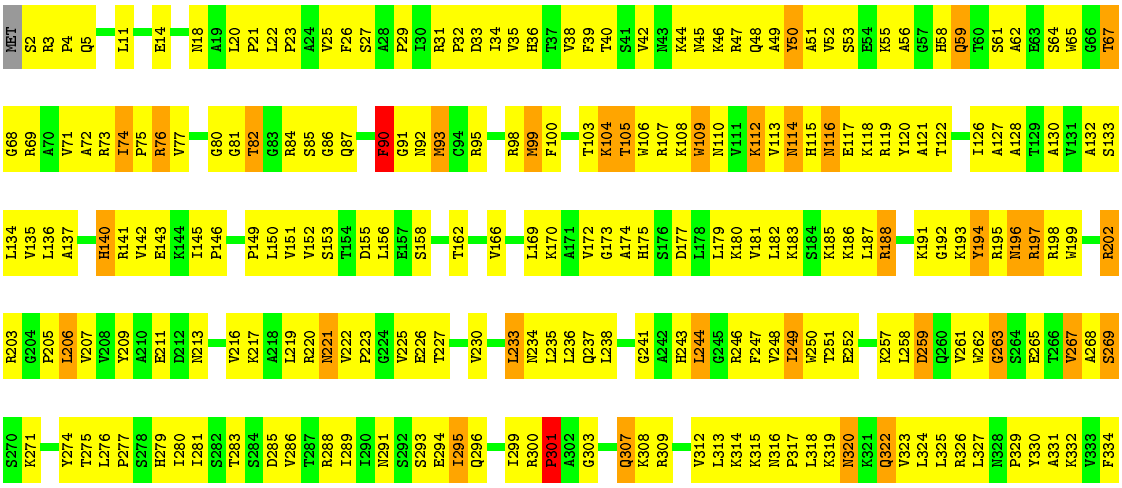
Chain G:

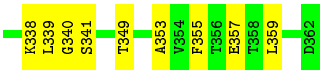




• Molecule 8: uL4 (yeast L4)

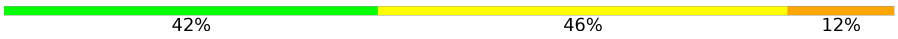
Chain H:

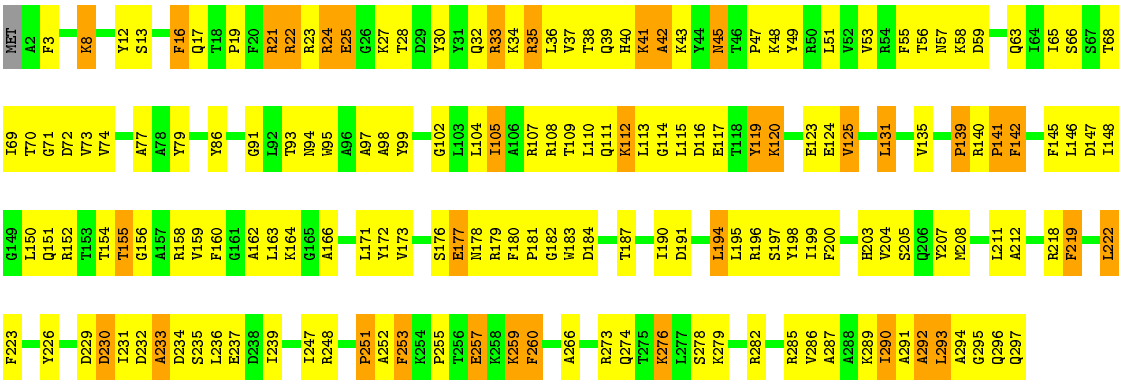




- Molecule 9: uL18 (yeast L5)

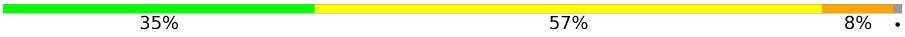
Chain I:

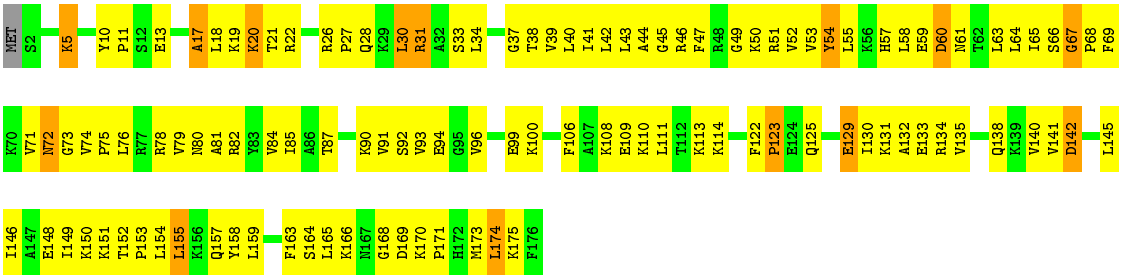




- Molecule 10: eL6 (yeast L6)

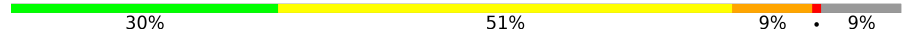
Chain J:

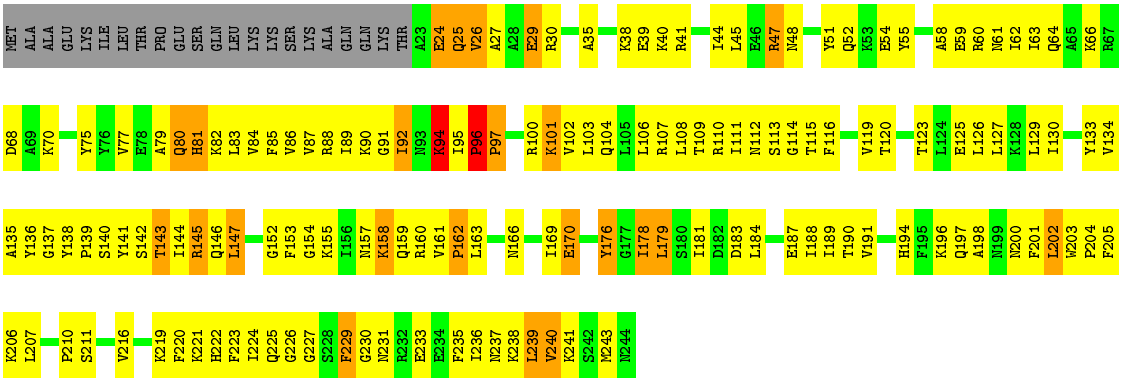




- Molecule 11: uL30 (yeast L7)

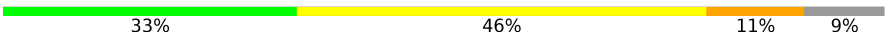
Chain K:

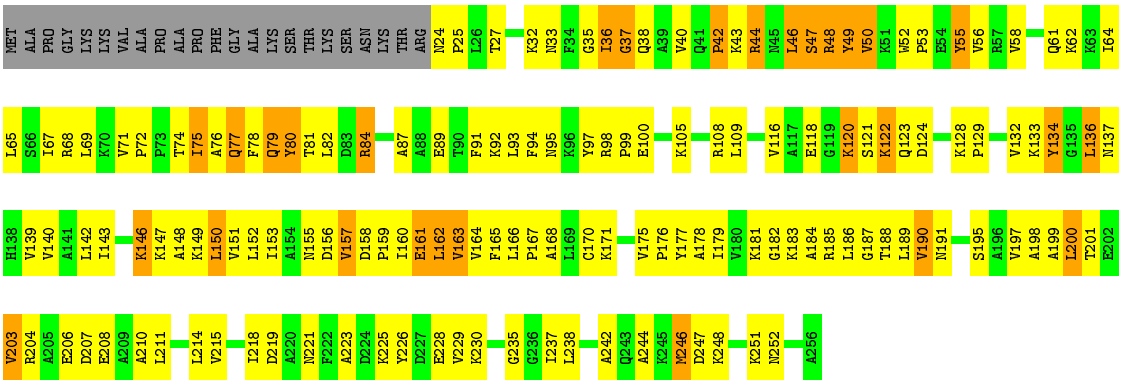




- Molecule 12: eL8 (yeast L8)

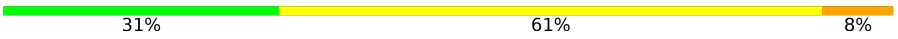
Chain L:

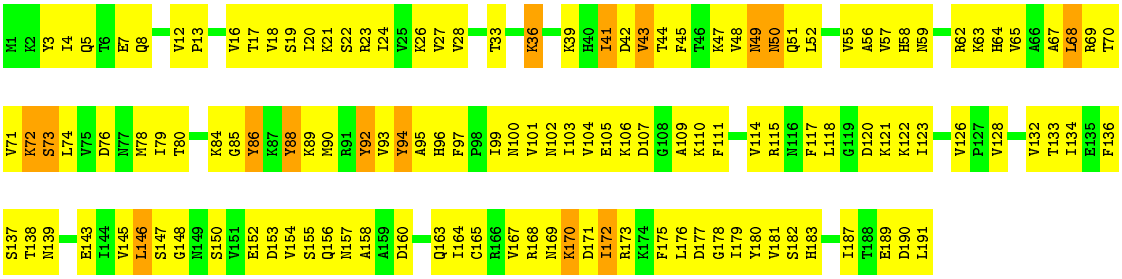




- Molecule 13: uL6 (yeast L9)

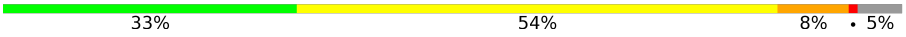
Chain M:

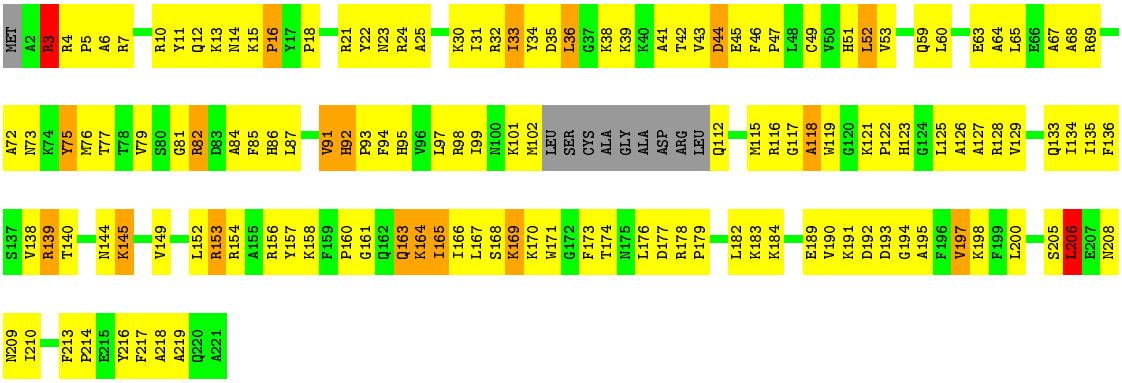




- Molecule 14: uL16 (yeast L10)

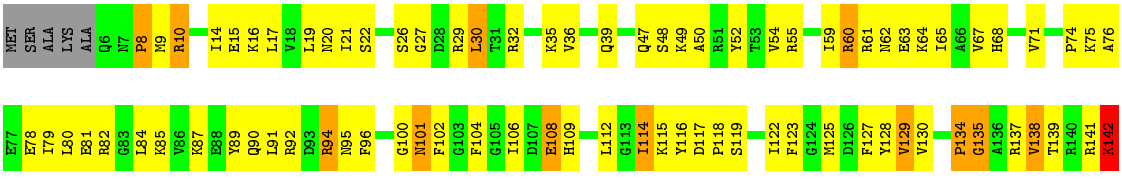
Chain N:





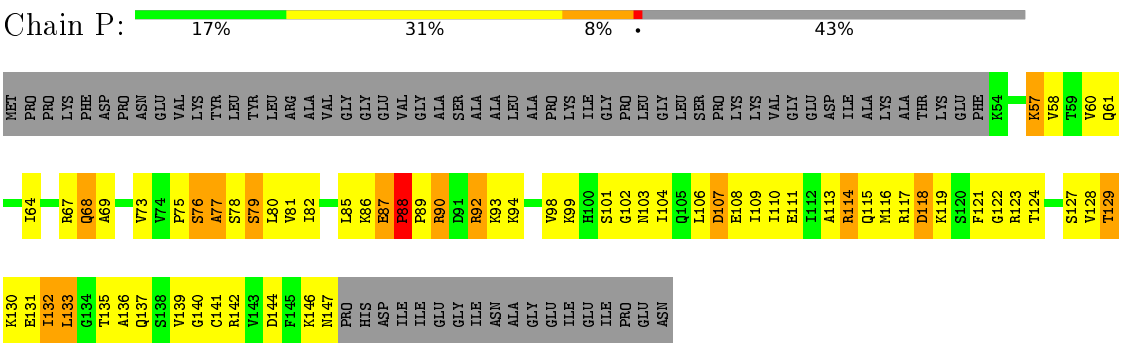
- Molecule 15: uL5 (yeast L11)

Chain O:



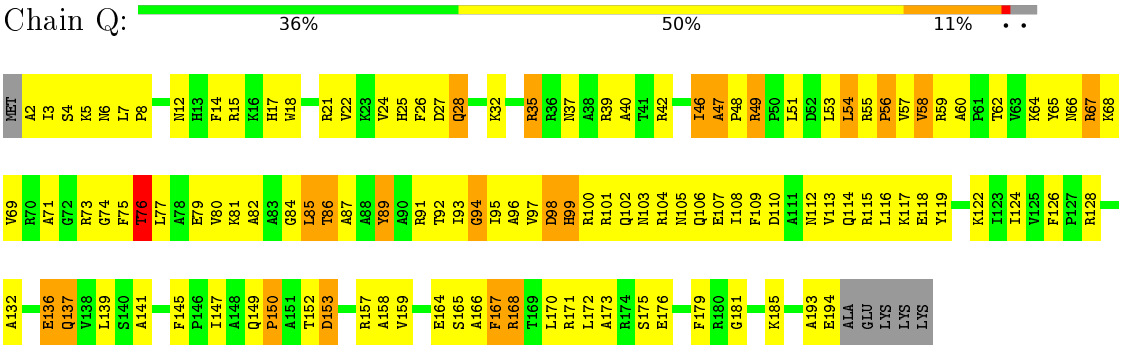
- Molecule 16: uL11 (yeast L12)

Chain P:



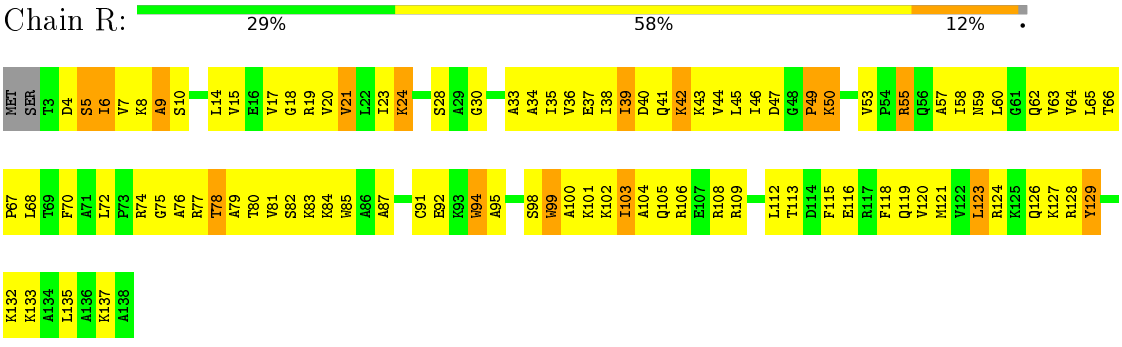
- Molecule 17: eL13 (yeast L13)

Chain Q:



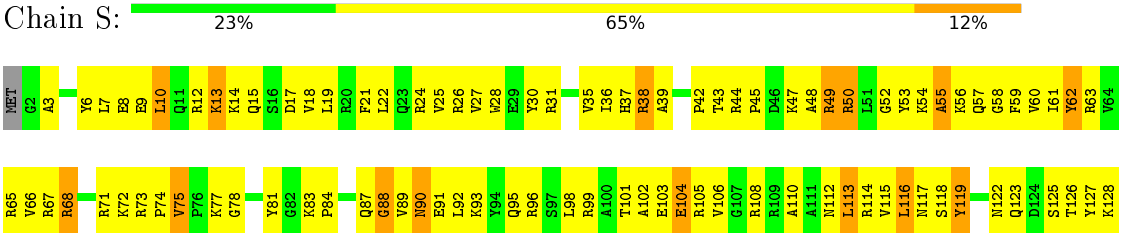
- Molecule 18: eL14 (yeast L14)

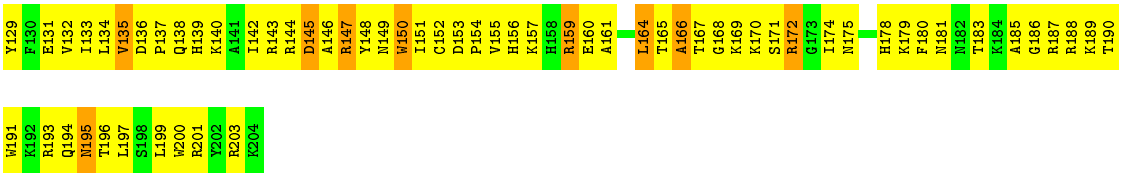
Chain R:



- Molecule 19: eL15 (yeast L15)

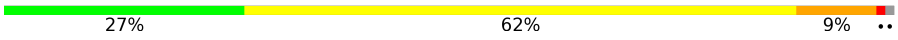
Chain S:

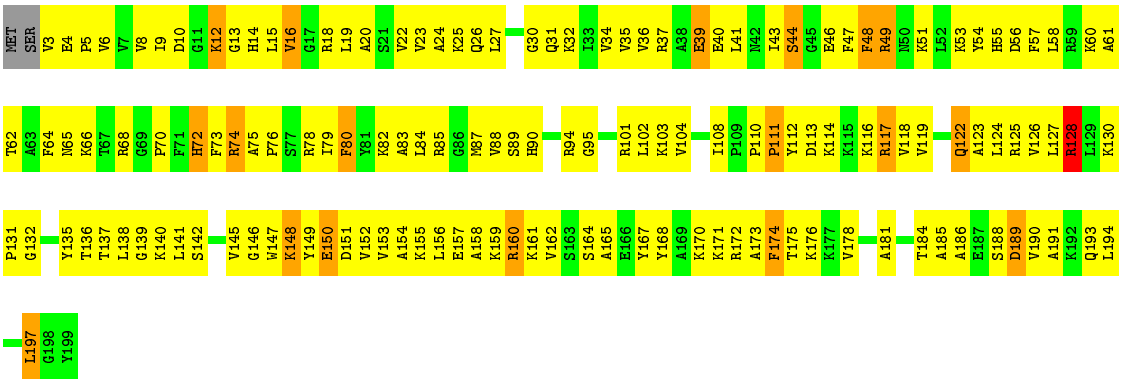




• Molecule 20: uL13 (yeast L16)

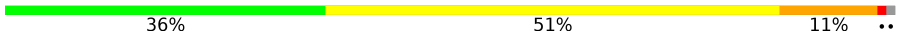
Chain T:

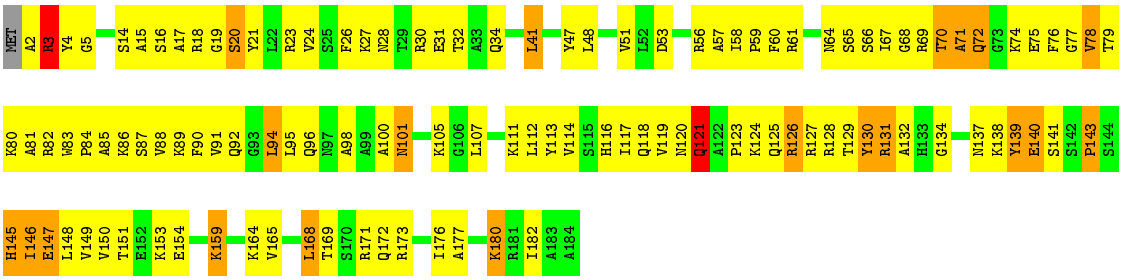




• Molecule 21: uL22 (yeast L17)

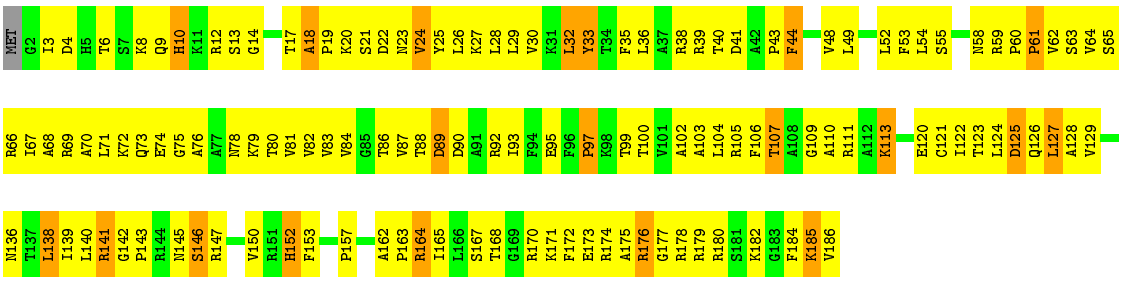
Chain U:





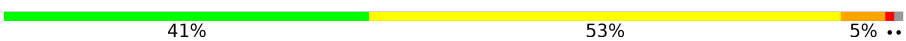
• Molecule 22: eL18 (yeast L18)

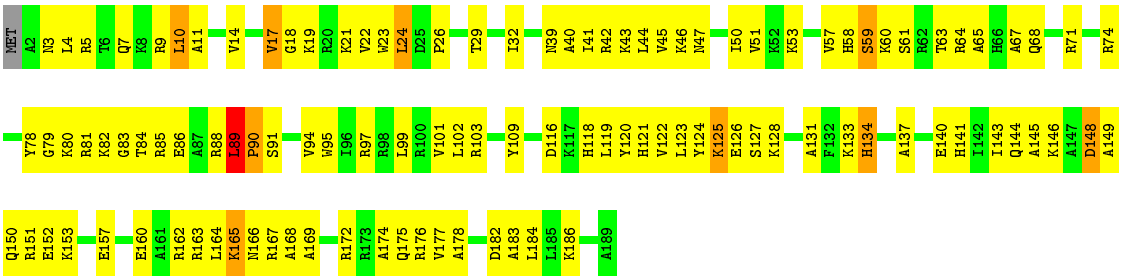
Chain V:



• Molecule 23: eL19 (yeast L19)

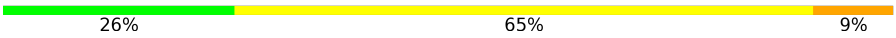
Chain W:

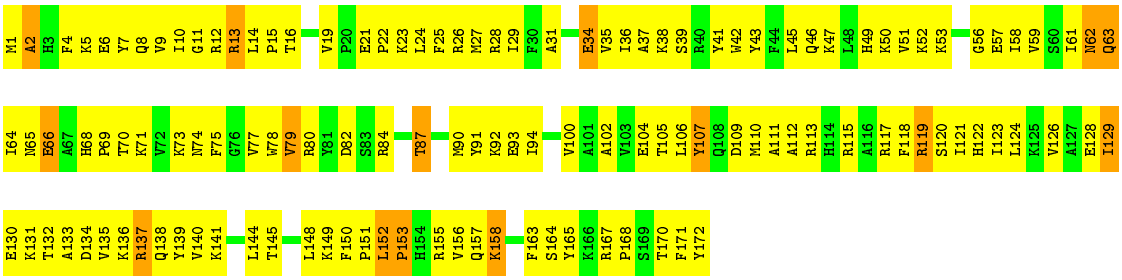




- Molecule 24: eL20 (yeast L20)

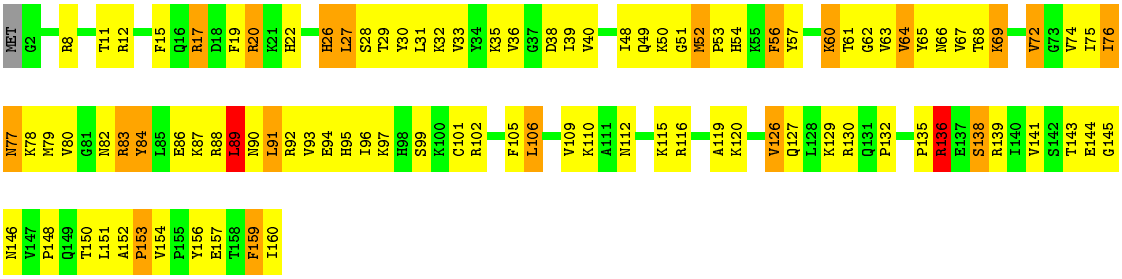
Chain X:





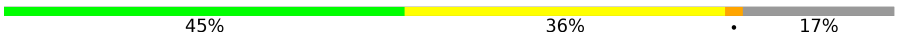
- Molecule 25: eL21 (yeast L21)

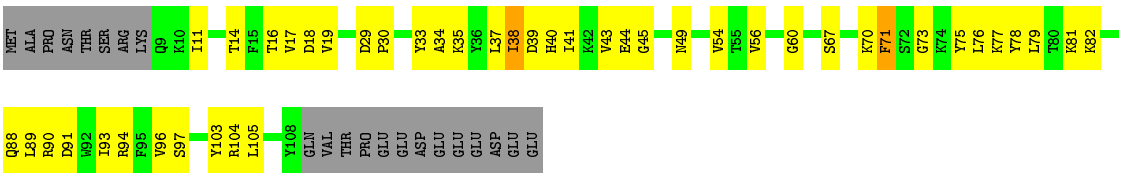
Chain Y:



- Molecule 26: eL22 (yeast L22)

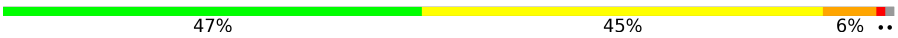
Chain Z:

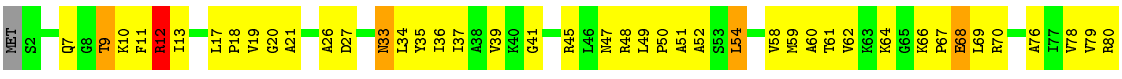


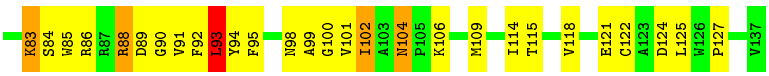


- Molecule 27: uL14 (yeast L23)

Chain AA:

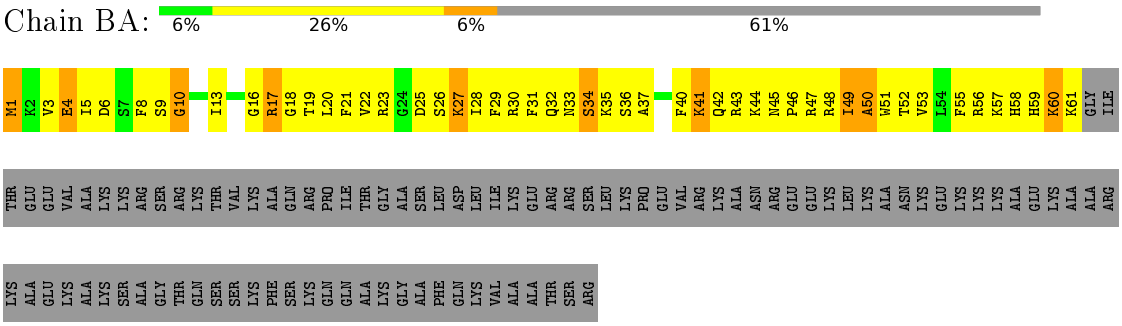






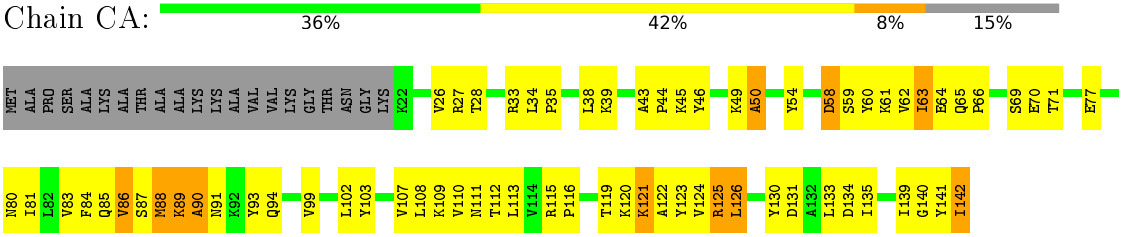
- Molecule 28: eL24 (yeast L24)

Chain BA:



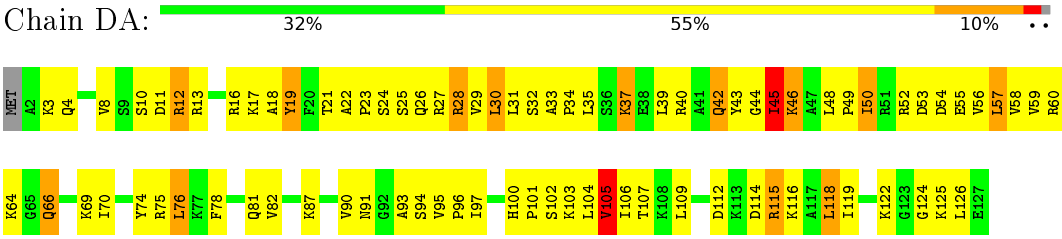
- Molecule 29: uL23 (yeast L25)

Chain CA:



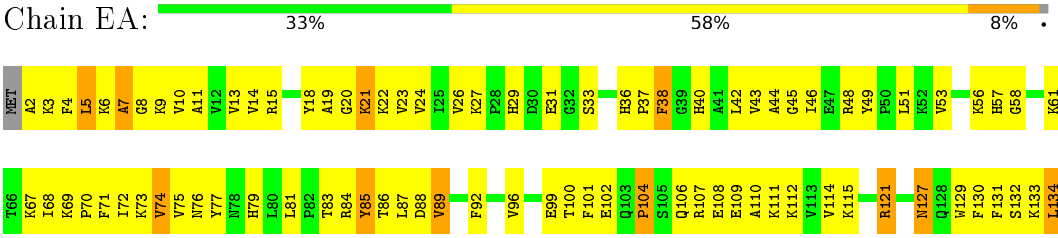
- Molecule 30: uL24 (yeast L26)

Chain DA:



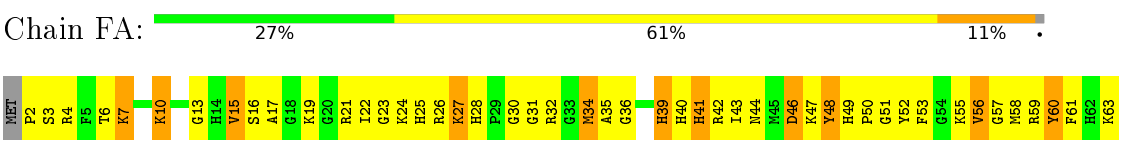
- Molecule 31: eL27 (yeast L27)

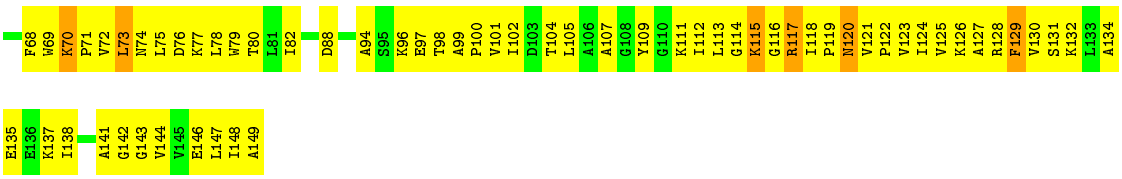
Chain EA:



- Molecule 32: uL15 (yeast L28)

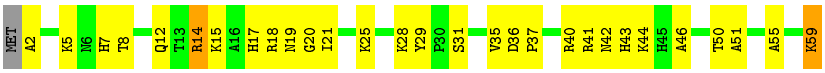
Chain FA:





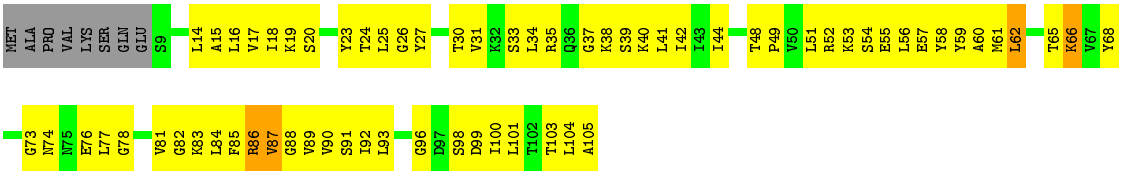
- Molecule 33: eL29 (yeast L29)

Chain GA:



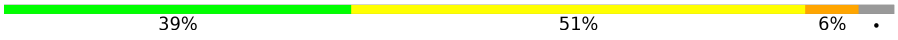
- Molecule 34: eL30 (yeast L30)

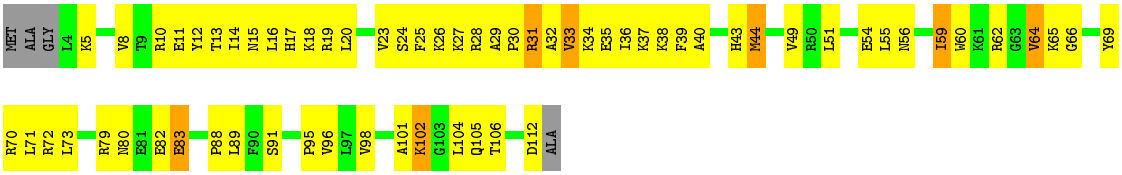
Chain HA:



- Molecule 35: eL31 (yeast L31)

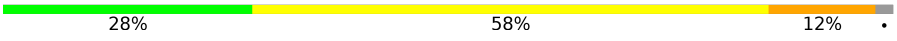
Chain IA:





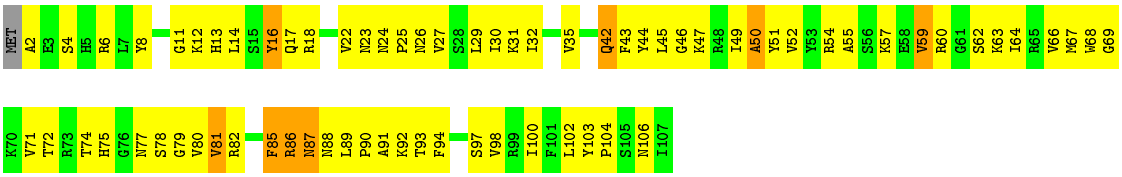
- Molecule 36: eL32 (yeast L32)

Chain JA:



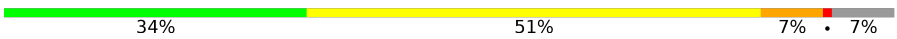
- Molecule 37: eL33 (yeast L33)

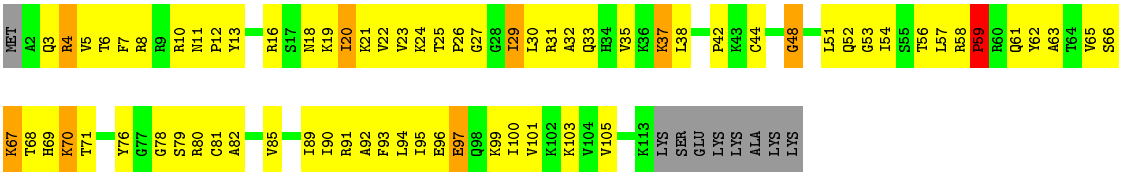
Chain KA:



- Molecule 38: eL34 (yeast L34)

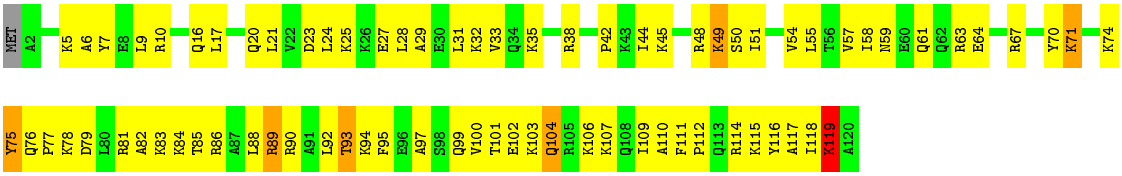
Chain LA:





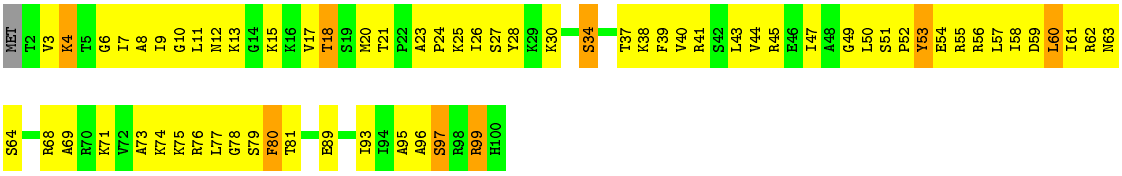
- Molecule 39: uL29 (yeast L35)

Chain MA:



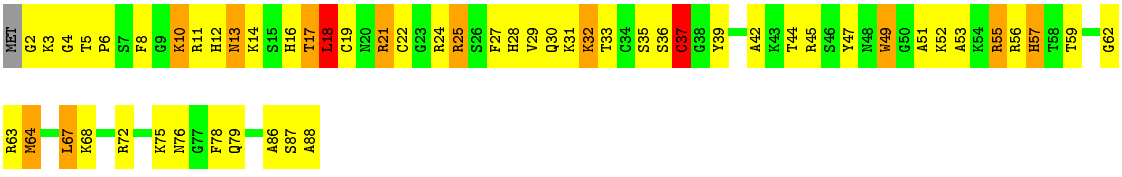
- Molecule 40: eL36 (yeast L36)

Chain NA:



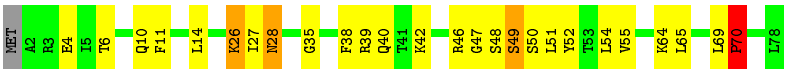
- Molecule 41: eL37 (yeast L37)

Chain OA:

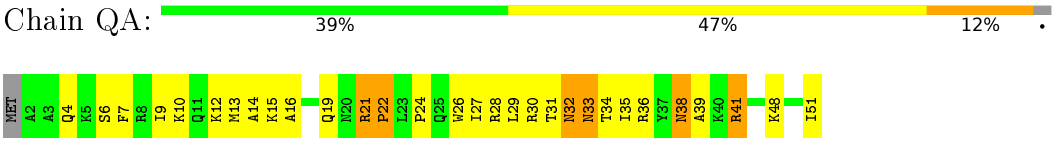


- Molecule 42: eL38 (yeast L38)

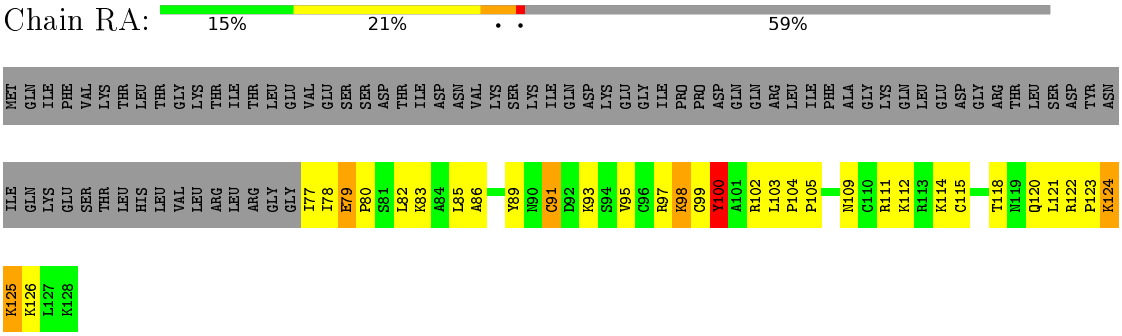
Chain PA:



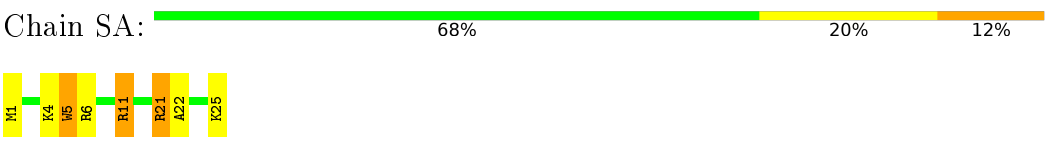
- Molecule 43: eL39 (yeast L39)



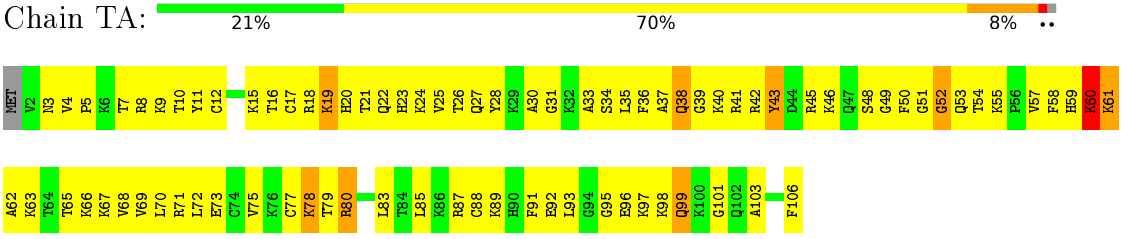
- Molecule 44: eL40 (yeast L40)



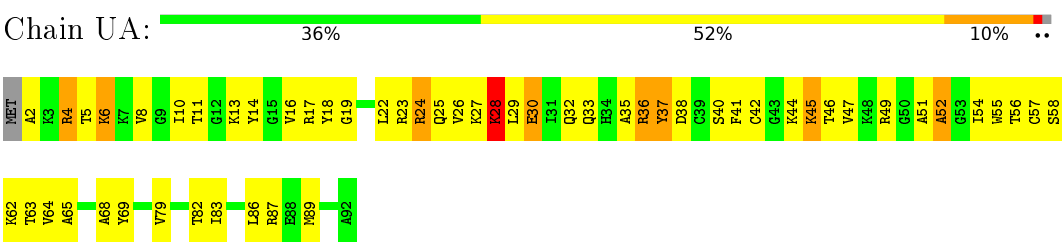
- Molecule 45: eL41 (yeast L41)



- Molecule 46: eL42 (yeast L42)

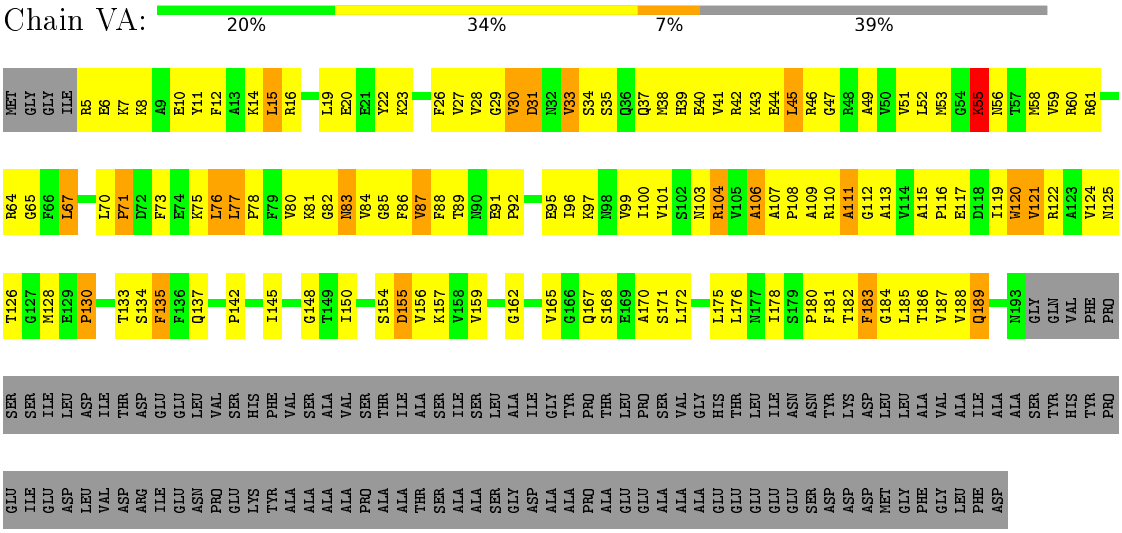


- Molecule 47: eL43 (yeast L43)



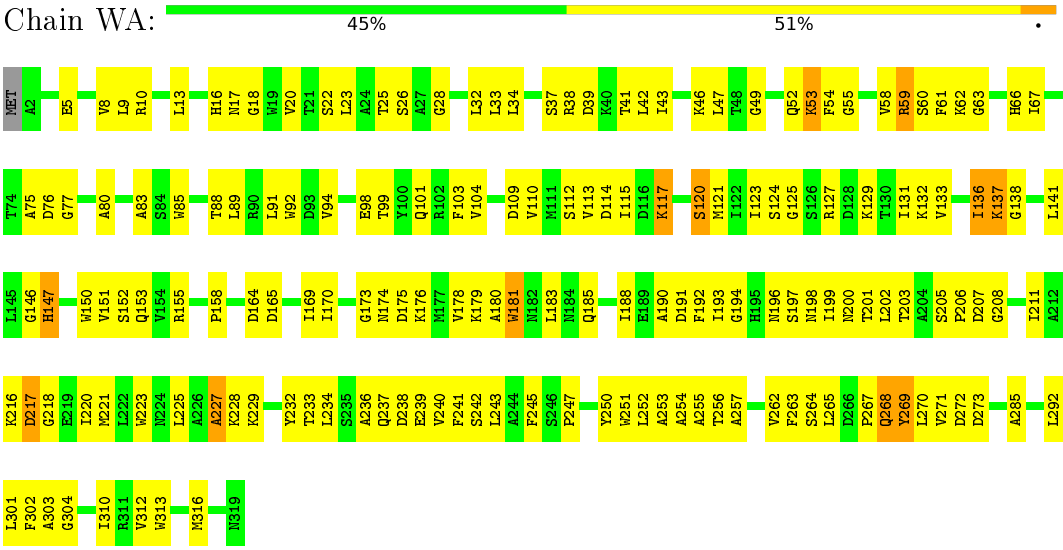
- Molecule 48: uL10 (yeast P0)

Chain VA:



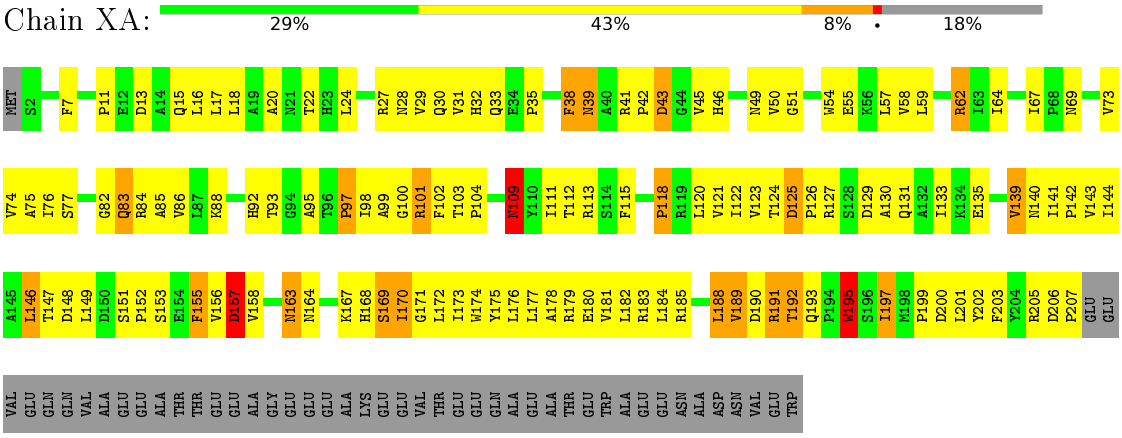
- Molecule 49: RACK1 (yeast Asc1)

Chain WA:



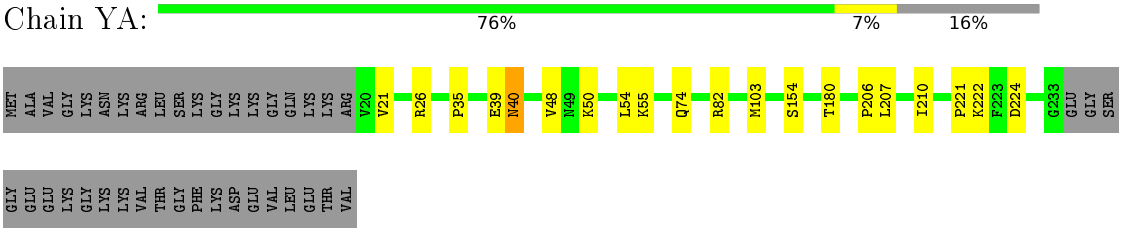
- Molecule 50: uS2 (yeast S0)

Chain XA:



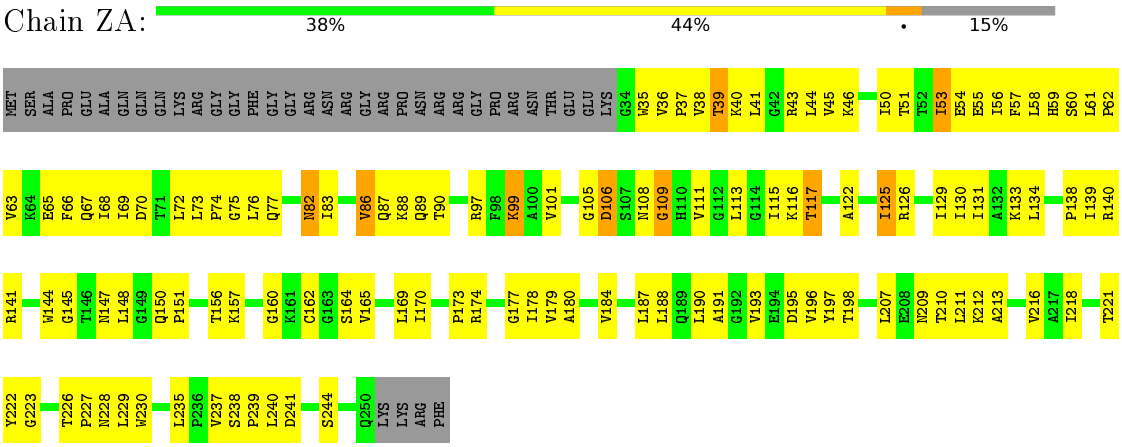
- Molecule 51: eS1 (yeast S1)

Chain YA:



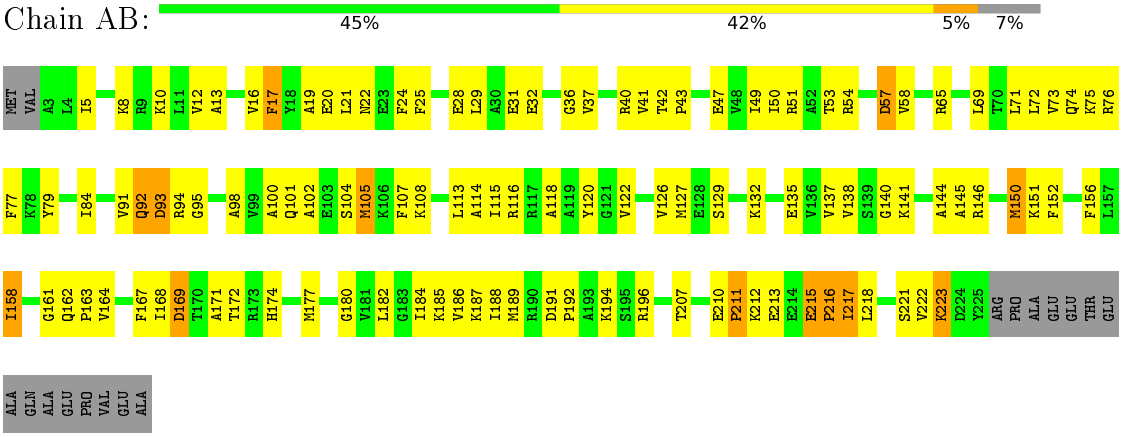
- Molecule 52: uS5 (yeast S2)

Chain ZA:



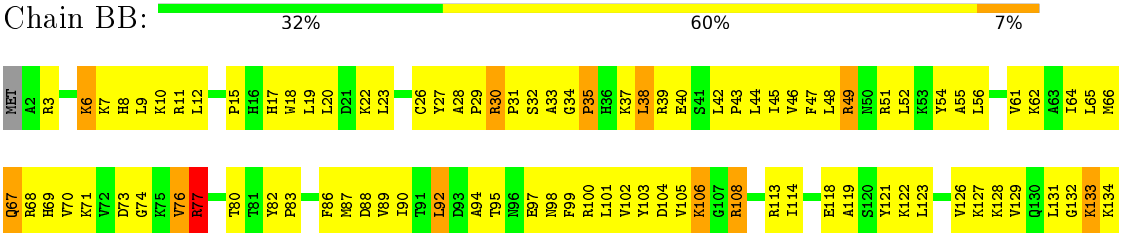
- Molecule 53: uS3 (yeast S3)

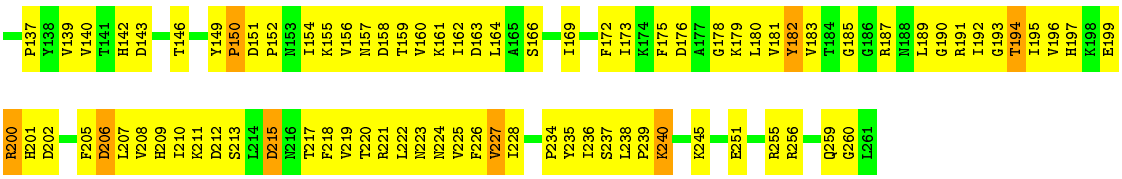
Chain AB:



- Molecule 54: eS4 (yeast S4)

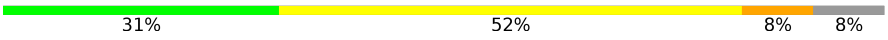
Chain BB:

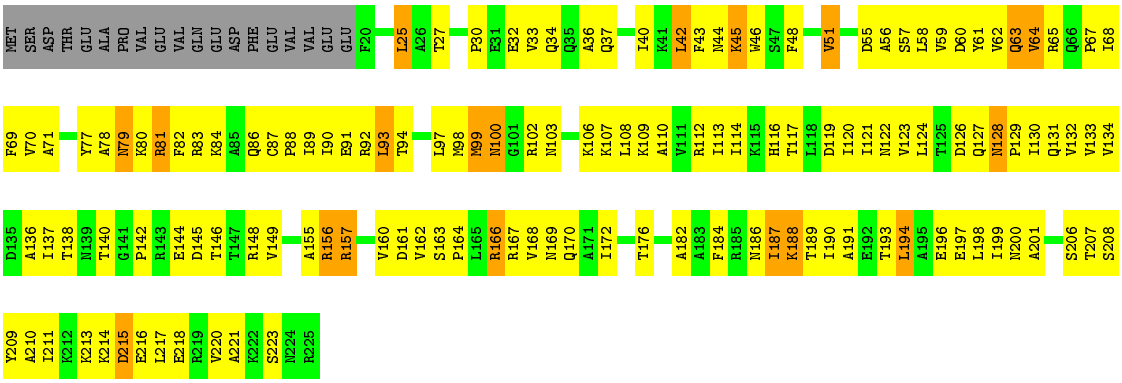




- Molecule 55: uS7 (yeast S5)

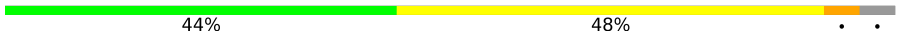
Chain CB:

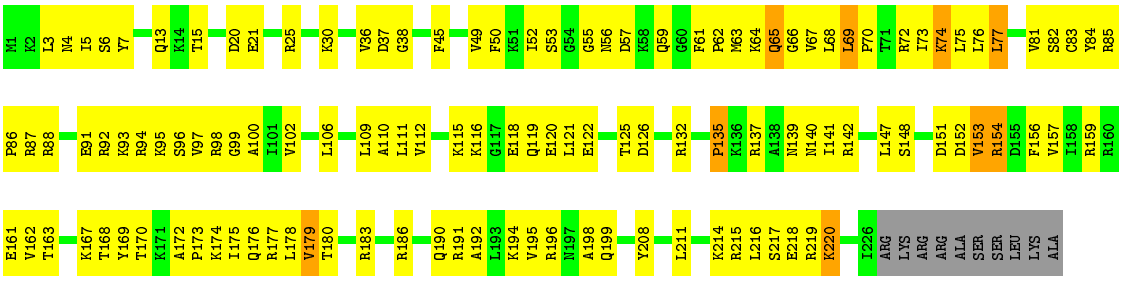




- Molecule 56: eS6 (yeast S6)

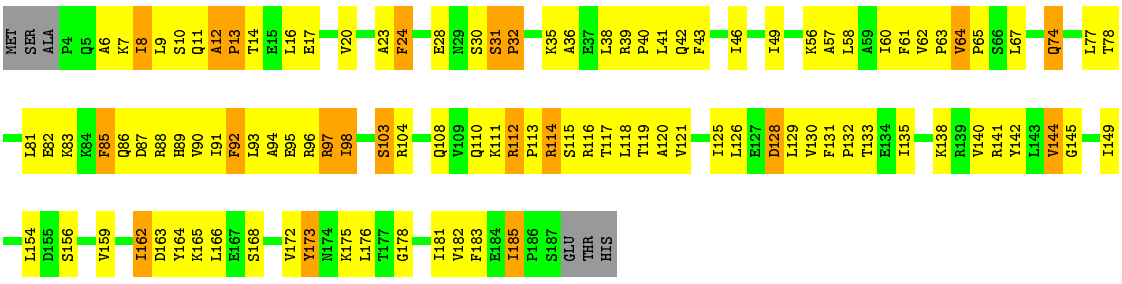
Chain DB:





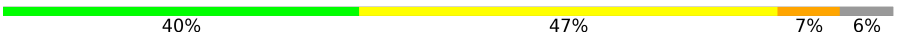
- Molecule 57: eS7 (yeast S7)

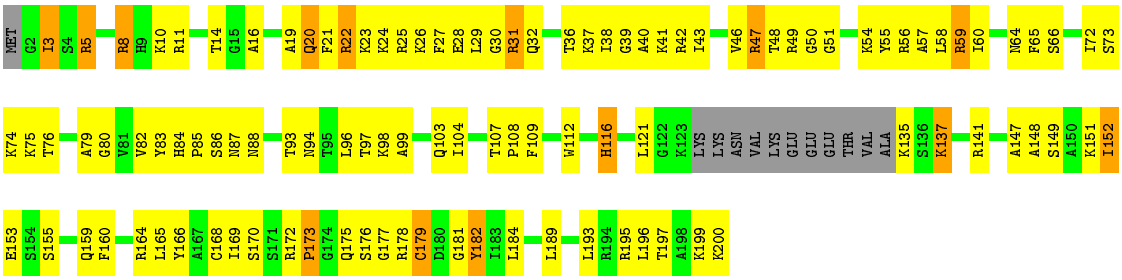
Chain EB:



- Molecule 58: eS8 (yeast S8)

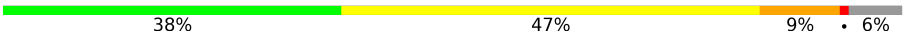
Chain FB:

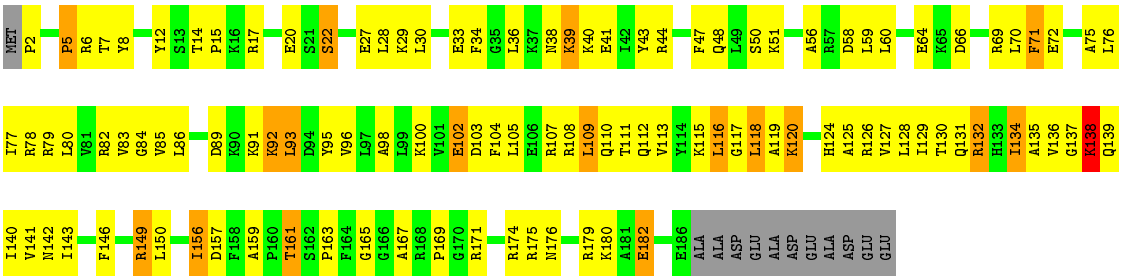




- Molecule 59: uS4 (yeast S9)

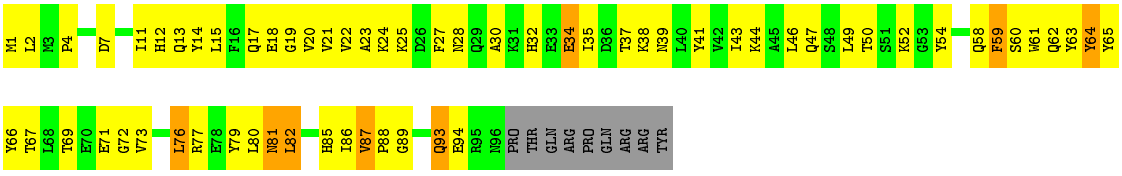
Chain GB:





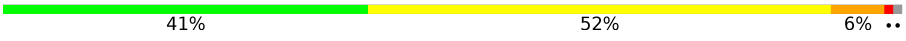
- Molecule 60: eS10 (yeast S10)

Chain HB:



- Molecule 61: uS17 (yeast S11)

Chain IB:

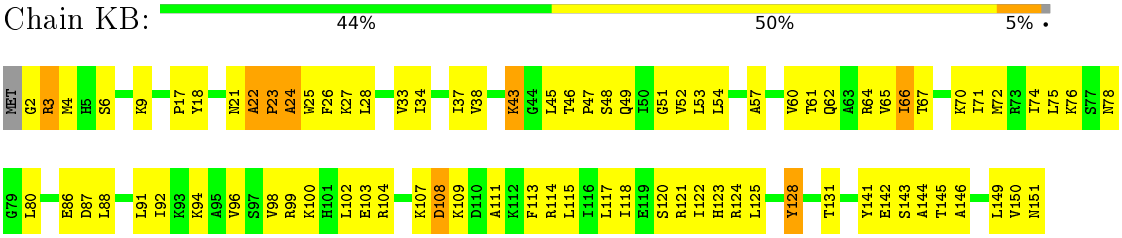


- Molecule 62: eS12 (yeast S12)

Chain JB:

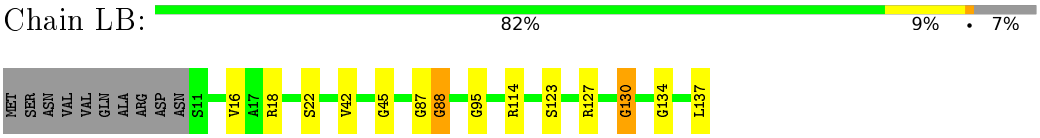
- Molecule 63: uS15 (yeast S13)

Chain KB:



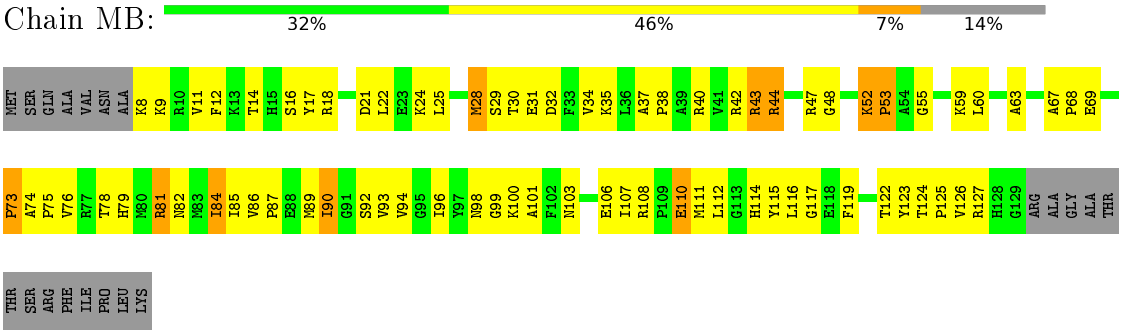
- Molecule 64: uS11 (yeast S14)

Chain LB:



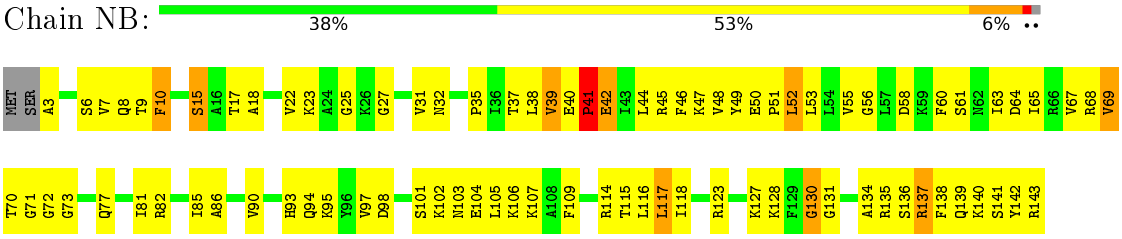
- Molecule 65: uS19 (yeast S15)

Chain MB:



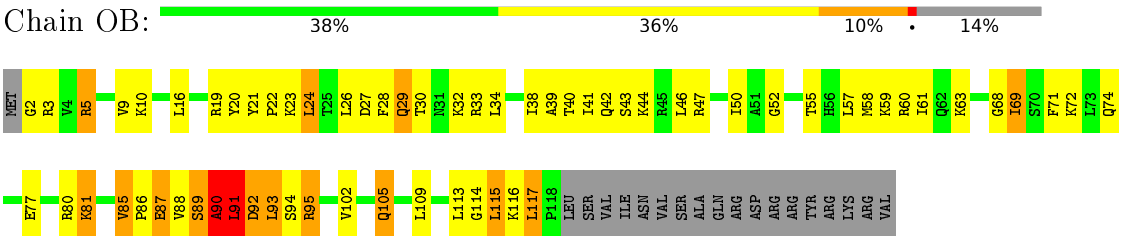
- Molecule 66: uS9 (yeast S16)

Chain NB:



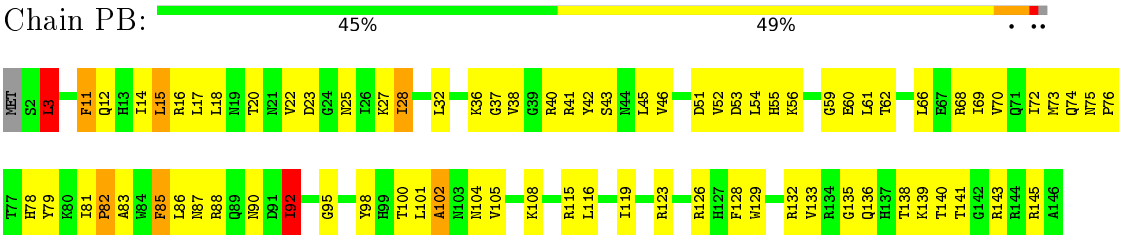
- Molecule 67: eS17 (yeast S17)

Chain OB:



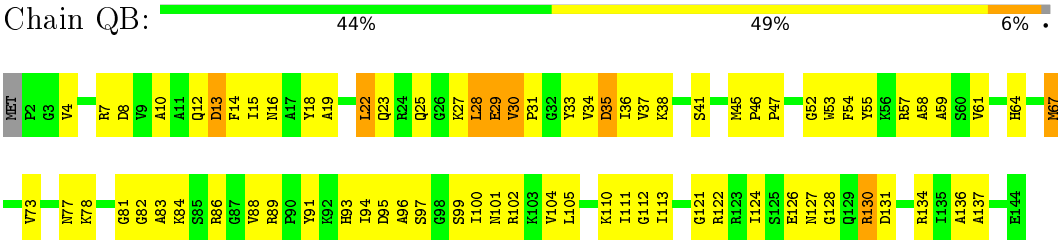
- Molecule 68: uS13 (yeast S18)

Chain PB:



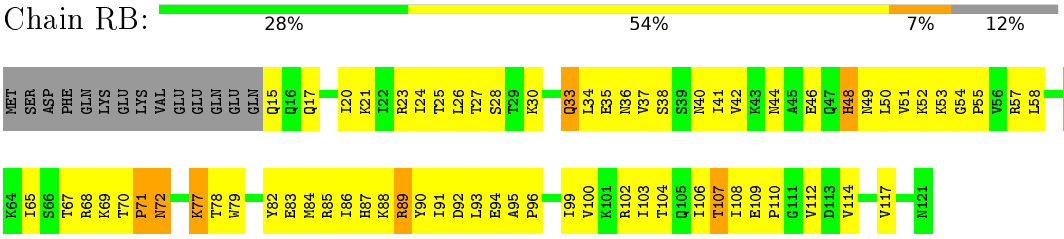
• Molecule 69: eS19 (yeast S19)

Chain QB:



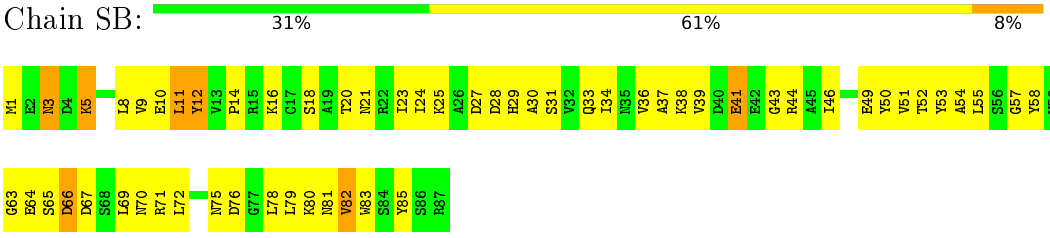
• Molecule 70: uS10 (yeast S20)

Chain RB:



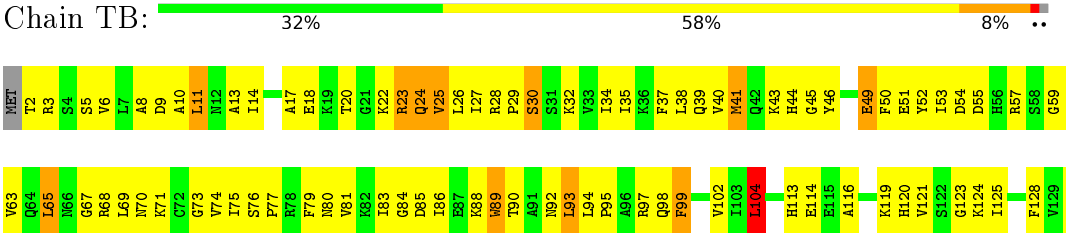
• Molecule 71: eS21 (yeast S21)

Chain SB:



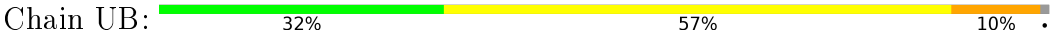
• Molecule 72: uS8 (yeast S22)

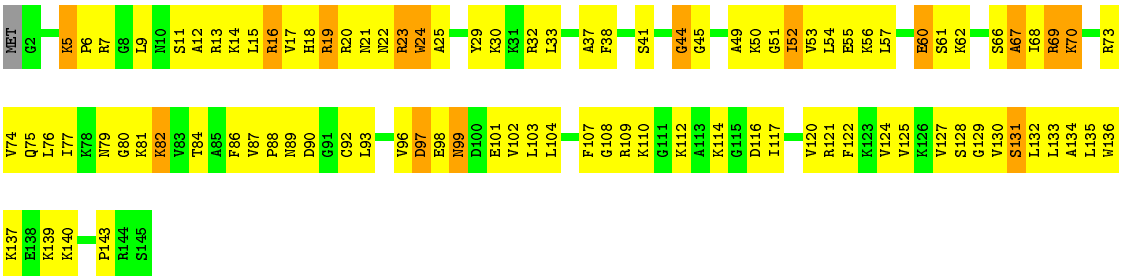
Chain TB:



• Molecule 73: uS12 (yeast S23)

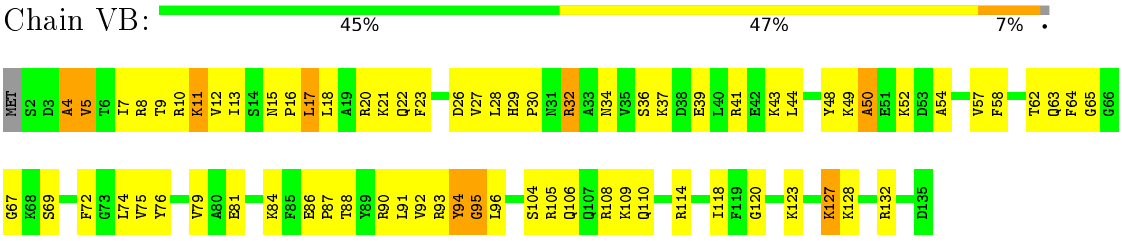
Chain UB:





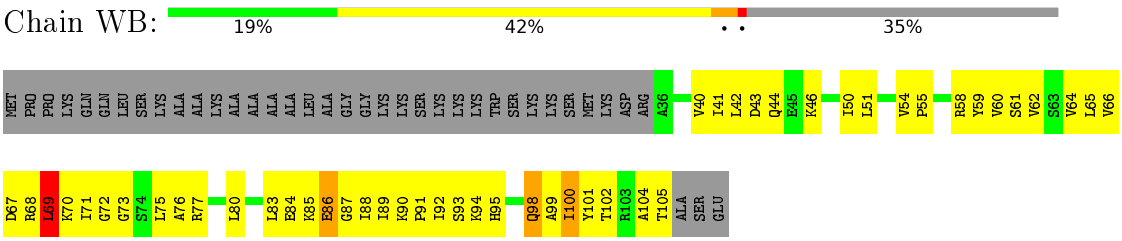
• Molecule 74: eS24 (yeast S24)

Chain VB:



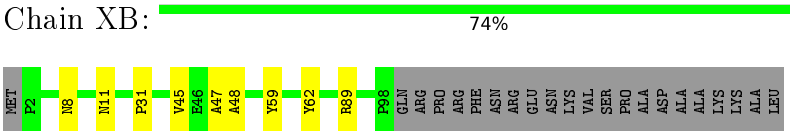
• Molecule 75: eS25 (yeast S25)

Chain WB:



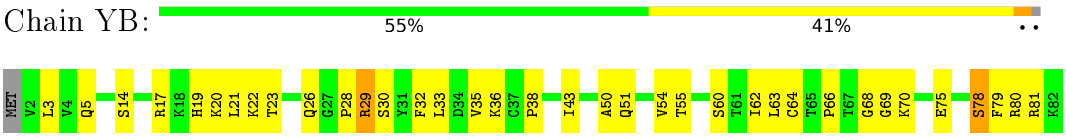
• Molecule 76: eS26 (yeast S26)

Chain XB:



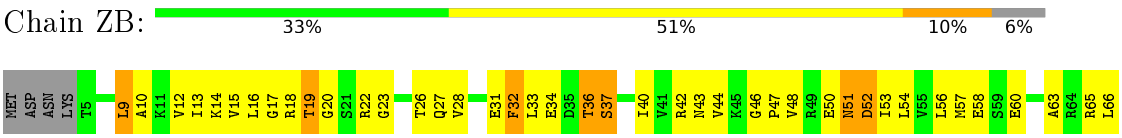
• Molecule 77: eS27 (yeast S27)

Chain YB:



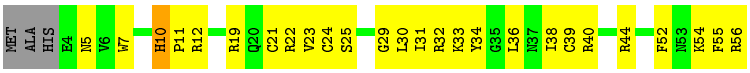
• Molecule 78: eS28 (yeast S28)

Chain ZB:



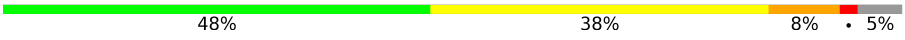
- Molecule 79: uS14 (yeast S29)

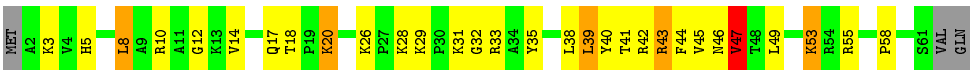
Chain AC:



- Molecule 80: eS30 (yeast S30)

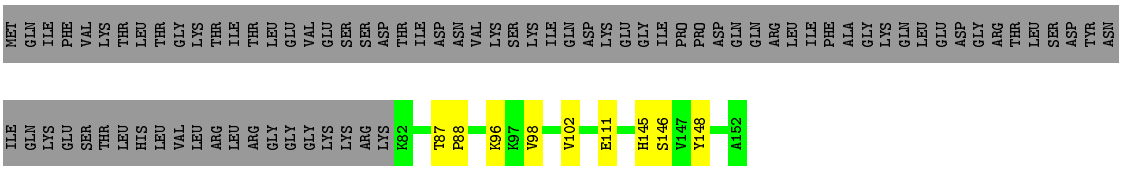
Chain BC:





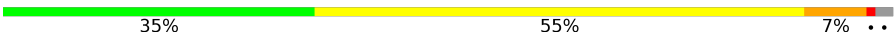
- Molecule 81: eS31 (yeast S31)

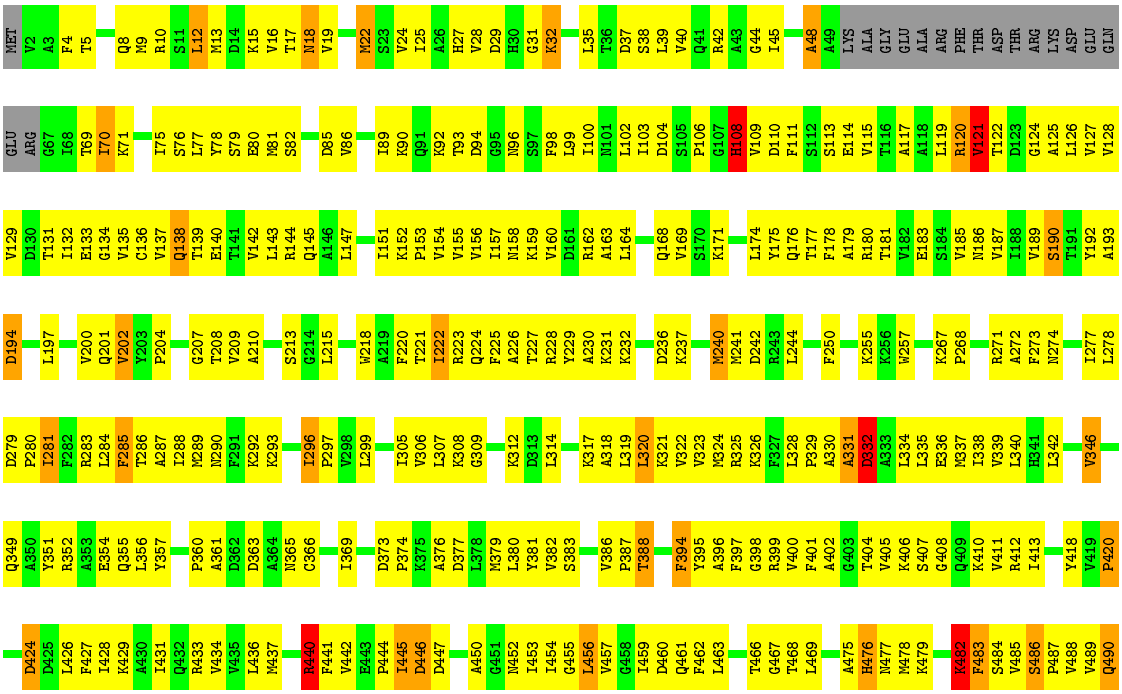
Chain CC:

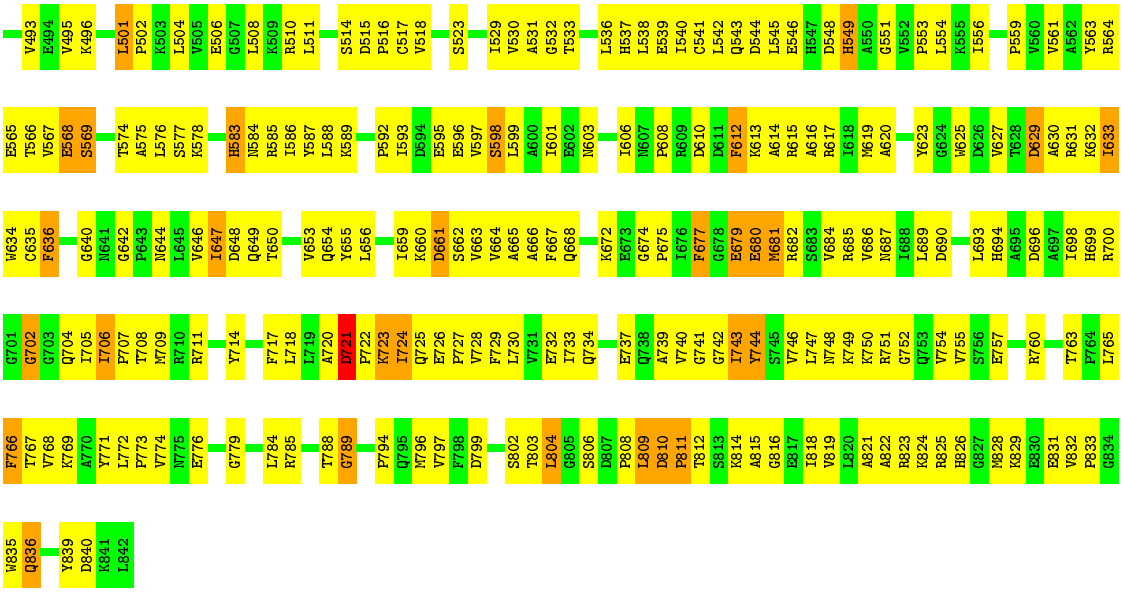


- Molecule 82: yeast eEF2

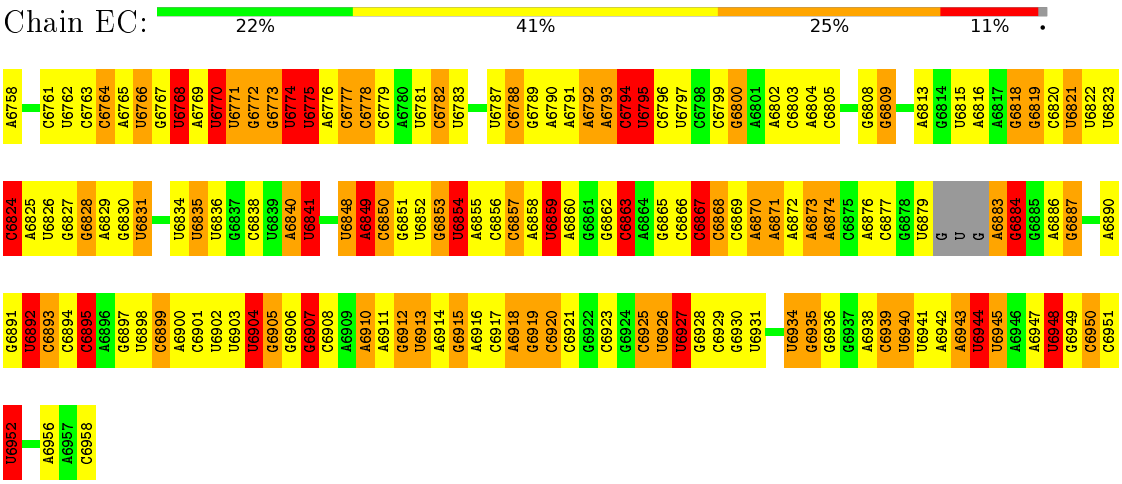
Chain DC:







- Molecule 83: IRES



4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	38054	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, SO1, MG, DDE

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	#$\|Z\|>2$	RMSZ	#$\|Z\|>2$
1	A	1.15	8/41014 (0.0%)	0.77	15/63809 (0.0%)
10	J	1.34	0/1425	0.66	0/1912
11	K	1.49	1/1822 (0.1%)	0.68	0/2451
12	L	1.15	0/1850	0.65	0/2495
13	M	1.27	0/1540	0.65	0/2073
14	N	1.32	0/1754	0.65	1/2350 (0.0%)
15	O	1.03	0/1375	0.57	0/1842
16	P	1.82	0/728	0.73	0/975
17	Q	1.32	0/1568	0.68	0/2106
18	R	1.40	1/1069 (0.1%)	0.67	0/1438
19	S	1.43	0/1758	0.70	0/2354
2	B	1.62	229/78631 (0.3%)	0.82	50/122552 (0.0%)
20	T	1.45	0/1586	0.67	0/2128
21	U	1.46	0/1466	0.70	1/1968 (0.1%)
22	V	1.43	0/1466	0.70	0/1965
23	W	1.13	0/1539	0.65	0/2050
24	X	1.54	0/1482	0.67	0/1990
25	Y	1.47	0/1301	0.64	1/1743 (0.1%)
26	Z	0.99	0/812	0.54	0/1099
27	AA	1.37	0/1019	0.66	1/1369 (0.1%)
28	BA	1.50	0/521	0.66	0/691
29	CA	1.33	0/984	0.65	0/1325
3	C	1.60	10/3747 (0.3%)	0.79	0/5832
30	DA	1.34	0/1005	0.73	3/1341 (0.2%)
31	EA	1.06	0/1119	0.54	0/1497
32	FA	1.41	0/1205	0.67	0/1612
33	GA	1.28	0/474	0.68	0/629
34	HA	1.02	0/751	0.60	0/1008
35	IA	1.23	0/904	0.63	0/1213
36	JA	1.47	0/1041	0.67	1/1394 (0.1%)
37	KA	1.56	0/869	0.70	0/1168
38	LA	1.22	0/891	0.65	0/1191

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >2	RMSZ	#|Z| >2
39	MA	1.22	0/979	0.64	0/1301
4	D	1.44	6/2884 (0.2%)	0.77	2/4491 (0.0%)
40	NA	1.17	0/779	0.63	0/1034
41	OA	1.53	0/697	0.70	1/923 (0.1%)
42	PA	1.06	0/619	0.61	0/826
43	QA	1.38	0/444	0.77	0/588
44	RA	1.31	0/424	0.66	0/562
45	SA	1.57	0/235	0.71	0/300
46	TA	1.30	0/861	0.70	0/1136
47	UA	1.30	0/702	0.65	0/934
48	VA	1.78	0/1498	0.83	3/2025 (0.1%)
49	WA	0.92	0/2498	0.56	0/3398
5	E	1.93	0/1377	0.71	0/1844
50	XA	0.78	0/1653	0.58	0/2261
51	YA	1.13	0/855	0.51	0/1067
52	ZA	0.91	0/1665	0.59	0/2263
53	AB	0.97	0/1759	0.56	0/2368
54	BB	0.89	0/2110	0.59	0/2839
55	CB	0.85	0/1630	0.56	0/2202
56	DB	0.89	0/1844	0.57	0/2464
57	EB	0.92	0/1506	0.58	0/2028
58	FB	1.07	0/1515	0.61	0/2021
59	GB	0.84	0/1519	0.59	0/2035
6	F	1.35	0/1952	0.67	2/2622 (0.1%)
60	HB	1.03	0/837	0.57	0/1131
61	IB	1.16	0/1273	0.62	0/1712
62	JB	1.06	0/495	0.56	0/617
63	KB	1.01	0/1216	0.59	0/1638
64	LB	1.02	0/507	0.53	0/632
65	MB	1.03	0/996	0.60	0/1335
66	NB	0.94	0/1126	0.55	0/1510
67	OB	1.04	2/844 (0.2%)	0.90	4/1120 (0.4%)
68	PB	0.93	0/1212	0.59	2/1628 (0.1%)
69	QB	0.89	0/1131	0.58	0/1517
7	G	1.35	0/3153	0.65	0/4239
70	RB	0.97	0/866	0.56	0/1169
71	SB	0.85	0/694	0.55	0/935
72	TB	0.95	0/1039	0.62	2/1395 (0.1%)
73	UB	1.12	0/1140	0.62	0/1518
74	VB	0.89	0/1088	0.54	0/1449
75	WB	0.87	0/571	0.57	0/768
76	XB	1.09	0/387	0.62	0/482
77	YB	0.87	0/621	0.55	0/838

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >2	RMSZ	#|Z| >2
78	ZB	0.85	0/500	0.56	0/670
79	AC	1.09	0/454	0.57	0/602
8	H	1.45	0/2802	0.70	0/3792
80	BC	0.96	0/483	0.59	0/643
81	CC	0.97	0/283	0.59	0/352
82	DC	1.63	0/6521	0.69	1/8830 (0.0%)
83	EC	2.33	88/4608 (1.9%)	0.94	11/7166 (0.2%)
9	I	1.15	0/2426	0.60	0/3271
All	All	1.41	345/227994 (0.2%)	0.75	101/334061 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	14
2	B	0	72
3	C	0	6
4	D	0	2
50	XA	0	1
83	EC	0	5
All	All	0	100

The worst 5 of 345 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	627	C	O3'-P	-14.02	1.44	1.61
2	B	1285	G	O3'-P	-9.98	1.49	1.61
2	B	3318	G	O3'-P	8.71	1.71	1.61
2	B	493	G	P-OP2	-8.52	1.34	1.49
67	OB	91	LEU	C-O	8.41	1.39	1.23

The worst 5 of 101 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	493	G	O5'-P-OP1	-40.69	61.87	110.70
2	B	493	G	O5'-P-OP2	19.84	134.51	110.70
2	B	487	U	P-O3'-C3'	16.13	139.06	119.70
1	A	627	C	O3'-P-O5'	9.79	122.59	104.00
67	OB	93	LEU	C-N-CA	-8.61	100.19	121.70

There are no chirality outliers.

5 of 100 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	313	U	Sidechain
1	A	324	U	Sidechain
1	A	447	U	Sidechain
1	A	53	G	Sidechain
1	A	568	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	A	36760	0	18348	1356	0
2	B	70288	0	35262	3569	0
3	C	3354	0	1695	188	0
4	D	2580	0	1304	125	0
5	E	1359	0	1425	98	0
6	F	1918	0	1987	258	0
7	G	3082	0	3165	358	0
8	H	2750	0	2863	326	0
9	I	2376	0	2325	219	0
10	J	1401	0	1501	144	0
11	K	1785	0	1862	193	0
12	L	1818	0	1908	192	0
13	M	1519	0	1587	156	0
14	N	1718	0	1754	166	0
15	O	1354	0	1383	86	0
16	P	723	0	774	98	0
17	Q	1543	0	1608	208	0
18	R	1054	0	1149	157	0
19	S	1721	0	1779	241	0
20	T	1556	0	1659	203	0
21	U	1443	0	1485	146	0
22	V	1442	0	1543	197	0
23	W	1522	0	1617	117	0
24	X	1446	0	1487	196	0
25	Y	1277	0	1323	148	0
26	Z	796	0	812	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	AA	1004	0	1048	93	0
28	BA	509	0	537	68	0
29	CA	969	0	1036	71	0
30	DA	994	0	1081	114	0
31	EA	1093	0	1155	116	0
32	FA	1174	0	1215	163	0
33	GA	463	0	491	45	0
34	HA	743	0	797	88	0
35	IA	890	0	938	78	0
36	JA	1020	0	1090	117	0
37	KA	851	0	880	95	0
38	LA	881	0	949	103	0
39	MA	970	0	1078	112	0
40	NA	772	0	849	83	0
41	OA	682	0	687	96	0
42	PA	613	0	682	20	0
43	QA	437	0	475	46	0
44	RA	418	0	459	48	0
45	SA	234	0	284	16	0
46	TA	848	0	918	110	0
47	UA	695	0	738	72	0
48	VA	1473	0	1514	177	0
49	WA	2445	0	2401	155	0
50	XA	1612	0	1623	146	0
51	YA	856	0	226	2	0
52	ZA	1635	0	1723	137	0
53	AB	1734	0	1817	122	0
54	BB	2069	0	2154	223	0
55	CB	1610	0	1675	162	0
56	DB	1820	0	1918	118	0
57	EB	1481	0	1572	129	0
58	FB	1490	0	1525	152	0
59	GB	1494	0	1573	121	0
60	HB	817	0	804	61	0
61	IB	1245	0	1314	104	0
62	JB	496	0	141	0	0
63	KB	1193	0	1255	99	0
64	LB	508	0	151	4	0
65	MB	975	0	1017	68	0
66	NB	1106	0	1166	121	0
67	OB	836	0	827	84	0
68	PB	1193	0	1222	80	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	QB	1113	0	1124	90	0
70	RB	856	0	917	75	0
71	SB	685	0	672	74	0
72	TB	1022	0	1060	107	0
73	UB	1122	0	1196	123	0
74	VB	1074	0	1132	76	0
75	WB	563	0	603	55	0
76	XB	388	0	96	0	0
77	YB	611	0	633	38	0
78	ZB	498	0	535	48	0
79	AC	444	0	436	30	0
80	BC	475	0	525	27	0
81	CC	284	0	76	0	0
82	DC	6419	0	6493	587	0
83	EC	4129	0	2078	97	0
84	DC	28	0	12	2	0
85	DC	1	0	0	0	0
86	DC	35	0	41	2	0
All	All	212680	0	156239	12389	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 34.

The worst 5 of 12389 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:KA:67:MET:CE	37:KA:67:MET:SD	2.03	1.47
66:NB:93:HIS:HA	66:NB:97:VAL:HB	1.20	1.19
2:B:1494:U:H4'	2:B:1495:U:H5'	1.24	1.14
2:B:2954:U:H4'	2:B:2955:U:H5'	1.26	1.13
2:B:1719:G:H4'	2:B:1732:U:H4'	1.30	1.11

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	165/217 (76%)	129 (78%)	26 (16%)	10 (6%)	2	27
6	F	250/254 (98%)	177 (71%)	56 (22%)	17 (7%)	1	24
7	G	384/387 (99%)	293 (76%)	70 (18%)	21 (6%)	2	30
8	H	359/362 (99%)	259 (72%)	77 (21%)	23 (6%)	2	26
9	I	294/297 (99%)	226 (77%)	49 (17%)	19 (6%)	1	26
10	J	173/176 (98%)	125 (72%)	33 (19%)	15 (9%)	1	17
11	K	220/244 (90%)	165 (75%)	39 (18%)	16 (7%)	1	22
12	L	231/256 (90%)	180 (78%)	38 (16%)	13 (6%)	2	29
13	M	189/191 (99%)	150 (79%)	36 (19%)	3 (2%)	12	57
14	N	207/221 (94%)	169 (82%)	28 (14%)	10 (5%)	3	32
15	O	167/174 (96%)	128 (77%)	31 (19%)	8 (5%)	3	32
16	P	92/165 (56%)	62 (67%)	20 (22%)	10 (11%)	0	11
17	Q	191/199 (96%)	144 (75%)	35 (18%)	12 (6%)	2	27
18	R	134/138 (97%)	103 (77%)	23 (17%)	8 (6%)	2	27
19	S	201/204 (98%)	144 (72%)	46 (23%)	11 (6%)	2	30
20	T	195/199 (98%)	160 (82%)	27 (14%)	8 (4%)	3	36
21	U	181/184 (98%)	133 (74%)	35 (19%)	13 (7%)	1	22
22	V	183/186 (98%)	131 (72%)	39 (21%)	13 (7%)	1	23
23	W	186/189 (98%)	162 (87%)	19 (10%)	5 (3%)	6	47
24	X	170/172 (99%)	130 (76%)	31 (18%)	9 (5%)	2	30
25	Y	157/160 (98%)	124 (79%)	25 (16%)	8 (5%)	2	31
26	Z	98/121 (81%)	69 (70%)	23 (24%)	6 (6%)	2	27
27	AA	134/137 (98%)	107 (80%)	24 (18%)	3 (2%)	8	51
28	BA	59/155 (38%)	43 (73%)	11 (19%)	5 (8%)	1	17
29	CA	119/142 (84%)	84 (71%)	29 (24%)	6 (5%)	3	31
30	DA	124/127 (98%)	89 (72%)	28 (23%)	7 (6%)	2	29
31	EA	133/136 (98%)	108 (81%)	19 (14%)	6 (4%)	3	34
32	FA	146/149 (98%)	106 (73%)	31 (21%)	9 (6%)	2	27
33	GA	56/59 (95%)	48 (86%)	8 (14%)	0	100	100
34	HA	95/105 (90%)	80 (84%)	13 (14%)	2 (2%)	9	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
35	IA	107/113 (95%)	87 (81%)	17 (16%)	3 (3%)	6 46
36	JA	125/130 (96%)	95 (76%)	23 (18%)	7 (6%)	2 29
37	KA	104/107 (97%)	81 (78%)	17 (16%)	6 (6%)	2 28
38	LA	110/121 (91%)	76 (69%)	26 (24%)	8 (7%)	1 22
39	MA	117/120 (98%)	93 (80%)	20 (17%)	4 (3%)	5 42
40	NA	97/100 (97%)	80 (82%)	10 (10%)	7 (7%)	1 22
41	OA	85/88 (97%)	62 (73%)	18 (21%)	5 (6%)	2 28
42	PA	75/78 (96%)	64 (85%)	8 (11%)	3 (4%)	4 37
43	QA	48/51 (94%)	35 (73%)	9 (19%)	4 (8%)	1 18
44	RA	50/128 (39%)	32 (64%)	10 (20%)	8 (16%)	0 5
45	SA	23/25 (92%)	23 (100%)	0	0	100 100
46	TA	103/106 (97%)	75 (73%)	22 (21%)	6 (6%)	2 28
47	UA	89/92 (97%)	63 (71%)	18 (20%)	8 (9%)	1 16
48	VA	187/312 (60%)	132 (71%)	39 (21%)	16 (9%)	1 17
49	WA	316/319 (99%)	247 (78%)	63 (20%)	6 (2%)	10 54
50	XA	204/252 (81%)	146 (72%)	40 (20%)	18 (9%)	1 17
51	YA	212/255 (83%)	159 (75%)	36 (17%)	17 (8%)	1 19
52	ZA	215/254 (85%)	169 (79%)	37 (17%)	9 (4%)	3 35
53	AB	221/240 (92%)	191 (86%)	24 (11%)	6 (3%)	6 47
54	BB	258/261 (99%)	185 (72%)	60 (23%)	13 (5%)	3 31
55	CB	204/225 (91%)	159 (78%)	33 (16%)	12 (6%)	2 28
56	DB	224/236 (95%)	192 (86%)	21 (9%)	11 (5%)	3 32
57	EB	182/190 (96%)	130 (71%)	34 (19%)	18 (10%)	1 13
58	FB	184/200 (92%)	141 (77%)	36 (20%)	7 (4%)	4 39
59	GB	183/197 (93%)	144 (79%)	27 (15%)	12 (7%)	1 25
60	HB	94/105 (90%)	73 (78%)	15 (16%)	6 (6%)	2 26
61	IB	153/156 (98%)	113 (74%)	30 (20%)	10 (6%)	1 26
62	JB	122/143 (85%)	90 (74%)	21 (17%)	11 (9%)	1 16
63	KB	148/151 (98%)	124 (84%)	19 (13%)	5 (3%)	5 42
64	LB	125/137 (91%)	88 (70%)	26 (21%)	11 (9%)	1 17
65	MB	120/142 (84%)	91 (76%)	15 (12%)	14 (12%)	0 9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
66	NB	139/143 (97%)	108 (78%)	24 (17%)	7 (5%)	3 31
67	OB	115/136 (85%)	79 (69%)	24 (21%)	12 (10%)	1 12
68	PB	143/146 (98%)	111 (78%)	24 (17%)	8 (6%)	2 29
69	QB	141/144 (98%)	122 (86%)	16 (11%)	3 (2%)	9 52
70	RB	105/121 (87%)	85 (81%)	15 (14%)	5 (5%)	3 32
71	SB	85/87 (98%)	63 (74%)	17 (20%)	5 (6%)	2 28
72	TB	127/130 (98%)	99 (78%)	24 (19%)	4 (3%)	5 44
73	UB	142/145 (98%)	108 (76%)	22 (16%)	12 (8%)	1 17
74	VB	132/135 (98%)	105 (80%)	20 (15%)	7 (5%)	2 30
75	WB	68/108 (63%)	47 (69%)	17 (25%)	4 (6%)	2 28
76	XB	95/119 (80%)	54 (57%)	32 (34%)	9 (10%)	1 15
77	YB	79/82 (96%)	59 (75%)	17 (22%)	3 (4%)	4 39
78	ZB	61/67 (91%)	43 (70%)	15 (25%)	3 (5%)	3 32
79	AC	51/56 (91%)	39 (76%)	11 (22%)	1 (2%)	9 53
80	BC	58/63 (92%)	38 (66%)	16 (28%)	4 (7%)	1 24
81	CC	69/152 (45%)	42 (61%)	18 (26%)	9 (13%)	0 7
82	DC	819/842 (97%)	646 (79%)	137 (17%)	36 (4%)	3 34
All	All	12207/13416 (91%)	9316 (76%)	2192 (18%)	699 (6%)	4 28

5 of 699 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	70	ASP
6	F	29	LEU
6	F	34	TYR
6	F	68	LYS
7	G	187	SER

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
5	E	157/198 (79%)	136 (87%)	21 (13%)	5 30
6	F	194/196 (99%)	172 (89%)	22 (11%)	7 37
7	G	322/323 (100%)	295 (92%)	27 (8%)	14 51
8	H	288/289 (100%)	249 (86%)	39 (14%)	5 30
9	I	244/245 (100%)	220 (90%)	24 (10%)	10 43
10	J	152/153 (99%)	141 (93%)	11 (7%)	18 58
11	K	186/205 (91%)	165 (89%)	21 (11%)	7 37
12	L	191/208 (92%)	169 (88%)	22 (12%)	7 36
13	M	171/171 (100%)	154 (90%)	17 (10%)	10 43
14	N	180/187 (96%)	161 (89%)	19 (11%)	8 39
15	O	147/150 (98%)	134 (91%)	13 (9%)	12 48
16	P	81/136 (60%)	70 (86%)	11 (14%)	5 29
17	Q	154/159 (97%)	136 (88%)	18 (12%)	7 35
18	R	107/109 (98%)	96 (90%)	11 (10%)	9 40
19	S	175/176 (99%)	150 (86%)	25 (14%)	4 28
20	T	160/162 (99%)	141 (88%)	19 (12%)	6 34
21	U	145/146 (99%)	122 (84%)	23 (16%)	3 23
22	V	150/151 (99%)	134 (89%)	16 (11%)	8 39
23	W	153/154 (99%)	138 (90%)	15 (10%)	10 43
24	X	156/156 (100%)	141 (90%)	15 (10%)	10 44
25	Y	136/137 (99%)	114 (84%)	22 (16%)	3 22
26	Z	87/107 (81%)	85 (98%)	2 (2%)	58 83
27	AA	104/105 (99%)	93 (89%)	11 (11%)	8 39
28	BA	54/129 (42%)	45 (83%)	9 (17%)	3 21
29	CA	105/118 (89%)	97 (92%)	8 (8%)	16 56
30	DA	109/110 (99%)	94 (86%)	15 (14%)	4 29
31	EA	115/116 (99%)	105 (91%)	10 (9%)	13 48
32	FA	118/119 (99%)	105 (89%)	13 (11%)	8 38
33	GA	46/47 (98%)	42 (91%)	4 (9%)	13 48
34	HA	81/88 (92%)	75 (93%)	6 (7%)	17 56
35	IA	96/97 (99%)	89 (93%)	7 (7%)	17 57
36	JA	109/111 (98%)	100 (92%)	9 (8%)	14 51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
37	KA	90/91 (99%)	80 (89%)	10 (11%)	8 38
38	LA	95/103 (92%)	90 (95%)	5 (5%)	28 67
39	MA	104/105 (99%)	96 (92%)	8 (8%)	16 55
40	NA	81/82 (99%)	75 (93%)	6 (7%)	17 56
41	OA	70/71 (99%)	60 (86%)	10 (14%)	4 28
42	PA	68/69 (99%)	63 (93%)	5 (7%)	17 56
43	QA	45/46 (98%)	39 (87%)	6 (13%)	5 30
44	RA	47/116 (40%)	44 (94%)	3 (6%)	22 61
45	SA	23/23 (100%)	20 (87%)	3 (13%)	5 31
46	TA	90/91 (99%)	80 (89%)	10 (11%)	8 38
47	UA	71/72 (99%)	65 (92%)	6 (8%)	13 51
48	VA	160/254 (63%)	147 (92%)	13 (8%)	15 52
49	WA	261/262 (100%)	246 (94%)	15 (6%)	25 65
50	XA	173/210 (82%)	155 (90%)	18 (10%)	9 40
52	ZA	176/205 (86%)	170 (97%)	6 (3%)	44 77
53	AB	182/195 (93%)	167 (92%)	15 (8%)	14 52
54	BB	221/222 (100%)	202 (91%)	19 (9%)	13 50
55	CB	173/191 (91%)	162 (94%)	11 (6%)	22 61
56	DB	193/201 (96%)	187 (97%)	6 (3%)	47 78
57	EB	165/170 (97%)	157 (95%)	8 (5%)	31 69
58	FB	150/161 (93%)	141 (94%)	9 (6%)	24 63
59	GB	158/166 (95%)	143 (90%)	15 (10%)	11 44
60	HB	89/98 (91%)	83 (93%)	6 (7%)	20 60
61	IB	136/137 (99%)	127 (93%)	9 (7%)	21 60
63	KB	127/128 (99%)	119 (94%)	8 (6%)	22 61
65	MB	103/118 (87%)	98 (95%)	5 (5%)	31 69
66	NB	117/119 (98%)	108 (92%)	9 (8%)	16 55
67	OB	82/124 (66%)	77 (94%)	5 (6%)	23 63
68	PB	128/129 (99%)	116 (91%)	12 (9%)	11 45
69	QB	115/116 (99%)	105 (91%)	10 (9%)	13 48
70	RB	100/114 (88%)	90 (90%)	10 (10%)	9 42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
71	SB	74/74 (100%)	66 (89%)	8 (11%)	8 39
72	TB	110/111 (99%)	99 (90%)	11 (10%)	9 42
73	UB	119/120 (99%)	110 (92%)	9 (8%)	16 56
74	VB	112/113 (99%)	103 (92%)	9 (8%)	15 53
75	WB	61/89 (68%)	56 (92%)	5 (8%)	14 52
77	YB	70/71 (99%)	69 (99%)	1 (1%)	74 89
78	ZB	56/60 (93%)	49 (88%)	7 (12%)	6 32
79	AC	47/49 (96%)	44 (94%)	3 (6%)	22 61
80	BC	51/54 (94%)	45 (88%)	6 (12%)	6 35
82	DC	699/714 (98%)	641 (92%)	58 (8%)	14 51
All	All	9865/10602 (93%)	8962 (91%)	903 (9%)	16 46

5 of 903 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	Y	136	ARG
37	KA	42	GLN
78	ZB	58	GLU
27	AA	102	ILE
31	EA	38	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 283 such sidechains are listed below:

Mol	Chain	Res	Type
35	IA	56	ASN
41	OA	30	GLN
72	TB	98	GLN
36	JA	13	HIS
37	KA	24	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1682/1798 (93%)	312 (18%)	11 (0%)
2	B	3267/3396 (96%)	632 (19%)	27 (0%)
3	C	157/158 (99%)	32 (20%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	D	120/121 (99%)	12 (10%)	0
83	EC	189/201 (94%)	74 (39%)	2 (1%)
All	All	5415/5674 (95%)	1062 (19%)	40 (0%)

5 of 1062 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	25	C
1	A	26	A
1	A	34	G
1	A	47	A

5 of 40 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	1144	U
2	B	1456	A
2	B	3317	U
2	B	1307	G
2	B	1815	U

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
82	DDE	DC	699	82	13,20,21	1.94	5 (38%)	12,28,30	2.05	3 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	DDE	DC	699	82	-	0/19/21/23	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	DC	699	DDE	CD2-NE2	2.08	1.39	1.36
82	DC	699	DDE	CB-CA	2.15	1.58	1.53
82	DC	699	DDE	CB-CG	2.19	1.59	1.51
82	DC	699	DDE	OAG-CBI	2.24	1.28	1.23
82	DC	699	DDE	CBW-CBI	4.45	1.60	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
82	DC	699	DDE	CAU-CBW-CBI	-2.51	105.65	110.72
82	DC	699	DDE	OAG-CBI-NAD	2.26	126.80	123.06
82	DC	699	DDE	CAU-CAT-CE1	5.10	140.11	112.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	DC	699	DDE	3	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
84	GDP	DC	901	85	24,30,30	2.21	8 (33%)	26,47,47	1.80	4 (15%)
86	SO1	DC	903	-	36,39,39	3.17	22 (61%)	36,64,64	1.68	8 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	GDP	DC	901	85	-	0/12/32/32	0/3/3/3
86	SO1	DC	903	-	-	0/15/104/104	0/2/5/5

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	DC	903	SO1	O56-C52	-3.67	1.32	1.41
86	DC	903	SO1	C7-C16	2.01	1.56	1.53
86	DC	903	SO1	C24-C18	2.02	1.59	1.54
86	DC	903	SO1	C54-C55	2.05	1.58	1.52
86	DC	903	SO1	C53-C54	2.37	1.58	1.52

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
84	DC	901	GDP	N3-C2-N1	-4.99	120.76	127.56
84	DC	901	GDP	C5-C6-N1	-3.84	118.50	123.52
86	DC	903	SO1	C7-C2-C8	-3.43	103.97	110.16
86	DC	903	SO1	C18-C9-C16	-3.27	98.83	103.42
86	DC	903	SO1	C12-C6-C10	-3.07	102.42	107.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	DC	901	GDP	2	0
86	DC	903	SO1	2	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.