



wwPDB EM Map/Model Validation Report ⓘ

Sep 29, 2016 – 05:36 PM EDT

PDB ID : 5JUP
EMDB ID: : EMD-6644
Title : Saccharomyces cerevisiae 80S ribosome bound with elongation factor eEF2-GDP-sordarin and Taura Syndrome Virus IRES, Structure II (mid-rotated 40S subunit)
Authors : Abeyrathne, P.; Koh, C.S.; Grant, T.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2016-05-10
Resolution : 3.50 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

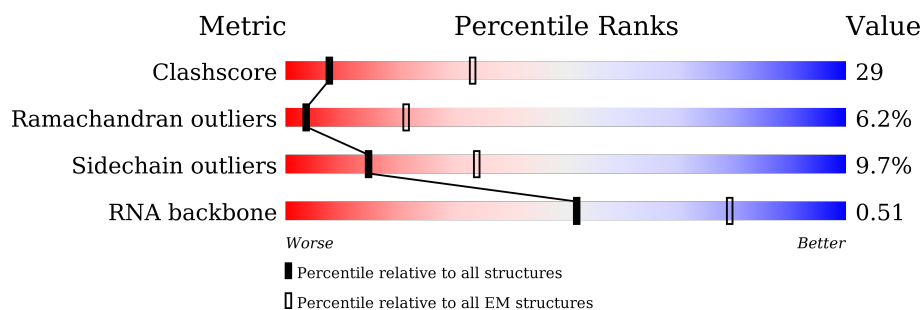
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



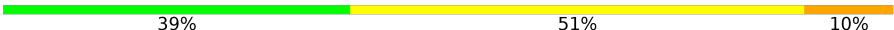


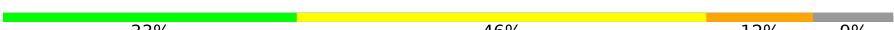
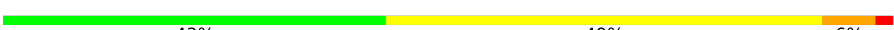
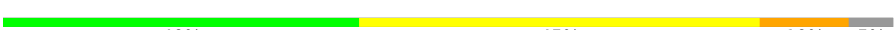




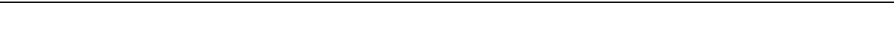

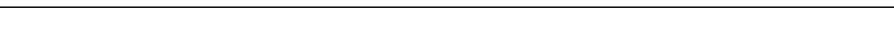
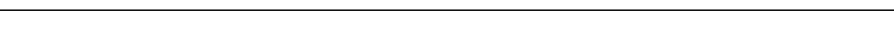







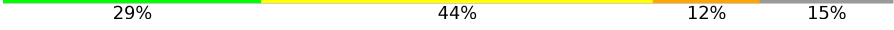


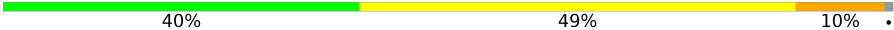
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	1798	28% 58% 12% ..
2	B	3396	31% 54% 11% ..
3	C	158	34% 52% 15%
4	D	121	23% 69% 7%
5	E	217	33% 35% 11% 21%
6	F	254	34% 57% 7% ..
7	G	387	47% 46% 7%
8	H	362	40% 47% 12% .




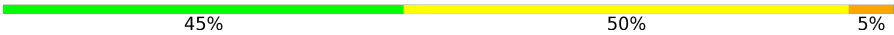
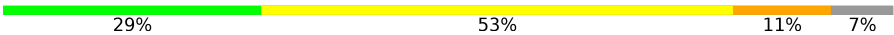
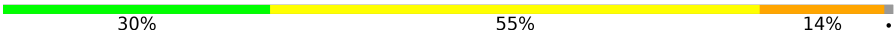



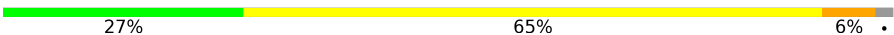

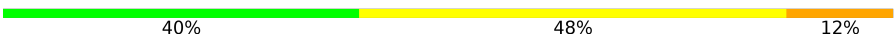




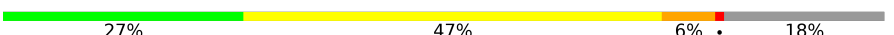








Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	I	297	
10	J	176	
11	K	244	
12	L	256	
13	M	191	
14	N	221	
15	O	174	
16	P	165	
17	Q	199	
18	R	138	
19	S	204	
20	T	199	
21	U	184	
22	V	186	
23	W	189	
24	X	172	
25	Y	160	
26	Z	121	
27	AA	137	
28	BA	155	
29	CA	142	
30	DA	127	
31	EA	136	
32	FA	149	
33	GA	59	


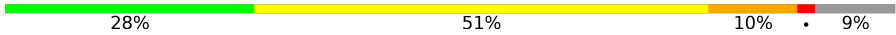


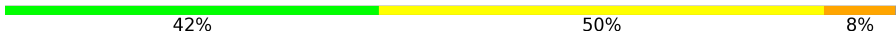

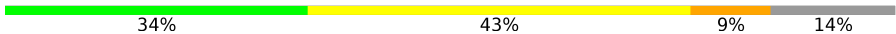
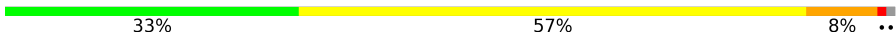
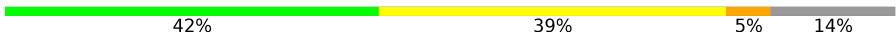
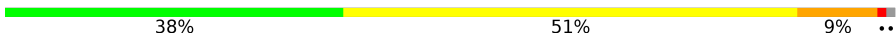
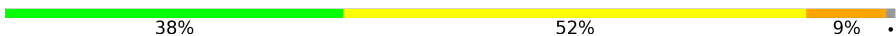
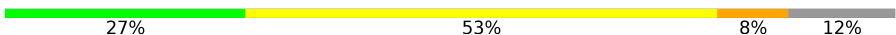
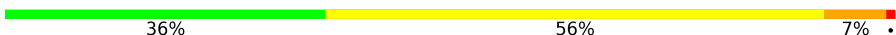
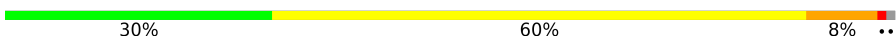











Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	HA	105	
35	IA	113	
36	JA	130	
37	KA	107	
38	LA	121	
39	MA	120	
40	NA	100	
41	OA	88	
42	PA	78	
43	QA	51	
44	RA	128	
45	SA	25	
46	TA	106	
47	UA	92	
48	VA	312	
49	WA	319	
50	XA	252	
51	YA	255	
52	ZA	254	
53	AB	240	
54	BB	261	
55	CB	225	
56	DB	236	
57	EB	190	
58	FB	200	

Continued on next page...

Continued from previous page...

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 [i](#)

There are 86 unique types of molecules in this entry. The entry contains 212656 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
1	A	1781	Total	C	N	O	P	0	0
			36760	16335	6359	12285	1781		

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

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

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

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

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

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

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

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

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

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

- 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	S	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	S	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
			4105	1826	718	1363	198		

- Molecule 84 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

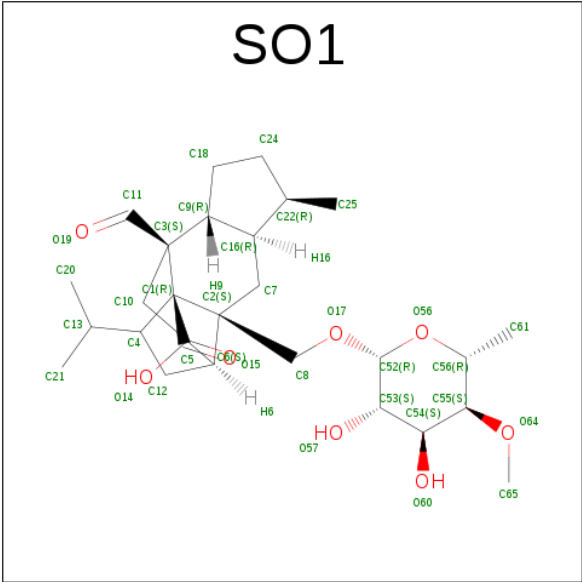


Mol	Chain	Residues	Atoms					AltConf
84	DC	1	Total 28	C 10	N 5	O 11	P 2	0

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

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

- 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: C₂₇H₄₂O₈).

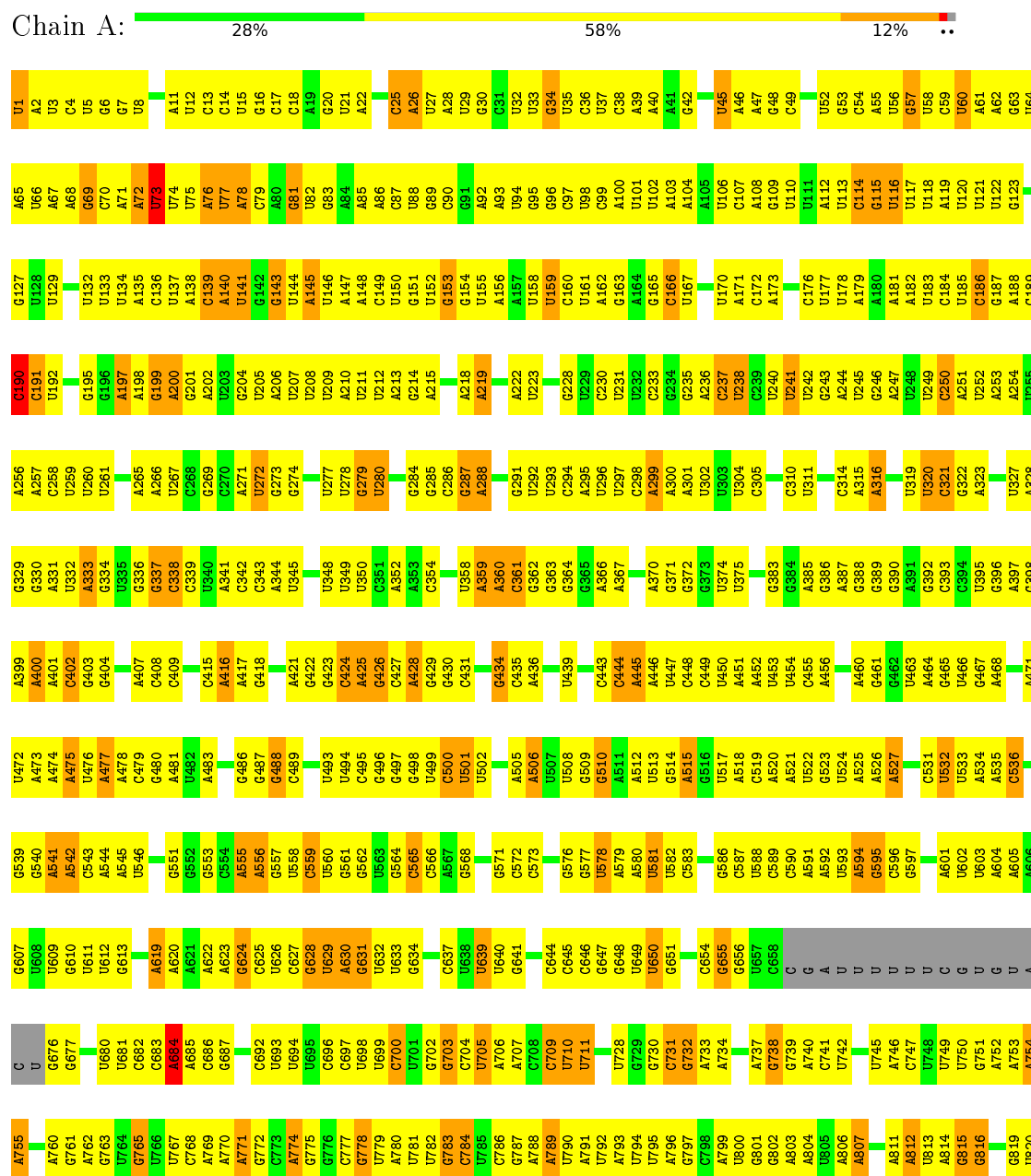


Mol	Chain	Residues	Atoms			AltConf
86	DC	1	Total	C	O	0
			35	27	8	

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. 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.

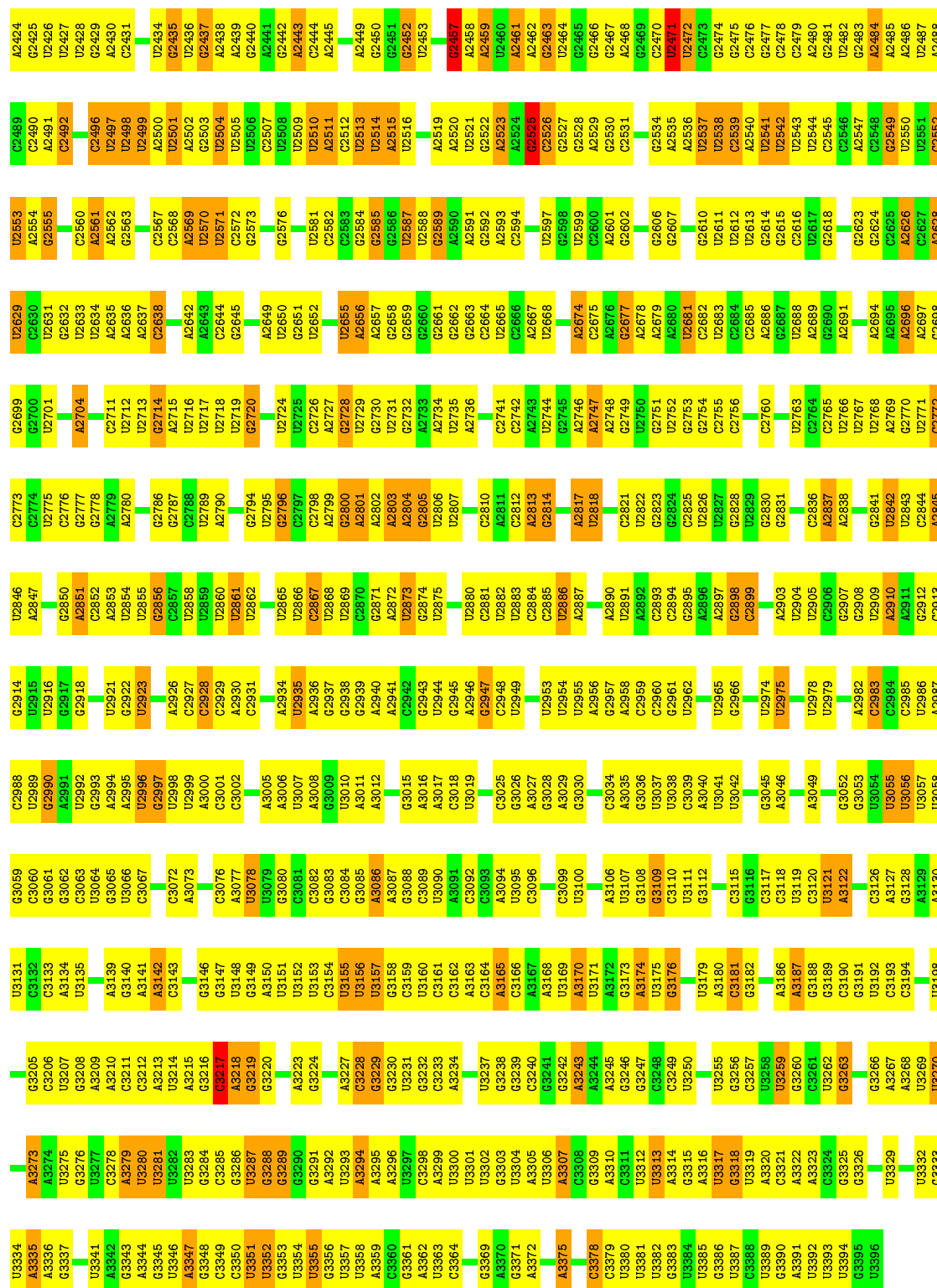
• Molecule 1: 18S ribosomal RNA



C1733	A1859	U1598	U1535	C1472	A1411	A1348	U1276	G1199	A1062	U988	C883	U821
C1734	A1860	U1599	G1536	U1473	G1412	A1349	G1277	G1200	U1063	C969	A884	U822
U1735	U1661	A1600	C1667	U1474	U1413	U1350	G1278	G1201	G1064	A970	G885	G823
G1736	G1662	G1601	U1538	A1475	U1414	G1351	C1279	A1202	A1065		U886	G824
G1737	G1663	C1602	G1539	C1476	U1415	G1352	C1280	A1203	A1138	A973	U887	U825
U1738	U1603	U1603	G1540	G1477	G1416	U1353	G1281		C1066	A974	U888	U826
G1739	A1867	U1604	G1541	G1478	A1417	U1356	U1282	C1207	C1067		U889	C827
A1740	G1668	U1605	G1542	A1479	G1418	A1357	U1283	G1208	C1068	C975	C890	U827
U1741	U1669	A1543	A1543	G1480	G1419	G1358	U1284	C1209	A1069	G976		
U1742	U1670	G1607	U1544	C1481	C1420	A1359	U1285	C1210	U1071	A977		
	A1571	U1608	A1545	C1482	A1421			G1211	C1072			
G1745	G1672	U1609	G1546	A1483	A1422	A1360	U1288	G1212	G1073	G991	G901	A829
A1746	U1673	U1610	A1547	G1484	U1423	U1361	U1289	G1213	G1074	A992	G902	U830
G1747	C1674	A1611	G1548	C1485	A1424	U1362	U1290	U1214	C1075	G994	U931	U831
G1748	C1675	U1612	C1549	G1486	A1425	U1363	U1291	C1215	A1076		U903	U832
A1749	U1676	U1613	A1550	A1487	C1426	G1364	G1292	C1216	C1077			G834
U1750	G1677	A1614	U1551	G1488	A1427	C1365	U1293	A1217	C1078		U911	U835
A1751	A1678	C1615	U1552	U1489	G1428	U1366	G1294	G1218		U1004	U918	U839
U1752	G1679	U1616	G1553	C1490	G1429	G1367		A1219	A1081	A1005	A919	U840
A1753	G1680	U1617	U1554	U1491	U1430	G1368	U1298		C1082	U1012		U841
A1754	A1681	C1618	A1555	A1492	C1431	U1369	U1301	U1225	G1158	U1015	A923	C842
A1755	U1682	U1619	A1556	A1493	U1432	U1370		A1226	G1159	C1016	A924	U843
G1756	G1683	C1620	U1557	C1494	G1433	A1371		A1227	A1084	C1013	G925	A844
U1757	U1684	U1621	U1558	C1495	U1434	U1372	G1304	G1228	G1085	A1026	A926	G845
G1757	U1685	G1622	A1559	G1498	U1435	C1373	U1305	G1229	A1086	A1023	C927	G846
A1761	G1686	C1623	U1560	C1499	A1436	C1374	U1306	A1230	A1087	U1024	A947	U847
A1762	U1687	U1624	U1561	G1498	U1437	A1375	U1307	U1231	U1089	A1025	A929	C848
A1763	G1688	C1625	G1562	C1500	G1438	C1376		G1232	A1090	A1026	C849	U849
G1764	U1689	U1626	C1563	C1501	U1439	U1377	U1314	G1233	A1091	A1027	A933	A850
A1765	G1696	U1627	U1564	G1502	C1440	U1378	U1315	A1234	C1096	C1033	G934	U851
U1766	G1697	U1628	C1565	A1503	G1441	C1379	C1316	G1235	U1097	G1034	U935	C852
A1767	G1698	U1629	U1566	G1504	U1442	U1380	C1317	C1236	U1098	G1035	G939	G853
G1768	U1701	A1630	C1567	U1505	U1443	U1381	A1319	G1241	G1036	A1030	A939	U854
U1769	A1702	G1632	A1569	G1506	A1444	A1382	U1320		C1096		A940	A855
U1770		A1633	C1570	G1507	G1445	G1383	A1321		U1097	C1033	A941	A856
U1771	C1706	G1634	C1571	U1511	G1448	A1384		A1244	U1099	G1036	G942	U857
C1772	U1771	A1635	G1572	G1512	C1449	G1386	A1322	G1245	G1100	C1037	A944	G858
G1773	C1711	C1636	A1573	G1513	U1450	G1387	C1323	U1250	G1101	U1038	U945	A859
G1774	A1712	G1637	G1574	U1514	C1451	C1388	A1325	U1251	G1178	A1039	U946	U860
	G1713	G1638	A1515	A1515	U1452	C1389	A1326		U1179	G1040	U947	U861
A1782	A1714	C1639	A1577	U1516	G1453	U1390	C1327	U1254	U1180	U1041	G948	A862
C1783	G1715	U1640	U1578	U1517	G1454	A1391	C1328	G1255	C1050	G1042	C949	U864
G1784	G1716	C1641	U1579	C1518	G1455	U1392	A1329	G1256	C1051	A1043	C950	A865
U1785	G1717		C1580	U1519	C1456	C1393	A1330	U1257	G1107	U1044	A951	G866
G1786	G1718	C1644		U1520	C1457	G1394	A1331	U1258	G1108	G1045	G952	G867
		G1645	G1584	G1521	G1458		A1332	U1259	G1109	G1046	G953	G868
G1789	G1719	C1646	U1585	U1522	C1459	U1397		U1260	G1110	G1047	G954	A869
A1790	G1720	U1647	U1586	G1523	U1460	U1398	U1335	G1263	G1114	G1048	A955	C870
A1791	A1721	C1648	A1587	C1461	C1399	C1399	A1336	G1264		U1049	C956	G871
G1792	G1722	U1649	G1588	A1525	G1462	G1265		G1265	U1117	U1052	G872	U873
G1793	U1724	U1650	A1589	A1526	G1463	G1402	G1339	U1266	G1118	G1053	U958	G874
A1794	U1725	U1651	G1590	C1527	G1464	C1403			G1119	G1054	U959	G875
	G1726	C1652	C1591	U1528	C1465	C1404	A1341	U1269	C1191	U1055	U960	G876
U1798	G1727	C1653	A1592	C1529	G1466	G1405	C1342	G1270	C1192	U1056	U961	G877
	A1728	G1654	A1593	C1530	C1467	A1406	U1343	G1271	A1193	C1121	U1057	G878
G1729	C1730	U1655	G1594	G1531	U1468	U1407	A1344	U1272	C1194	U1058	U964	G879
A1730	A1730	U1656	U1595	U1532	A1469	G1408	A1345	G1273	C1195	U1059	U965	C880
A1731	A1731	C1657	C1596	C1533	C1470	G1409	A1346	C1274	A1125	G1126	A966	U881
	A1732	U1658	A1597	C1534	C1471	U1410	U1347	G1275	C1197	U1060	U967	U882

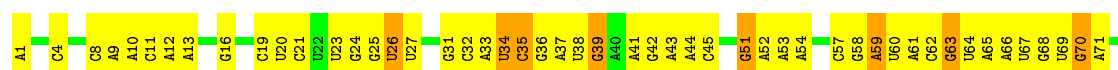
A1193	A1129	A1061	A993	A926	U850	C700	G635	U558	C489	A416	A338	C271	A199	G138	A66
G1194	A1130	A1062	G994	C927	C851	A705	C536	A559	A490	A417	C339	G272	C200	U129	A67
C1195	A1131	A1063	U995	C928	U852	A706	C638	G560	C491	A418	C340	U275	G206	C131	A70
A1196	C1132	A1064	A996	A929	G853	A707	C639	C561	U492	G419	G341	U276	U207	C132	A71
A1197	A1133	A1065	A997	A930	G854	G708	C640	U562	G493	G420	C346	G277	C208	U133	C73
	G1134	A1066	A998	A933	U855	A709	C641	U564	G494	A422	G347	U278	A209	U134	C74
C1201		U1067	G999	G934	G856	A710	U642	G567	C500	A423	A348	U279	U210	C135	G75
A1202	C1137	C1068	G1000	U935	G857	A711	U643	G568	A501	G424	A349	U280	A211	G137	G76
A1203	U1138	C1069	G1001	A936	U858	G712	U644	G569	A502	G425	C350	U281	G212	U138	G77
A1204	U1070	G859	A1002	G937	G860	G713	A645	U574	A504	G426	G353	A284	G215	G139	U78
	C1141	C938	A1003	C938	C861	G714	A646	U575	A505	G427	U354	A285	G216	C140	U79
G1207	G1142	U939	U1007	G940		A715	A647	G576	C503		A351	G282	A213	U139	U78
U1208	A1143	G941	U1008	G941	G869		C648	G575	A506		G352	A286	G217	G143	G80
G1209	U1144	G942	A1009	G942	U870	G718	C649	C576	C506		A353	U287	G218	G144	C81
U1210	G1145	U943	G1010	U943	U871	U719	C650	C577	U507		C356	G288	G219	G145	C82
U1211	C1146	G1078	A1010	U944	U872	G720	C651	G579	U508		A357	A289	A219	U146	U84
A1212	G1147	A1079	A1011	C945	C873	G722	G652		U509		G358	G290	A221	U147	A85
G1213		A1080	G1012	U946	U874	U723		G583	G510		G359	C291	A222	G148	G86
U1214	A1150	U1081	G1013	U947	G875	U724	C655	G584	G511		G360	C292	U223	U149	U87
U1215		U1082	U1014	G947	A876	G725	A656	G585	U512		A361	C293	U224	U150	A88
	A1153	G1083	U1015	C948	G877	G726	A657	A585	G513		G362	C294	C225	A151	A89
C1218	A1154		C1016	C949	C878	G727		A589	C514		G363	A295	C226	U152	G90
C1219	C1155	G1089	G1017	G953	G879	G728	U660	A592	C515		G364	A296	C227	G91	G92
U1220	C1156	A1090	C1018	U954	U880	G729	U661	G595	G518		U370	U298	U230	G155	
A1221	G1157	A1091	G1019	U955	G881	C734	U662	G596	A519		G371	G299	U231	G156	A95
G1222	A1158	C1092	G1020	U956	C882	A735	U663	C596	U520		A372	G300	G232	G158	G96
A1223	A1159	U1093	G1021		A882		U664	G597	A521		A373	G301		G162	U97
C1224	C1160	U1094		C959	A883		U665	A598	A522		A374	G303	A238	C163	A99
U1225	U1095	G1095	G1024	C961	U892	U741	U666	G599	A523		A375	G304	U240	A165	A100
G1226	U1162	U1096	A1027	C962	C893	G742	U667	G600	C525		G376	U305	G241	G103	C102
C1227	A1163	G1097	C1027	A962	C894	G743	U668	A603	U528			A306	C242	U168	G104
G1228	G1164	U1098	U1028	G963	C895	G744	U669	G604	A529			A307	G243	U169	G105
C1229	A1165	A1099	G1029		A896	C745	U670		G530			A308	G244	G170	C105
G1230	G1166	U1100		U966	U897	U746	U671	A608	U531				U245	C174	A106
A1231	U1167	G1101	U1033	U967	U898	U749	U672	G609	A532				U246	C175	A107
G1232	C1168	A1102	G1034	A967	U899	G750	U673	G610	A533					U181	A108
G1233	A1169	A1103	G1035	G968	U900	G751	U674	G611	U534					U182	G110
G1234	A1170	G1104	A1036	C969	G901	G752	U675	G612	G535					U183	C111
					G902	C753	A677	U613	U536					U184	U112
U1235	G1171	U1108	U1039	A970	U903	G754	U678	G614	U537					U185	C113
G1236	G1172	U1109	G1236	G971	G904	G755	U679	U615	G538					U186	A114
C1237	U1173	U1110	A1040	A972	U905	G756	U680	G616						U187	A115
G1238	G1174	U1111	U1041	A973	U906	G757	U681	G617	G542					U188	A116
C1239	C1175	U1112	U1042	A974	U907	G758	U682	U618	C543					U189	U117
A1240	U1176	G1113	G1043	C975	C907	U759	U683	U619	C544					U190	U118
U1241	G1177	U1114	U1044		G908	U760	U684	U620	U545					U191	U119
G1242		G1115	C1045	G978		A761	U685	A621	C546					U192	G120
		G1116	A1046	U979			U686		U547					U193	A121
A1245	A1180	G1117	A1047	A980			U687		C548					U194	A122
G1246	U1181	G1118	A1048	U981			U688		U549					U195	A123
U1247	A1182	C1118	C1049	C982			U689		A550					U196	U124
C1248	C1183	C1119	U1050	A983			U690		A551					U197	C125
G1249	A1184	U1120	U1051	G984			A691		G552					G198	U126
G1250	C1185	U1121	U1052	U985			A692		A557					G199	G127
A1251	G1186	U1122	A1053	U986			A693							U199	
U1252	C1187	U1123	A1054	A917			A694							U200	
C1253	U1188	U1124	U1055	U919			A695							U201	
G1254	U1189	U1125	U1056	U920			C696							U202	
C1255	A1190	G1126	U1057	C923			A697							U203	
G1256	U1191	G1127	A648	U990			U698							U204	
C1257	C1192	U1128	U1060	A925			A699							U205	

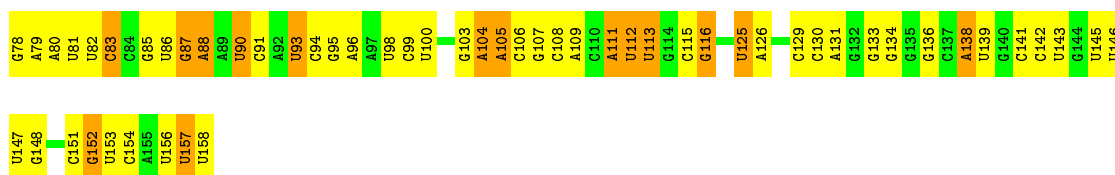


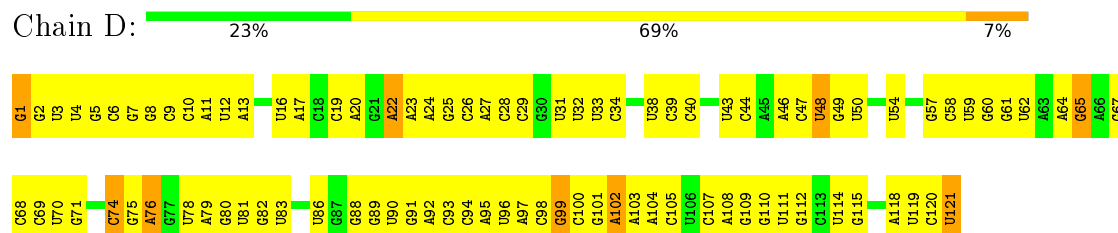
• Molecule 3: 5.8S ribosomal RNA

Chain C:

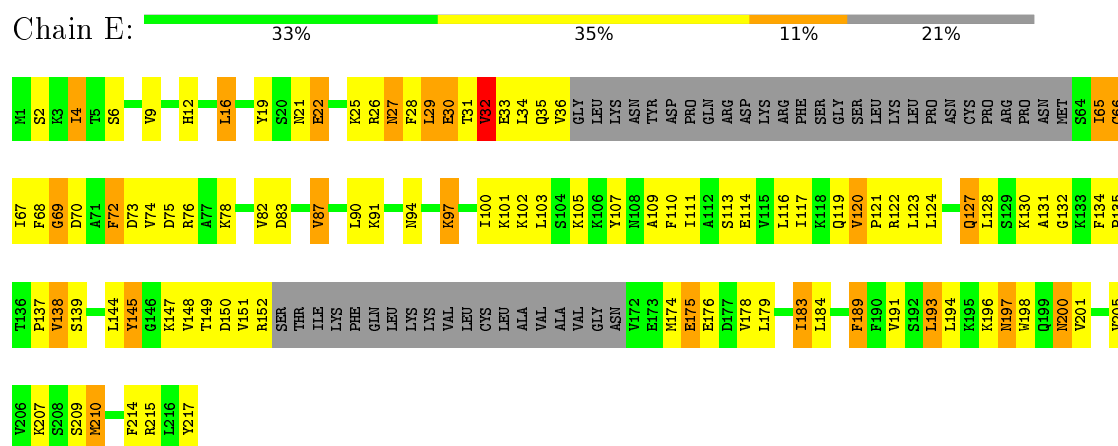




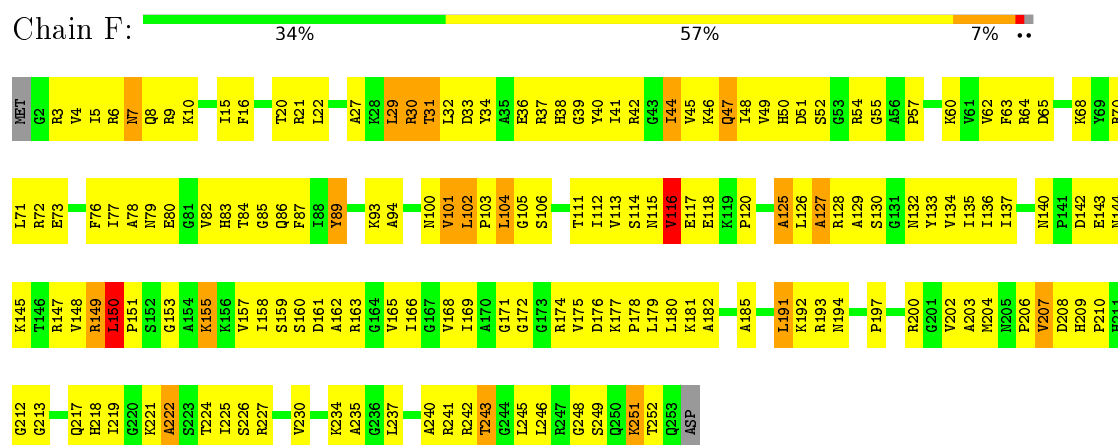
- Molecule 4: 5S ribosomal RNA



- Molecule 5: uL1 (yeast L1)

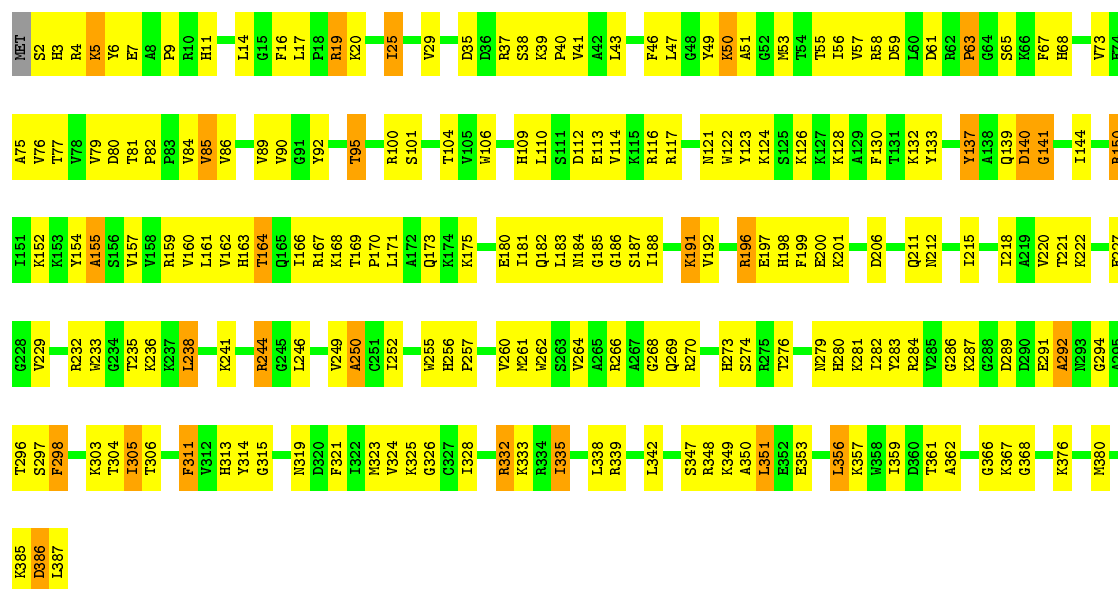


- Molecule 6: uL2 (yeast L2)



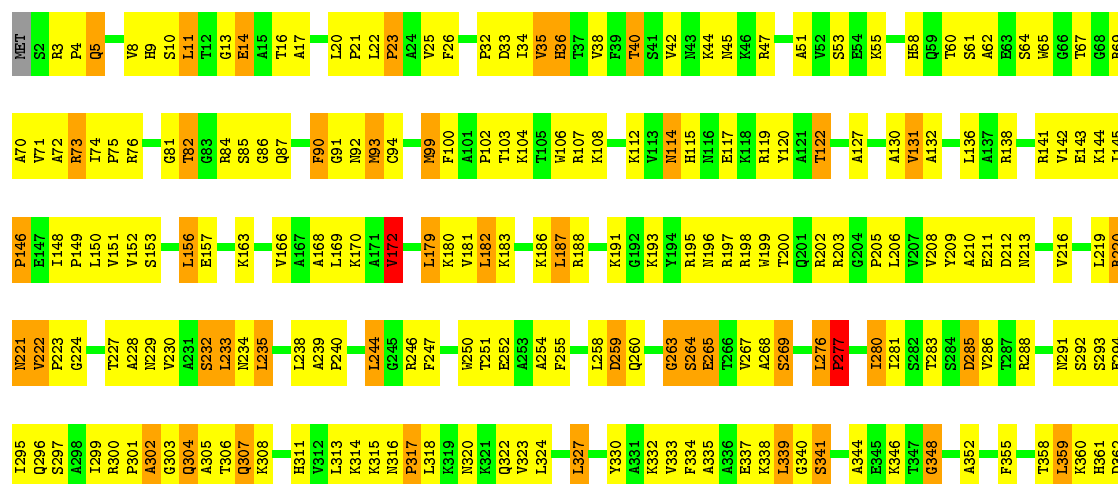
- Molecule 7: uL3 (yeast L3)





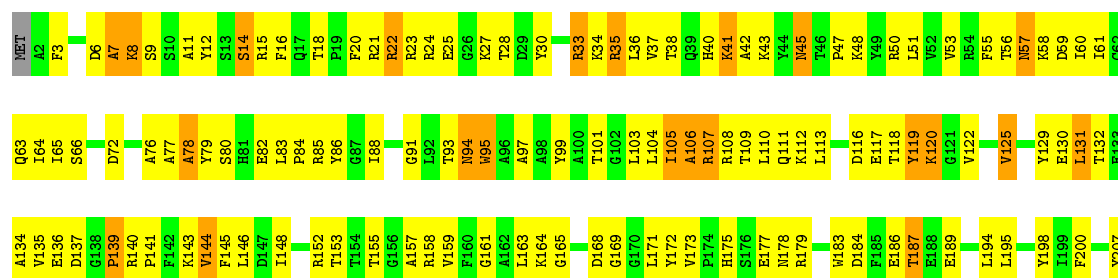
• Molecule 8: uL4 (yeast L4)

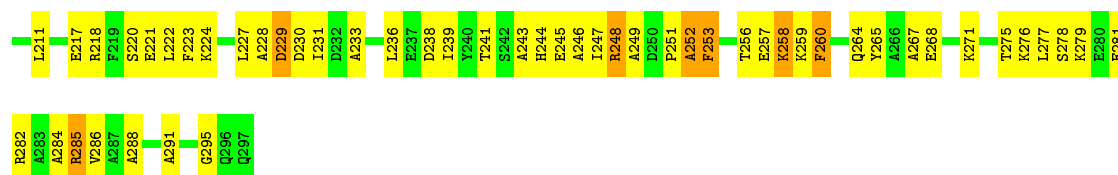
Chain H: 40% 47% 12%



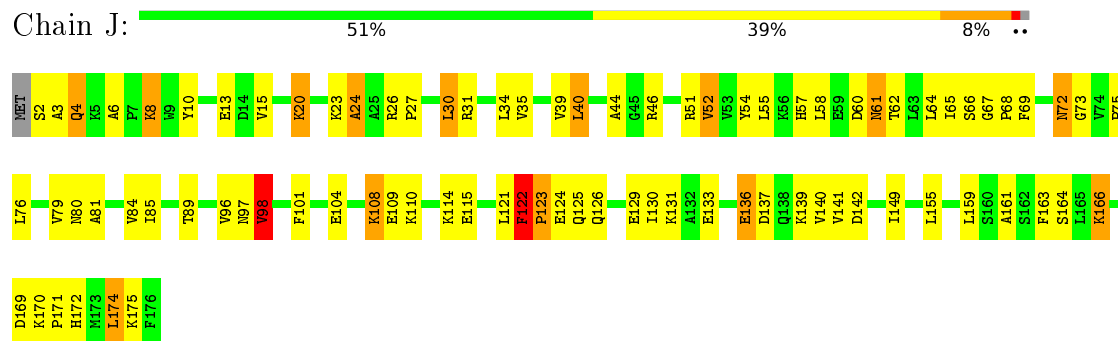
• Molecule 9: uL18 (yeast L5)

Chain I: 39% 51% 10%

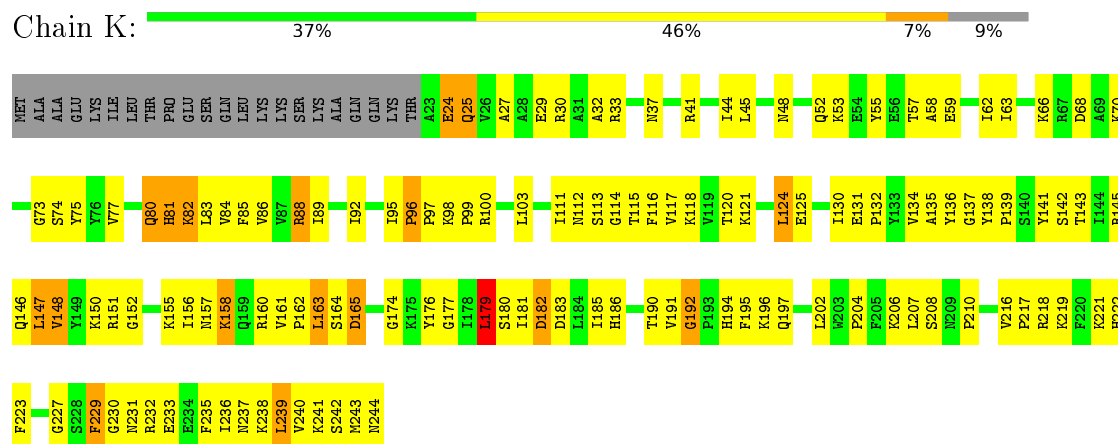




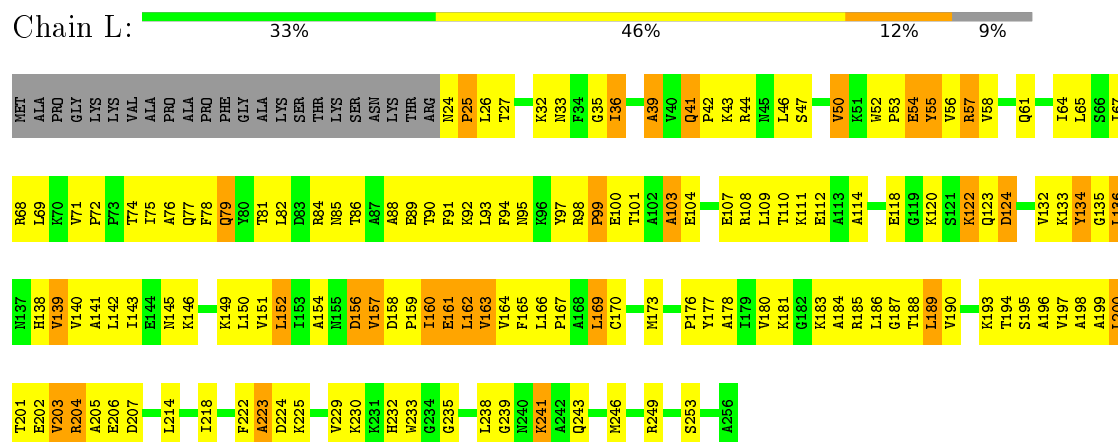
• Molecule 10: eL6 (yeast L6)



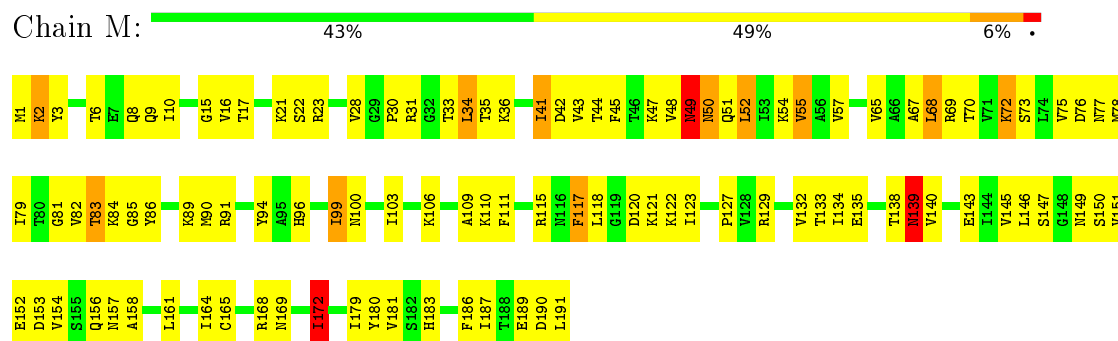
• Molecule 11: uL30 (yeast L7)



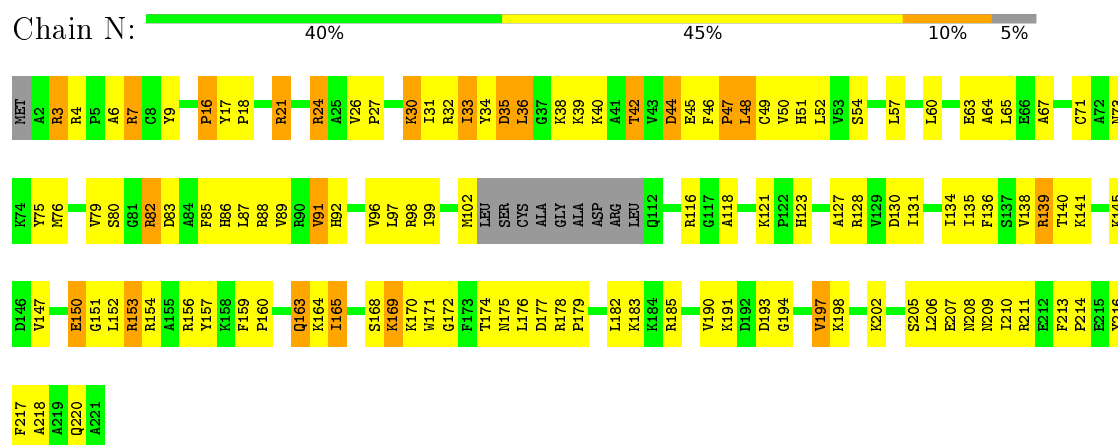
• Molecule 12: eL8 (yeast L8)



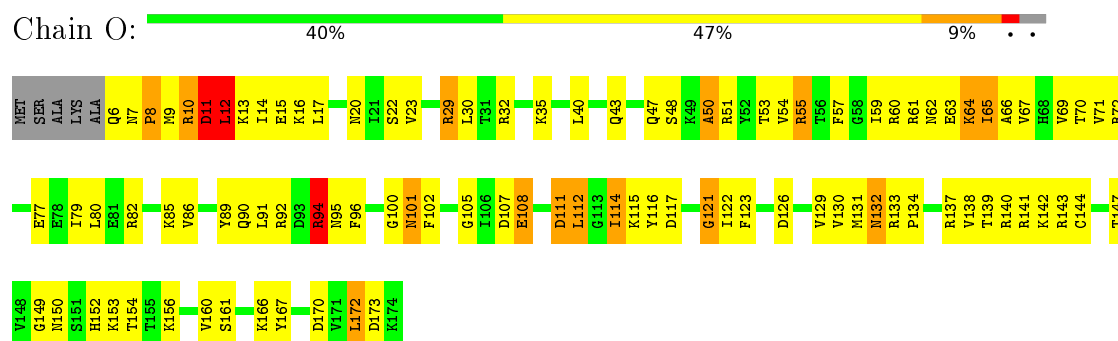
• Molecule 13: uL6 (yeast L9)



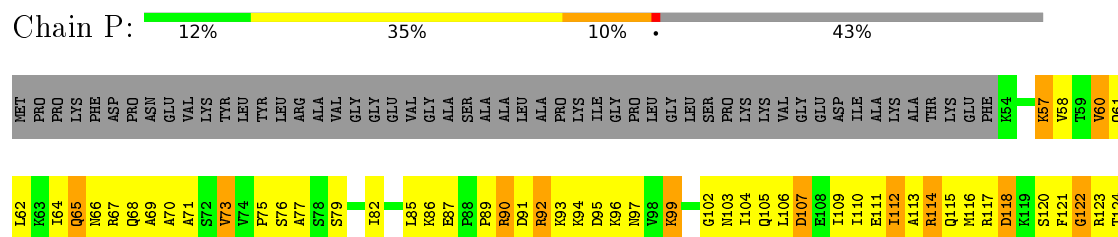
• Molecule 14: uL16 (yeast L10)



• Molecule 15: uL5 (yeast L11)



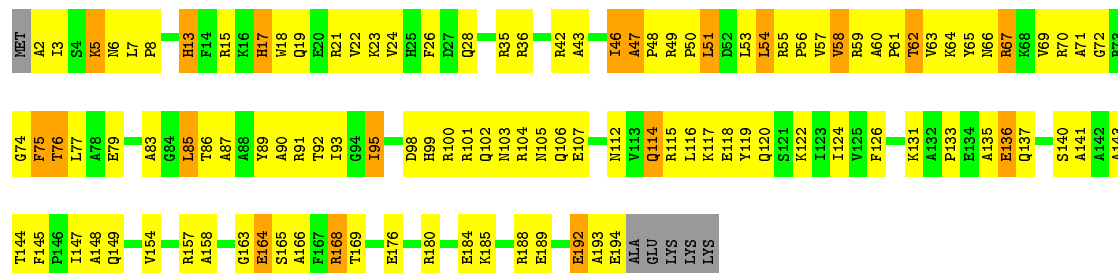
• Molecule 16: uL11 (yeast L12)





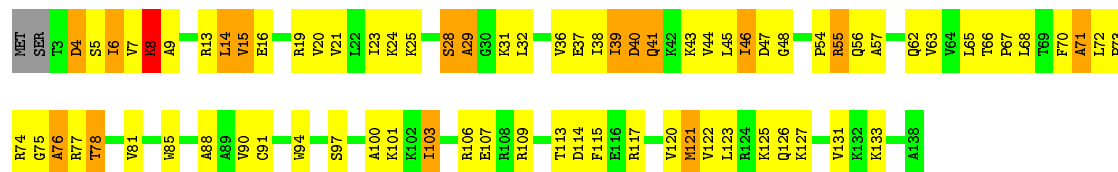
• Molecule 17: eL13 (yeast L13)

Chain Q: 40% 47% 10%



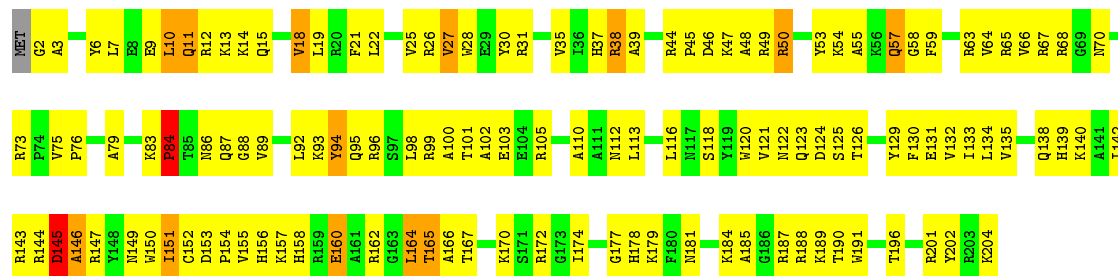
• Molecule 18: eL14 (yeast L14)

Chain R: 43% 43% 12%



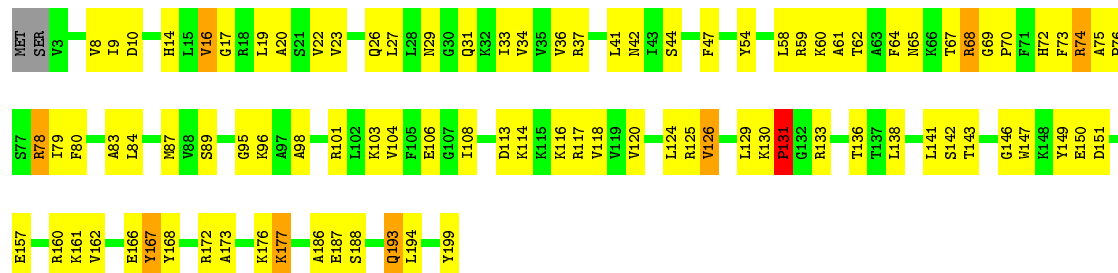
• Molecule 19: eL15 (yeast L15)

Chain S: 36% 56% 6%

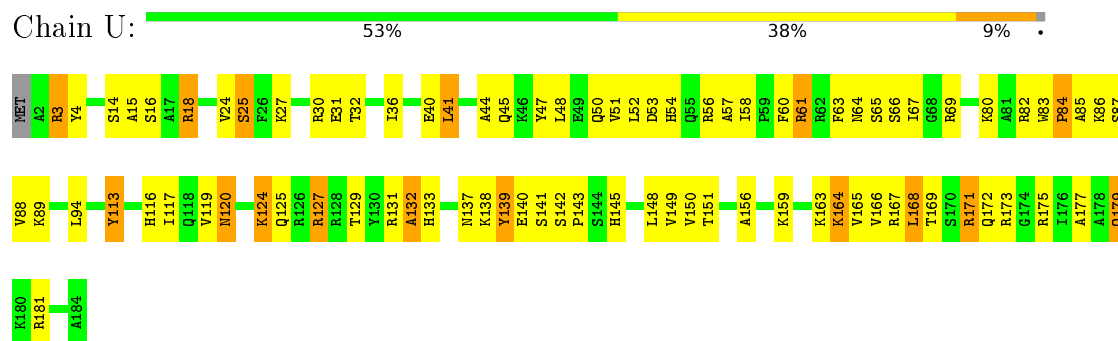


• Molecule 20: uL13 (yeast L16)

Chain T: 52% 43%



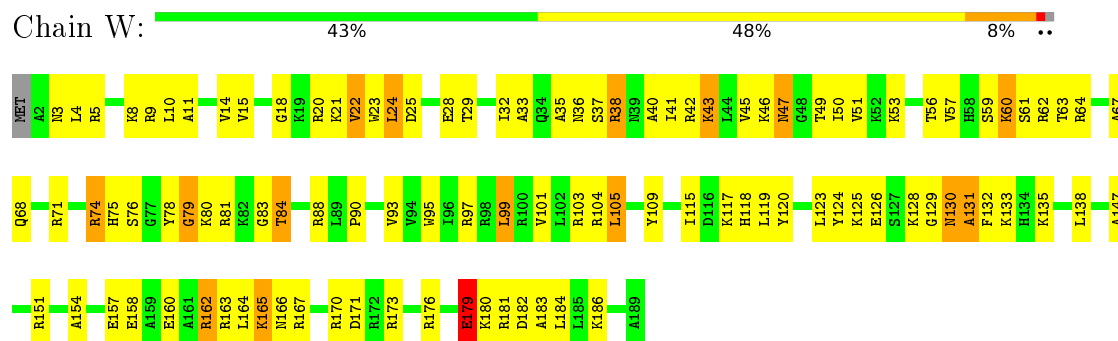
- Molecule 21: uL22 (yeast L17)



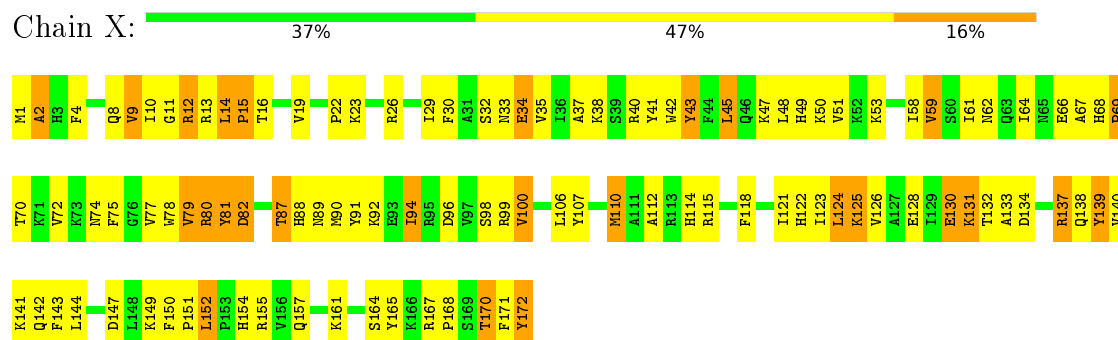
- Molecule 22: eL18 (yeast L18)



- Molecule 23: eL19 (yeast L19)

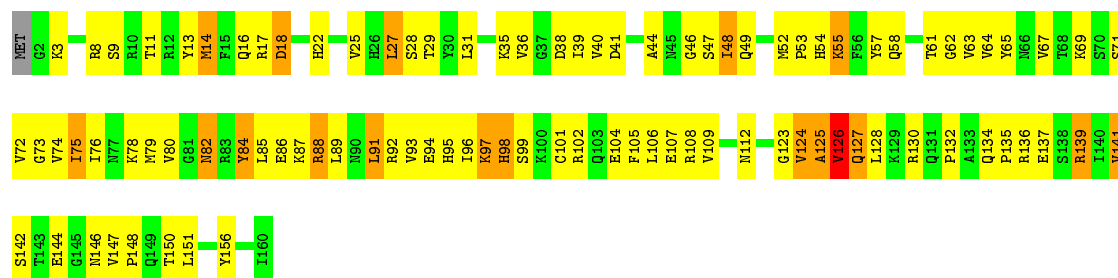


- Molecule 24: eL20 (yeast L20)



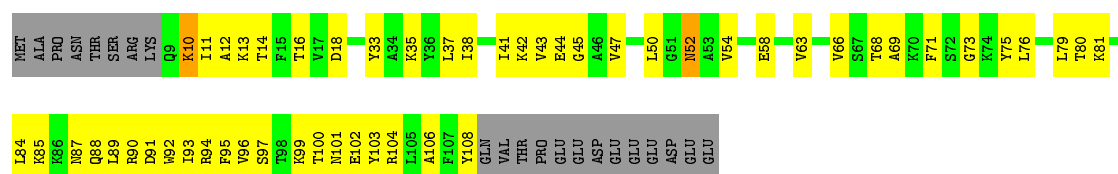
- Molecule 25: eL21 (yeast L21)

Chain Y:  40% 48% 11% ..



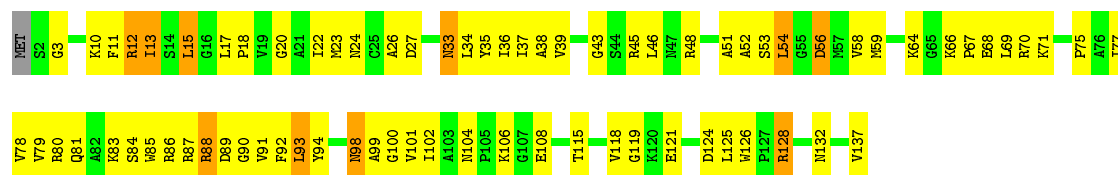
- Molecule 26: eL22 (yeast L22)

Chain Z:  39% 42% • 17%



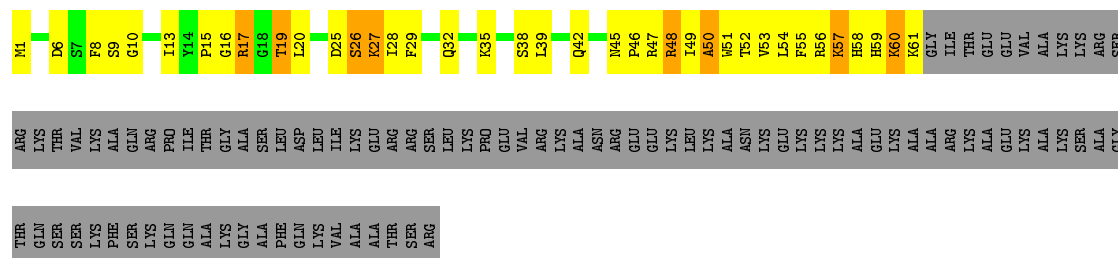
- Molecule 27: uL14 (yeast L23)

Chain AA:  45% 47% 7%



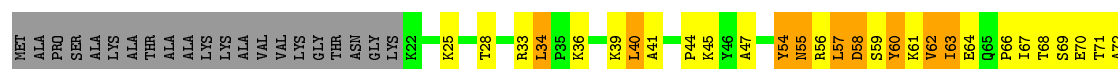
- Molecule 28: eL24 (yeast L24)

Chain BA:  15% 19% 5% 61%



- Molecule 29: uL23 (yeast L25)

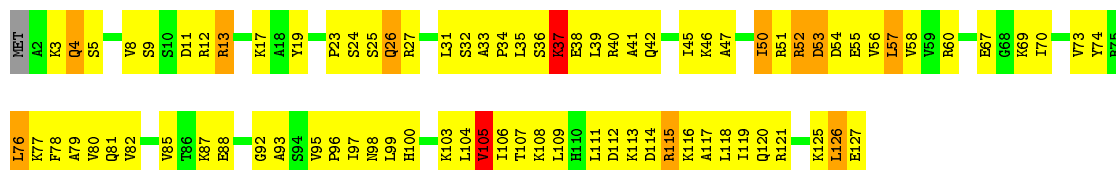
Chain CA:





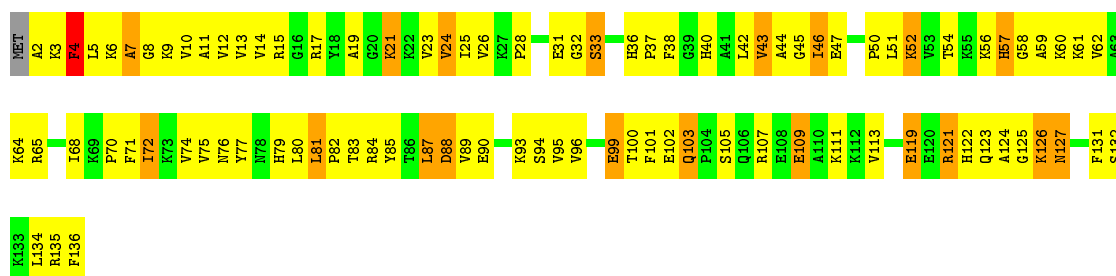
• Molecule 30: uL24 (yeast L26)

Chain DA: 33% 57% 8% ..



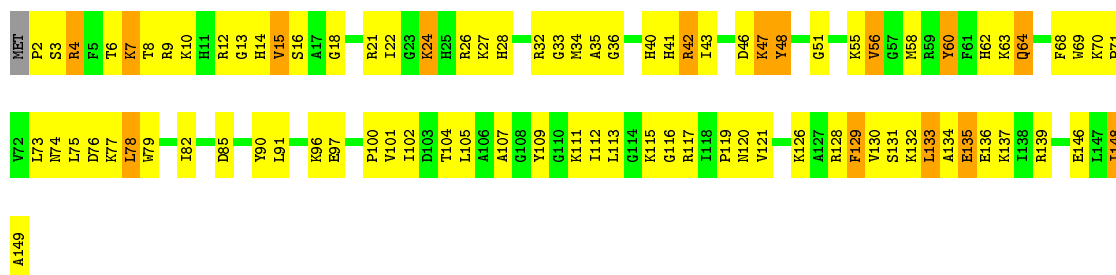
• Molecule 31: eL27 (yeast L27)

Chain EA: 30% 54% 14% ..



• Molecule 32: uL15 (yeast L28)

Chain FA: 40% 49% 10% .

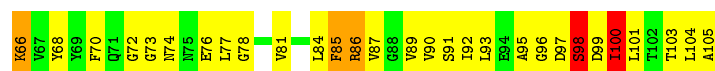
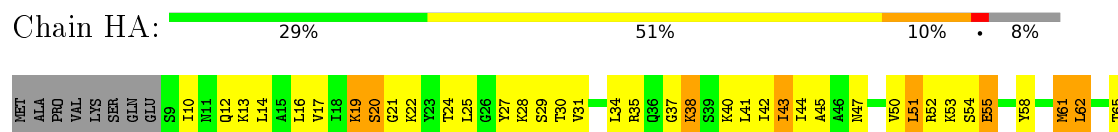


• Molecule 33: eL29 (yeast L29)

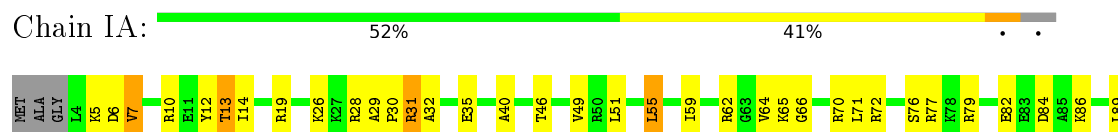
Chain GA: 58% 37% ..



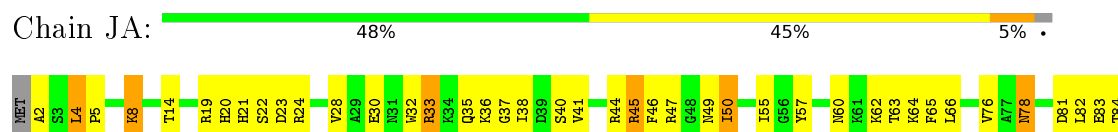
• Molecule 34: eL30 (yeast L30)



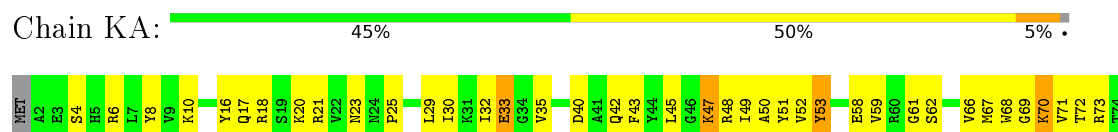
- Molecule 35: eL31 (yeast L31)



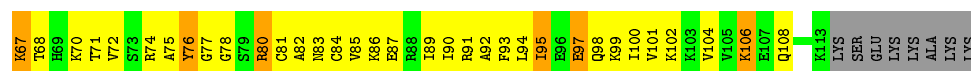
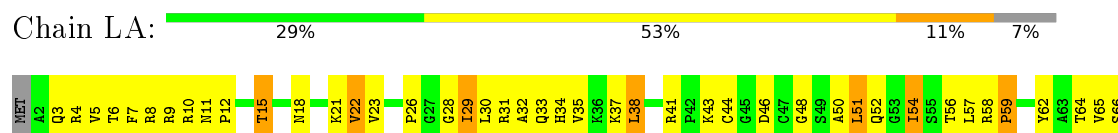
- Molecule 36: eL32 (yeast L32)



- Molecule 37: eL33 (yeast L33)

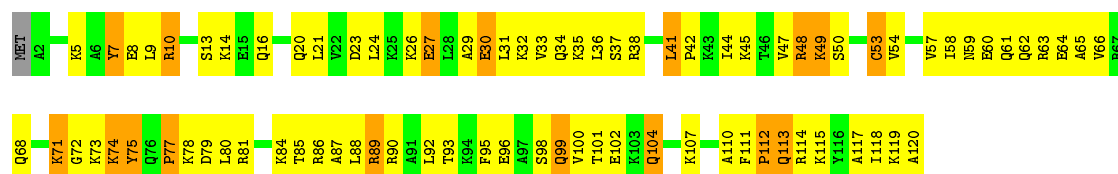


- Molecule 38: eL34 (yeast L34)

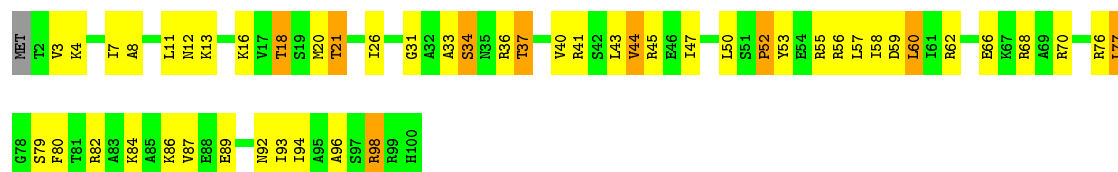


- Molecule 39: uL29 (yeast L35)

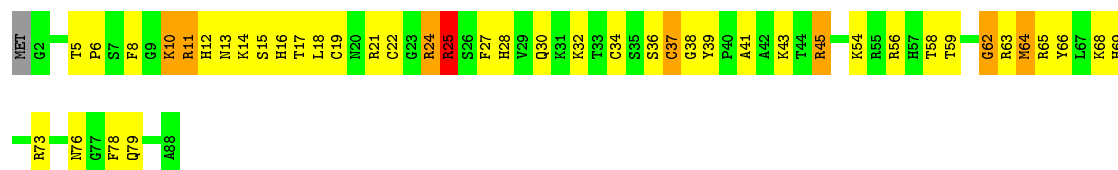




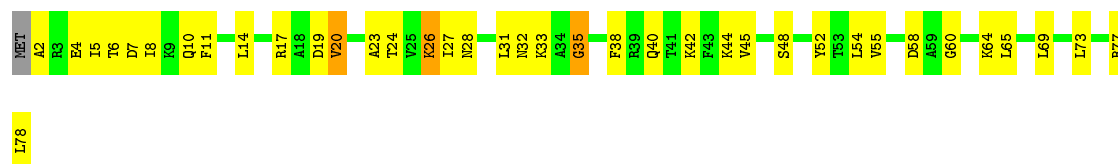
- Molecule 40: eL36 (yeast L36)



- Molecule 41: eL37 (yeast L37)



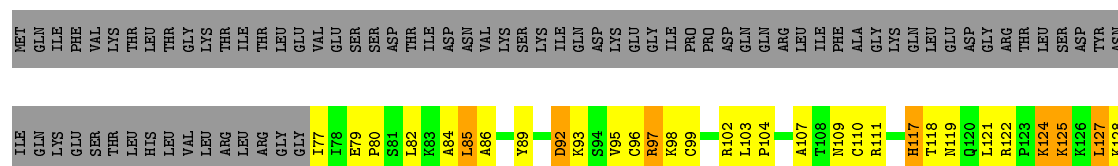
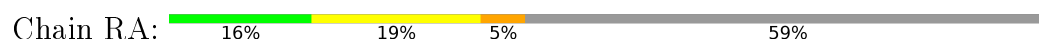
- Molecule 42: eL38 (yeast L38)



- Molecule 43: eL39 (yeast L39)



- Molecule 44: eL40 (yeast L40)



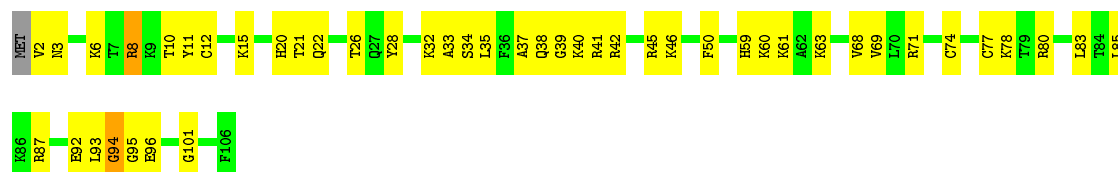
- Molecule 45: eL41 (yeast L41)

Chain SA: 



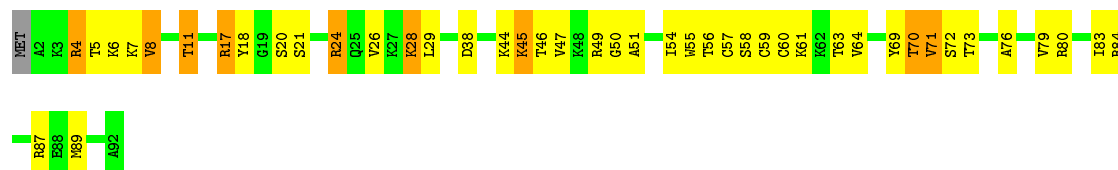
- Molecule 46: eL42 (yeast L42)

Chain TA: 



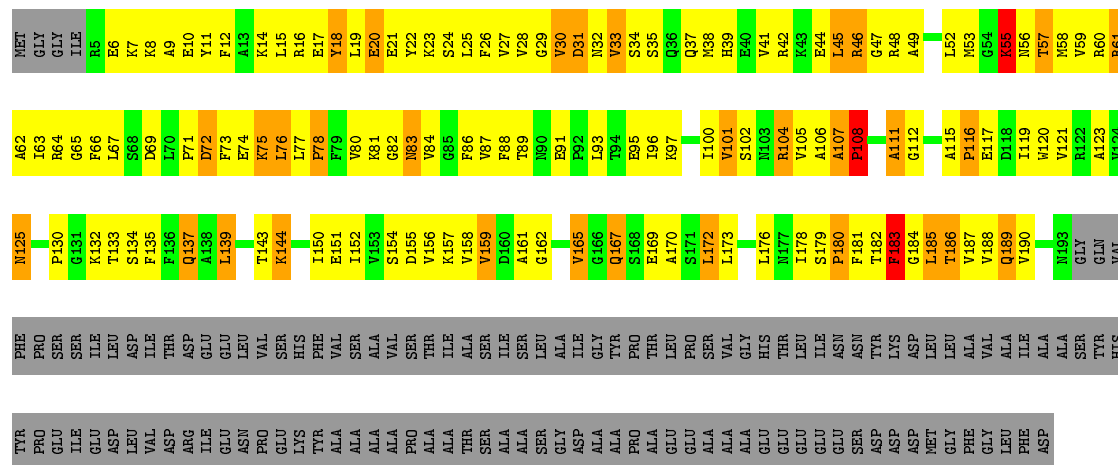
- Molecule 47: eL43 (yeast L43)

Chain UA:  51% 38% 10%



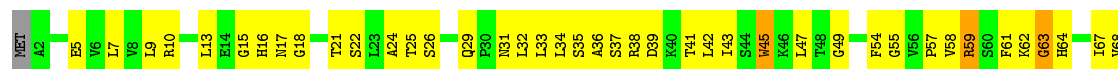
- Molecule 48: uL10 (yeast P0)

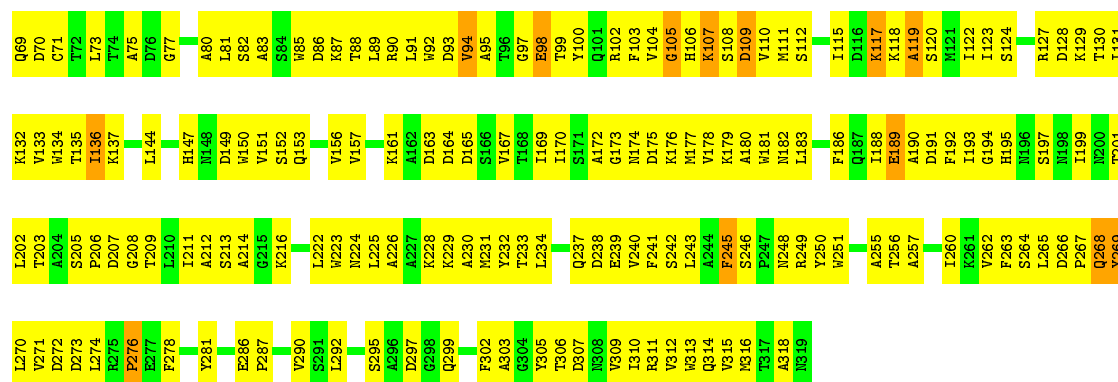
Chain VA:  17% 33% 10% 39%



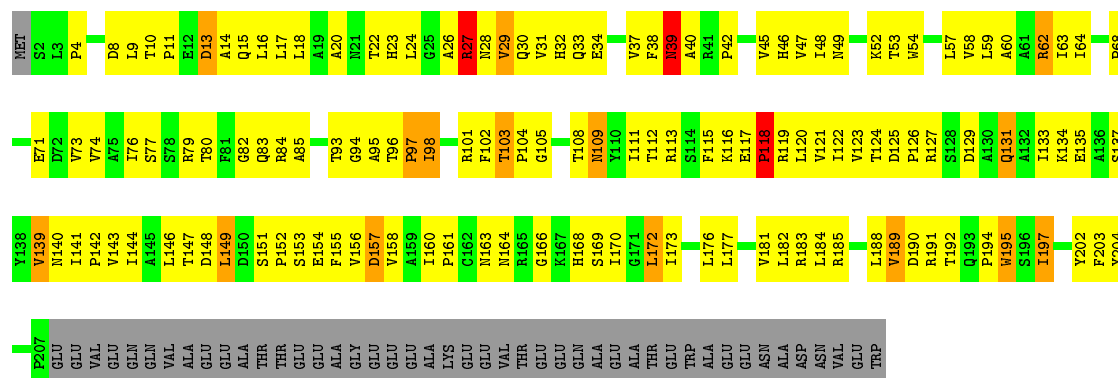
- Molecule 49: RACK1 (yeast Asc1)

Chain WA:  33% 62% 5%

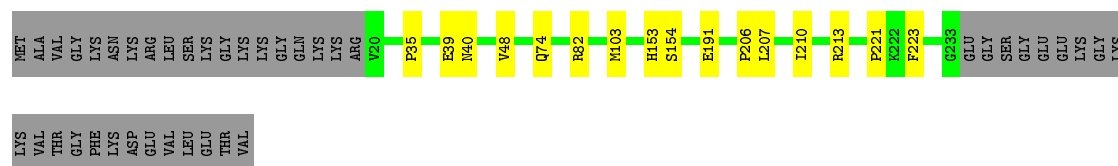
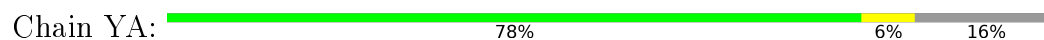




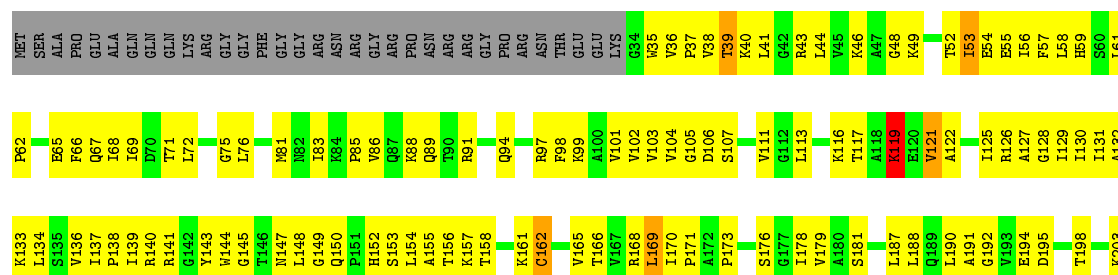
• Molecule 50: uS2 (yeast S0)

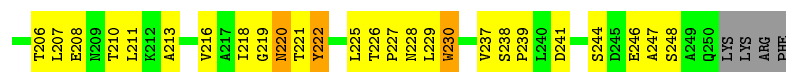


• Molecule 51: eS1 (yeast S1)



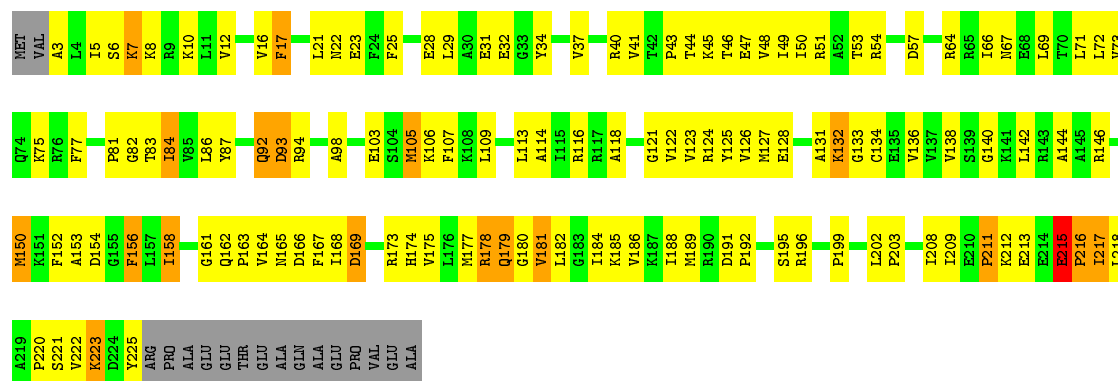
• Molecule 52: uS5 (yeast S2)





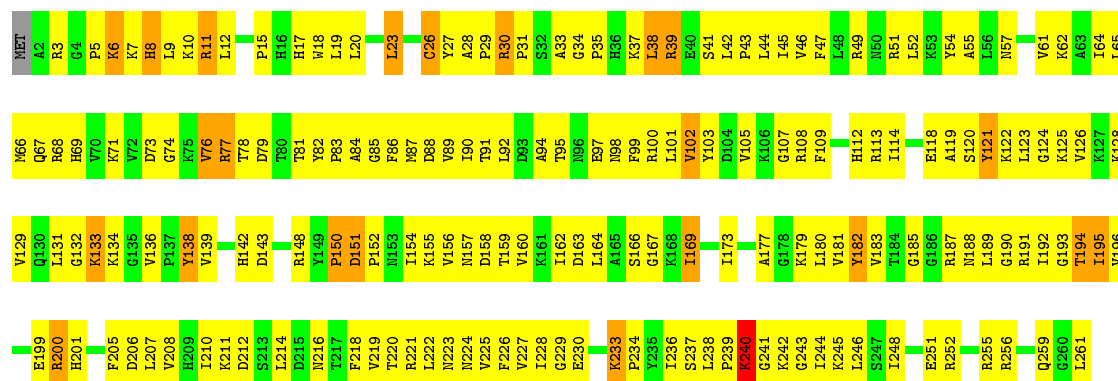
• Molecule 53: uS3 (yeast S3)

Chain AB: 39% 46% 8% 7%



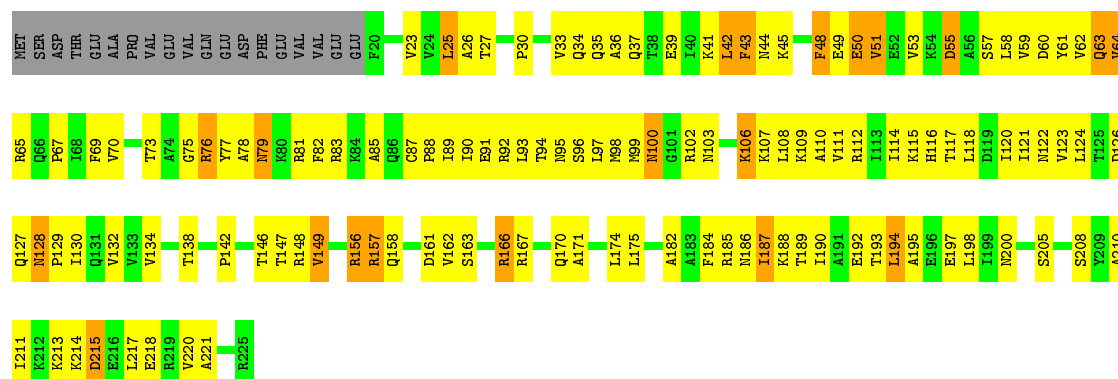
• Molecule 54: eS4 (yeast S4)

Chain BB: 30% 61% 8%



• Molecule 55: uS7 (yeast S5)

Chain CB: 35% 48% 9% 8%



• Molecule 56: eS6 (yeast S6)

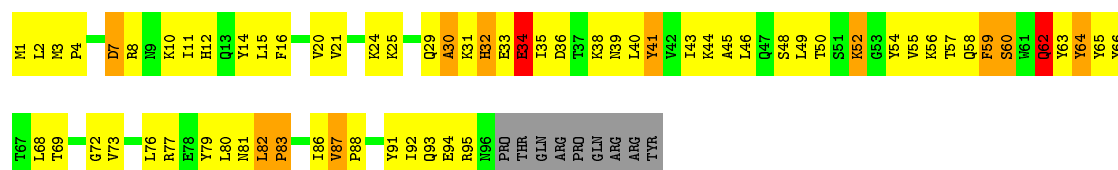
LVS	ARG	D152	L75	M1
	ARG	V153	L76	K2
	ARG	R154	L77	K3
	ALA			N4
	SER	R159	Y84	I5
	SER	R160	R85	S6
	LEU	E161	P86	Y7
	LVS	V162	R87	P8
	ALA	K163	R88	
		K164		
	K167	E91	Q13	
	K168	R95	K14	
	Y169	S96	T15	
	T170	V97	E17	
		R98	I18	
	P173	G99	D19	
	K174	A100	D20	
	I175	I101	E21	
	Q176	V102	E22	
	R177	G103	R23	
	K178	P104	I24	
	V179	D105	R25	
	T180	L106	V98	
	P181	A107	F27	
	Q182	V108	F28	
	R183	L109	D29	
	L184	A110	K30	
	Q185	I111	R31	
	R186	V112	I32	
	K187	I113	K33	
	R188	V114	Q34	
	H189	K115	E35	
	Q190	K116	V36	
	R191	G117		
	A192	E118	D43	
	L193	Q119		
		E120	Y48	
	R196	L121	V49	
		E122	F50	
	R202	G123	K51	
		L124	I52	
	E207	T125	S53	
	Y208	R132	N56	
	Q210	L133	D57	
	L211	G134	K58	
		P135	Q59	
		K136	G60	
	R215	R137		
	L216	A138	M63	
	E218	N139	K64	
	R219	N140	Q65	
	K220	I141	G66	
	A221	R142	V67	
	E222		L68	
	K223	L147	L69	
		S148	P70	
	L226		I73	
	A26	P151	E74	

R139	L67	Met
V140	A68	Ser
R141	G69	Ala
	F70	P4
V144	H71	Q5
G145	K72	A6
	V73	K7
I149	Q74	I8
Q150	L77	L9
K151	E80	S10
V152	L81	Q11
L153	E82	A12
L154	K83	P13
S156	K84	T14
	F85	L16
	K86	E17
V159	D87	E17
	R88	L18
I162	I91	Q19
D163	F92	V20
K164	L93	A21
K165	A94	A23
L166	E95	F24
E167	R97	
S168	I98	L27
	L99	E28
	K101	N29
	P100	S30
	K102	S31
	S103	P32
	R104	E33
G178	K111	L34
R179	R112	K35
Q180	P113	A36
L181	H114	E37
I181	S115	L38
V182	R116	R39
	T117	P40
	L118	L41
F183	I119	A42
E184	A120	F43
I185	V121	
P186	K124	I46
S187	I125	
	E127	I49
	L129	D50
GLU	F130	V51
THR	P132	
HIS	I135	K56
		A57
		L58
		A59
		I60
		F61
		V62
		P63
		V64
		P65
		S66

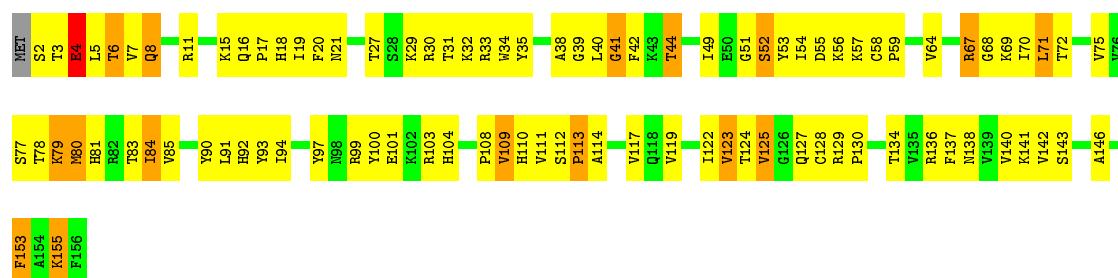
R194	LVS	F65	MET
R195	GLU	S66	I3
L196	GLU	w67	S4
K199	GLU	E70	R8
K200	THR	G71	H9
	VAL	S73	
	ALA		
	K135	T76	K10
	K137	R77	R11
	N138	I78	S12
	A139	A79	A13
	E140	G80	T14
	R141	R81	G15
	K142	R82	A16
	M143	R83	K17
		R84	R18
	R146		A19
	A147	R85	Q20
	A148	S86	F21
	S149	R87	R22
	A150	N88	K23
	K151	R89	K24
	I152	L90	R25
	E153	R91	R26
	S154	R92	F27
	S155	T93	F28
	V156	N94	L29
	E157	T95	G30
	S158	L96	R31
	Q159	T97	Q32
	F160	R98	
		A99	N35
	R164	A100	T36
	L165	I101	K37
	V166	R102	I38
	A167	Q103	G39
		I104	
	R172	A106	R42
	P173	T107	I43
	G174	P108	
	Q175	F109	V46
	S176	R110	R47
	R177	Q111	T48
	C179	M112	R49
	D180	F113	G50
	G181		G51
	I182		R52
	L183	H116	K53
	R184	V117	K54
	A185	G118	V55
	G186	Q119	R56
	E187	T120	A57
	E188	L121	L58
	L189	G122	R59
	A190	K123	I60
	F191	LVS	E61
	I192	TVS	T62
	L193	ASN	G63
		V11	N64

MET	P2	P3	A4	P5	R6	T7		K10	T11		T14	P15	K16	R17	P18	Y19	E20			L24		L28	K29	L30	A31	G32	E33	F34	G35	L36	K37	N38	K39	K40	E41	I42	Y43	R44	I45	S46	Q48	L49	S50	K51	I52	R53	R54	A55	A56	R57	D58	L59	L60		E64	K65	D66		P69
-----	----	----	----	----	----	----	--	-----	-----	--	-----	-----	-----	-----	-----	-----	-----	--	--	-----	--	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	-----	-----	-----	--	-----

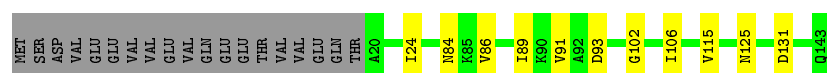
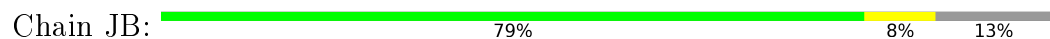
- Molecule 60: eS10 (yeast S10)



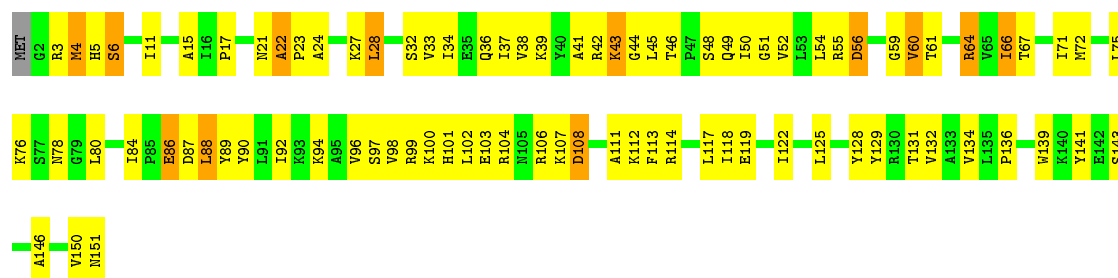
- Molecule 61: uS17 (yeast S11)



- Molecule 62: eS12 (yeast S12)



- Molecule 63: uS15 (yeast S13)



- Molecule 64: uS11 (yeast S14)

MET
SER
ASN
VAL
VAL
GLN
ALA
ARG
ASP
ASN
S11
L33
S34
V42
T43
G44
G45
G75
G87
R114
V118
S123
R127
G130
G134
L137

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| LVS | P75 | V76 | R77 | T78 | H79 | R80 | R81 | R84 | R85 | V86 | P87 | R90 | G91 | S92 | V93 | I96 | Y97 | N98 | A101 | F102 | N103 | E106 | I107 | R108 | P109 | E110 | M111 | L112 | Y115 | L116 | F119 | S120 | I121 | I122 | Y123 | P124 | P125 | V126 | R127 | H128 | G129 | ANG | A1A | GLY | ALA | ALA | THR | THR | SER | ANG | PHE | I1E | PRO | LEU |
| | MTT | SER | GLN | ALA | VAL | ASN | ALA | K8 | Y11 | F12 | K13 | T14 | H15 | S16 | Y17 | R18 | G19 | V20 | D21 | L22 | E23 | K24 | L25 | M28 | S29 | T30 | E31 | D32 | F33 | V34 | K35 | L36 | A37 | P38 | A39 | R40 | V41 | R42 | R43 | R44 | F45 | A46 | R47 | T50 | S51 | K52 | P53 | L60 | L65 | P68 | E69 | H73 | P74 | |

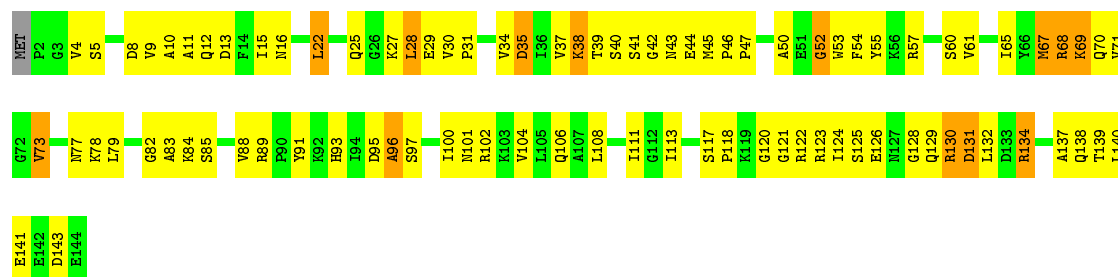
- | | | |
|------|------|-----|
| R137 | T70 | MET |
| F138 | G71 | SER |
| Q139 | G72 | A3 |
| K140 | G73 | V4 |
| S141 | H74 | P5 |
| Y142 | V75 | S6 |
| R143 | S76 | V7 |
| | Q77 | Q8 |
| | T78 | T9 |
| | Y79 | F10 |
| | A80 | G11 |
| | I81 | K12 |
| | R82 | |
| | Q83 | S15 |
| | A84 | A16 |
| | I85 | T17 |
| | A86 | A18 |
| | G88 | |
| | L89 | V22 |
| | V90 | K23 |
| | A91 | K26 |
| | Y92 | G27 |
| | H93 | L28 |
| | | I29 |
| | Y96 | K30 |
| | V97 | V31 |
| | D98 | N32 |
| | E99 | |
| | Q100 | P35 |
| | S101 | |
| | K102 | L38 |
| | N103 | V39 |
| | E104 | E40 |
| | L105 | P41 |
| | K106 | E42 |
| | | I43 |
| | F109 | L44 |
| | | R45 |
| | | F46 |
| | Y112 | K47 |
| | R113 | V48 |
| | T115 | V49 |
| | L116 | E50 |
| | L117 | P51 |
| | I118 | L52 |
| | A119 | L53 |
| | D120 | L54 |
| | | V55 |
| | R123 | S56 |
| | P124 | L57 |
| | E125 | D58 |
| | P126 | K59 |
| | K127 | F60 |
| | K128 | S61 |
| | F129 | N62 |
| | G130 | I63 |
| | G131 | D64 |
| | | L65 |
| | S136 | |

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| S70 | F71 | K72 | L73 | V85 | P86 | E87 | V88 | V89 | L100 | N101 | D102 | N104 | L109 | K116 | L117 | P118 | L1U | SER | VAL | ILE | ASN | VAL | SER | ALA | GLN | ARG | ASP | ARG | TTR | ARG | LYS | ARG | VAL | | | | | | | | | | | | | | | | | | | | |
| MET | G2 | R3 | V4 | R5 | V9 | K10 | K14 | A15 | L16 | I17 | E18 | R19 | Y20 | Y21 | P22 | K23 | L24 | T25 | L26 | D27 | P28 | Q29 | N31 | K32 | R33 | L34 | I38 | A39 | T40 | I41 | Q42 | S43 | K44 | R45 | L46 | R47 | M48 | R49 | I50 | Y53 | T54 | B55 | R56 | L57 | M58 | K59 | R60 | I61 | Q62 | K63 | R67 | G68 | T69 |

- [illegible]

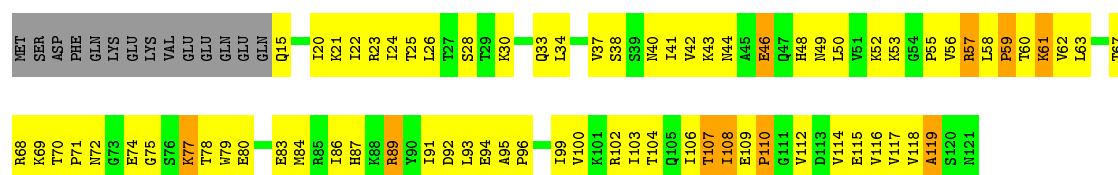
- 


Chain QB: 



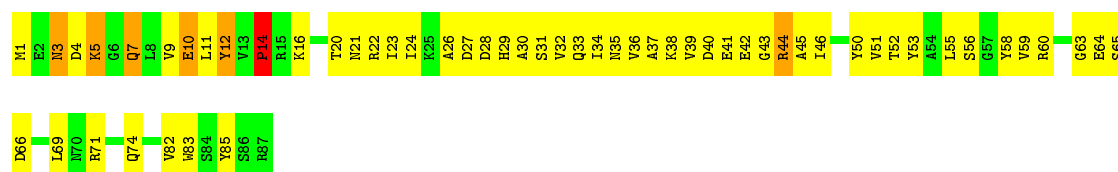
- Molecule 70: uS10 (yeast S20)

Chain RB: 



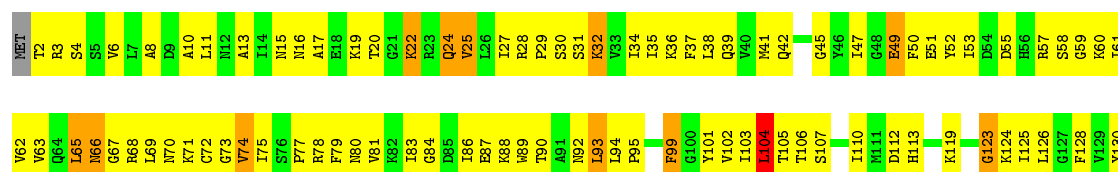
- Molecule 71: eS21 (yeast S21)

Chain SB: 



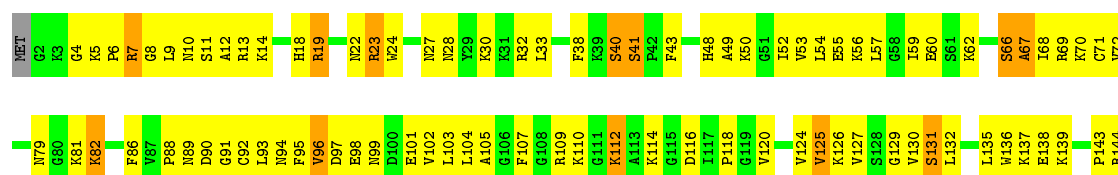
- Molecule 72: uS8 (yeast S22)

Chain TB: 



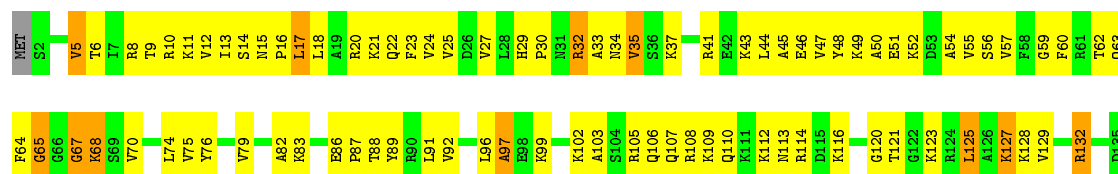
- Molecule 73: uS12 (yeast S23)

Chain UB: 



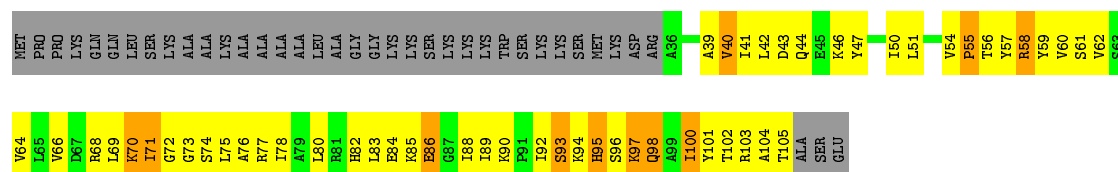
- Molecule 74: eS24 (yeast S24)

Chain VB: 36% 56% 8%



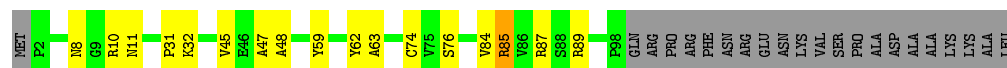
- Molecule 75: eS25 (yeast S25)

Chain WB: 



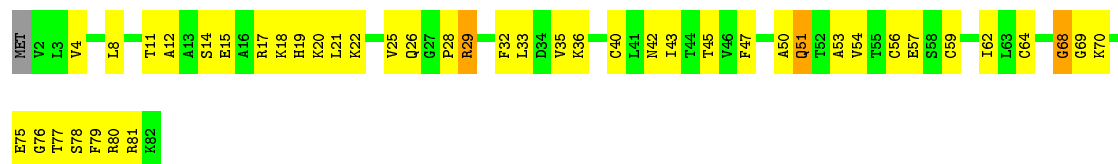
- Molecule 76: eS26 (yeast S26)

Chain XB:  67% 13% • 18%



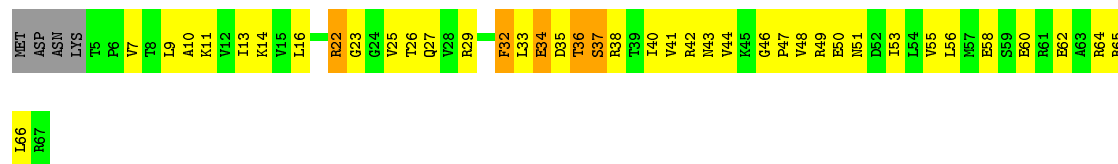
- Molecule 77: eS27 (yeast S27)

Chain YB:  45% 50% ..



- Molecule 78: eS28 (yeast S28)

Chain ZB:



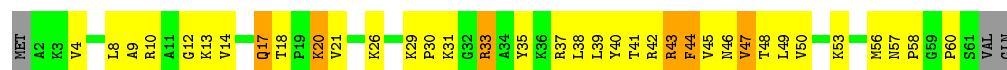
- Molecule 79: uS14 (yeast S29)

Chain AC: 



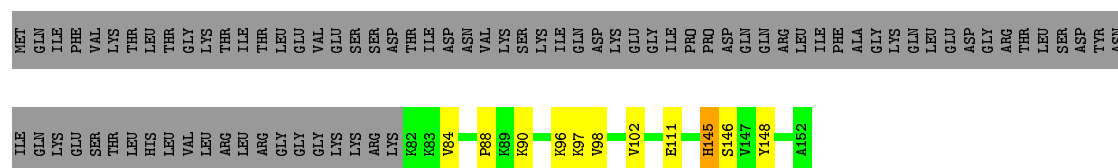
- Molecule 80: eS30 (yeast S30)

Chain BC: 



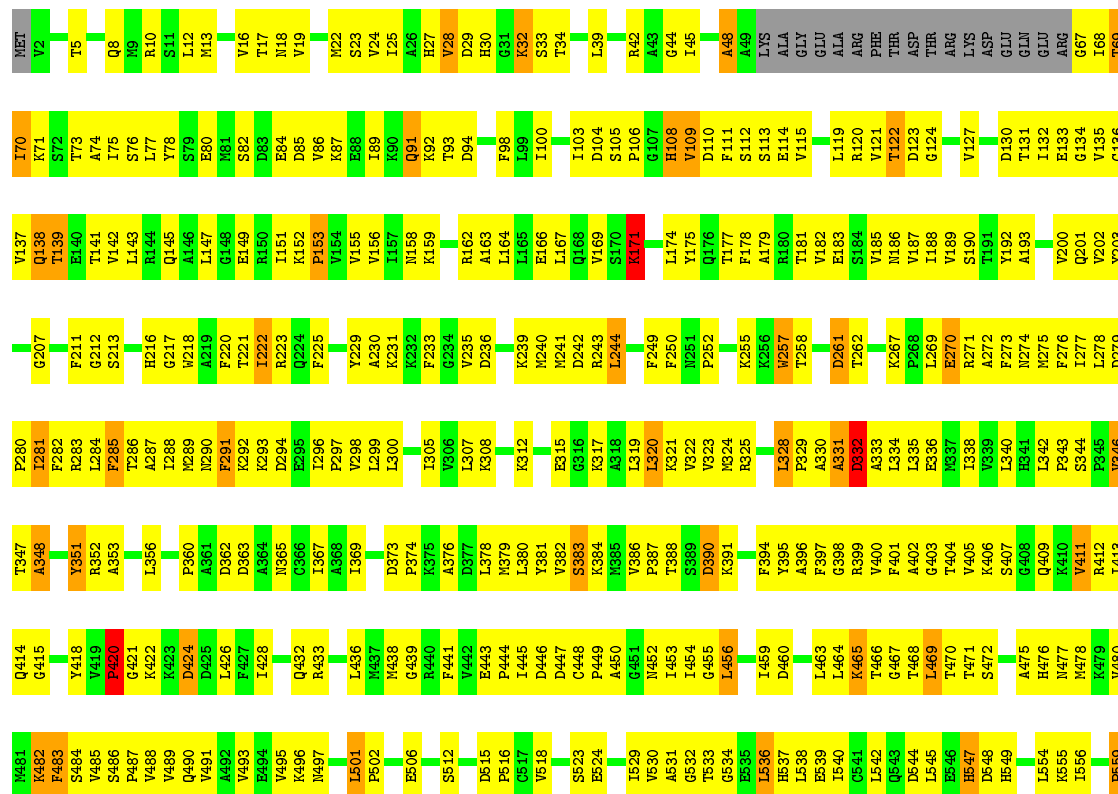
- Molecule 81: eS31 (yeast S31)

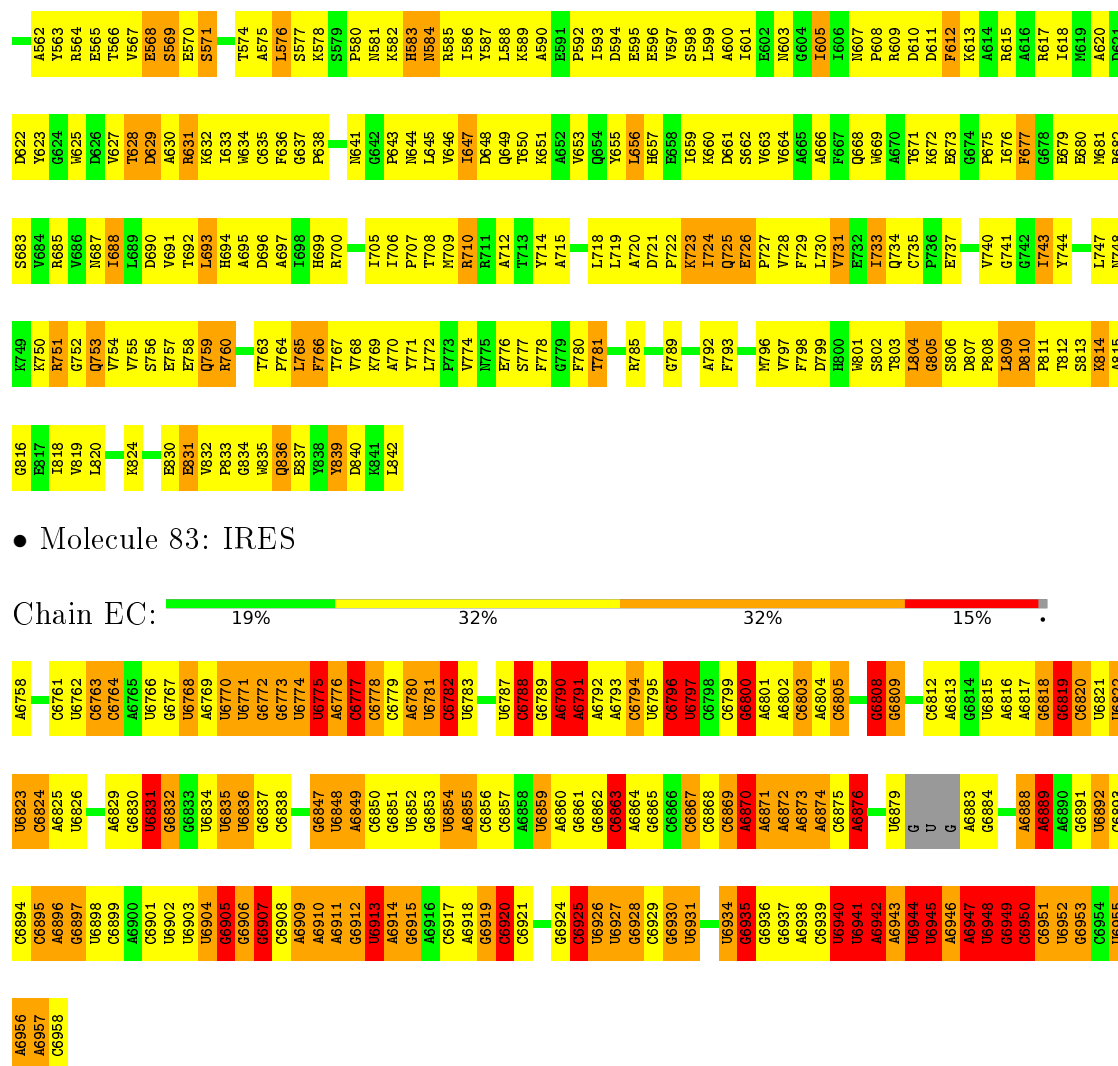
Chain CC: 



- Molecule 82: yeast eEF2

Chain DC: 





• Molecule 83: IRES

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	59570	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 ($e^-/\text{\AA}^2$)	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	0.90	3/41014 (0.0%)	0.75	14/63809 (0.0%)
10	J	0.96	0/1425	0.68	0/1912
11	K	0.90	0/1822	0.66	1/2451 (0.0%)
12	L	0.79	0/1850	0.65	0/2495
13	M	0.82	0/1540	0.66	0/2073
14	N	0.93	0/1754	0.62	0/2350
15	O	0.77	0/1375	0.60	0/1842
16	P	1.93	0/728	0.86	2/975 (0.2%)
17	Q	0.82	0/1568	0.62	0/2106
18	R	0.91	0/1069	0.65	0/1438
19	S	0.84	0/1758	0.65	0/2354
2	B	0.81	5/78631 (0.0%)	0.73	14/122552 (0.0%)
20	T	0.81	0/1586	0.62	0/2128
21	U	0.83	0/1466	0.60	0/1968
22	V	0.84	0/1466	0.68	0/1965
23	W	0.76	0/1539	0.63	0/2050
24	X	0.93	0/1482	0.70	0/1990
25	Y	0.92	0/1301	0.62	0/1743
26	Z	0.71	0/812	0.54	0/1099
27	AA	0.80	0/1019	0.61	0/1369
28	BA	0.98	0/521	0.58	0/691
29	CA	0.88	0/984	0.71	1/1325 (0.1%)
3	C	0.81	1/3747 (0.0%)	0.72	1/5832 (0.0%)
30	DA	0.87	0/1005	0.67	1/1341 (0.1%)
31	EA	0.77	0/1119	0.59	0/1497
32	FA	0.79	0/1205	0.66	0/1612
33	GA	0.79	0/474	0.59	0/629
34	HA	0.69	0/751	0.64	1/1008 (0.1%)
35	IA	0.72	0/904	0.61	0/1213
36	JA	0.85	0/1041	0.62	0/1394
37	KA	0.80	0/869	0.68	0/1168
38	LA	0.79	0/891	0.69	0/1191

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	MA	0.82	0/979	0.64	0/1301
4	D	0.78	1/2884 (0.0%)	0.68	0/4491
40	NA	0.81	0/779	0.63	0/1034
41	OA	0.90	0/697	0.70	0/923
42	PA	0.83	0/619	0.61	0/826
43	QA	0.85	0/444	0.69	0/588
44	RA	0.88	0/424	0.66	0/562
45	SA	1.55	0/235	0.81	0/300
46	TA	0.86	0/861	0.65	0/1136
47	UA	0.78	0/702	0.65	0/934
48	VA	1.80	0/1498	1.03	9/2025 (0.4%)
49	WA	0.90	0/2498	0.60	0/3398
5	E	2.02	2/1377 (0.1%)	0.83	1/1844 (0.1%)
50	XA	0.66	0/1653	0.57	0/2261
51	YA	1.17	0/855	0.56	0/1067
52	ZA	0.66	0/1665	0.58	0/2263
53	AB	0.86	0/1759	0.59	0/2368
54	BB	0.81	0/2110	0.63	0/2839
55	CB	0.83	0/1630	0.58	0/2202
56	DB	0.83	0/1844	0.59	0/2464
57	EB	0.87	0/1506	0.60	0/2028
58	FB	0.93	0/1515	0.63	0/2021
59	GB	0.70	0/1519	0.59	0/2035
6	F	0.80	0/1952	0.68	1/2622 (0.0%)
60	HB	0.98	0/837	0.59	0/1131
61	IB	0.95	0/1273	0.62	0/1712
62	JB	1.12	0/495	0.58	0/617
63	KB	0.88	0/1216	0.59	0/1638
64	LB	1.10	0/507	0.60	0/632
65	MB	0.97	0/996	0.63	0/1335
66	NB	0.90	0/1126	0.63	0/1510
67	OB	0.76	0/844	0.84	4/1120 (0.4%)
68	PB	0.88	0/1212	0.60	1/1628 (0.1%)
69	QB	0.86	0/1131	0.59	0/1517
7	G	0.75	0/3153	0.62	0/4239
70	RB	0.91	0/866	0.60	0/1169
71	SB	0.67	0/694	0.57	0/935
72	TB	0.74	0/1039	0.64	1/1395 (0.1%)
73	UB	0.82	0/1140	0.62	0/1518
74	VB	0.80	0/1088	0.57	0/1449
75	WB	0.87	0/571	0.59	0/768
76	XB	1.15	0/387	0.60	0/482
77	YB	0.81	0/621	0.59	0/838

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
78	ZB	0.84	0/500	0.60	0/670
79	AC	0.94	0/454	0.56	0/602
8	H	0.83	0/2802	0.67	0/3792
80	BC	0.82	0/483	0.62	0/643
81	CC	1.03	0/283	0.64	0/352
82	DC	1.42	0/6521	0.70	1/8830 (0.0%)
83	EC	2.32	82/4579 (1.8%)	0.94	15/7119 (0.2%)
9	I	0.83	0/2426	0.62	0/3271
All	All	0.94	94/227965 (0.0%)	0.71	68/334014 (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	18
2	B	0	70
3	C	0	4
48	VA	0	2
82	DC	0	1
83	EC	0	9
All	All	0	104

The worst 5 of 94 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	EC	6831	U	N1-C2	7.29	1.45	1.38
83	EC	6908	C	N1-C2	7.27	1.47	1.40
83	EC	6867	C	N1-C2	7.03	1.47	1.40
2	B	2263	C	N1-C2	6.96	1.47	1.40
4	D	1	G	OP3-P	-6.96	1.52	1.61

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	VA	108	PRO	CB-CA-C	-16.97	69.58	112.00
67	OB	73	LEU	N-CA-C	9.72	137.25	111.00
48	VA	108	PRO	CA-C-N	-8.74	97.97	117.20
83	EC	6788	C	N1-C1'-C2'	8.43	124.96	114.00
1	A	1339	C	N1-C1'-C2'	8.29	124.78	114.00

There are no chirality outliers.

5 of 104 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	143	G	Sidechain
1	A	199	G	Sidechain
1	A	207	U	Sidechain
1	A	287	G	Sidechain
1	A	60	U	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	36760	0	18348	1440	0
2	B	70288	0	35262	2381	0
3	C	3354	0	1695	114	0
4	D	2580	0	1304	103	0
5	E	1359	0	1425	110	0
6	F	1918	0	1987	209	0
7	G	3082	0	3165	226	0
8	H	2750	0	2863	225	0
9	I	2376	0	2325	197	0
10	J	1401	0	1501	88	0
11	K	1785	0	1862	134	0
12	L	1818	0	1908	178	0
13	M	1519	0	1587	116	0
14	N	1718	0	1754	136	0
15	O	1354	0	1383	102	0
16	P	723	0	774	128	0
17	Q	1543	0	1608	145	0
18	R	1054	0	1149	87	0
19	S	1721	0	1779	155	0
20	T	1556	0	1659	98	0
21	U	1443	0	1485	99	0
22	V	1442	0	1543	117	0
23	W	1522	0	1617	104	0
24	X	1446	0	1487	145	0
25	Y	1277	0	1323	107	0
26	Z	796	0	812	40	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	AA	1004	0	1048	71	0
28	BA	509	0	537	35	0
29	CA	969	0	1036	80	0
30	DA	994	0	1081	100	0
31	EA	1093	0	1155	102	0
32	FA	1174	0	1215	119	0
33	GA	463	0	491	20	0
34	HA	743	0	797	91	0
35	IA	890	0	938	44	0
36	JA	1020	0	1090	60	0
37	KA	851	0	880	59	0
38	LA	881	0	949	101	0
39	MA	970	0	1078	108	0
40	NA	772	0	849	43	0
41	OA	682	0	687	55	0
42	PA	613	0	682	36	0
43	QA	437	0	475	43	0
44	RA	418	0	459	33	0
45	SA	234	0	284	12	0
46	TA	848	0	918	36	0
47	UA	695	0	738	52	0
48	VA	1473	0	1514	186	0
49	WA	2445	0	2401	213	0
50	XA	1612	0	1623	134	0
51	YA	856	0	226	0	0
52	ZA	1635	0	1723	131	0
53	AB	1734	0	1817	132	0
54	BB	2069	0	2154	263	0
55	CB	1610	0	1675	140	0
56	DB	1820	0	1918	153	0
57	EB	1481	0	1572	131	0
58	FB	1490	0	1525	146	0
59	GB	1494	0	1573	154	0
60	HB	817	0	804	76	0
61	IB	1245	0	1314	106	0
62	JB	496	0	141	0	0
63	KB	1193	0	1255	87	0
64	LB	508	0	151	2	0
65	MB	975	0	1017	88	0
66	NB	1106	0	1166	101	0
67	OB	836	0	827	61	0
68	PB	1193	0	1222	94	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	QB	1113	0	1124	89	0
70	RB	856	0	917	91	0
71	SB	685	0	672	66	0
72	TB	1022	0	1060	84	0
73	UB	1122	0	1196	103	0
74	VB	1074	0	1132	112	0
75	WB	563	0	603	59	0
76	XB	388	0	96	3	0
77	YB	611	0	633	41	0
78	ZB	498	0	535	48	0
79	AC	444	0	436	34	0
80	BC	475	0	525	48	0
81	CC	284	0	76	1	0
82	DC	6419	0	6493	651	0
83	EC	4105	0	2063	133	0
84	DC	28	0	12	5	0
85	DC	1	0	0	0	0
86	DC	35	0	42	3	0
All	All	212656	0	156225	10781	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 29.

The worst 5 of 10781 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)
83:EC:6927:U:H3'	83:EC:6928:G:H5'	1.22	1.17
2:B:1235:U:H4'	2:B:1236:G:H5'	1.17	1.14
48:VA:108:PRO:HA	48:VA:179:SER:HA	1.14	1.13
1:A:230:C:H3'	1:A:231:U:H5''	1.31	1.12
58:FB:12:SER:HA	58:FB:18:ARG:HH21	1.10	1.11

There are no symmetry-related clashes.

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 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%)	128 (78%)	27 (16%)	10 (6%)	2	21
6	F	250/254 (98%)	175 (70%)	61 (24%)	14 (6%)	2	24
7	G	384/387 (99%)	305 (79%)	64 (17%)	15 (4%)	4	34
8	H	359/362 (99%)	255 (71%)	70 (20%)	34 (10%)	1	10
9	I	294/297 (99%)	217 (74%)	58 (20%)	19 (6%)	1	20
10	J	173/176 (98%)	131 (76%)	34 (20%)	8 (5%)	3	29
11	K	220/244 (90%)	171 (78%)	40 (18%)	9 (4%)	3	33
12	L	231/256 (90%)	168 (73%)	44 (19%)	19 (8%)	1	13
13	M	189/191 (99%)	140 (74%)	39 (21%)	10 (5%)	2	25
14	N	207/221 (94%)	161 (78%)	36 (17%)	10 (5%)	3	28
15	O	167/174 (96%)	126 (75%)	26 (16%)	15 (9%)	1	11
16	P	92/165 (56%)	65 (71%)	20 (22%)	7 (8%)	1	15
17	Q	191/199 (96%)	142 (74%)	40 (21%)	9 (5%)	3	29
18	R	134/138 (97%)	107 (80%)	16 (12%)	11 (8%)	1	13
19	S	201/204 (98%)	150 (75%)	45 (22%)	6 (3%)	5	42
20	T	195/199 (98%)	158 (81%)	33 (17%)	4 (2%)	9	50
21	U	181/184 (98%)	150 (83%)	24 (13%)	7 (4%)	4	34
22	V	183/186 (98%)	133 (73%)	43 (24%)	7 (4%)	4	35
23	W	186/189 (98%)	153 (82%)	26 (14%)	7 (4%)	4	35
24	X	170/172 (99%)	131 (77%)	28 (16%)	11 (6%)	1	20
25	Y	157/160 (98%)	124 (79%)	21 (13%)	12 (8%)	1	15
26	Z	98/121 (81%)	72 (74%)	21 (21%)	5 (5%)	2	26
27	AA	134/137 (98%)	114 (85%)	19 (14%)	1 (1%)	26	72
28	BA	59/155 (38%)	47 (80%)	7 (12%)	5 (8%)	1	13
29	CA	119/142 (84%)	92 (77%)	19 (16%)	8 (7%)	1	19
30	DA	124/127 (98%)	88 (71%)	30 (24%)	6 (5%)	3	28
31	EA	133/136 (98%)	95 (71%)	27 (20%)	11 (8%)	1	13
32	FA	146/149 (98%)	105 (72%)	30 (20%)	11 (8%)	1	15
33	GA	56/59 (95%)	43 (77%)	10 (18%)	3 (5%)	2	25
34	HA	95/105 (90%)	71 (75%)	19 (20%)	5 (5%)	2	25

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	IA	107/113 (95%)	89 (83%)	14 (13%)	4 (4%)	4	36
36	JA	125/130 (96%)	102 (82%)	20 (16%)	3 (2%)	7	47
37	KA	104/107 (97%)	89 (86%)	10 (10%)	5 (5%)	3	28
38	LA	110/121 (91%)	87 (79%)	18 (16%)	5 (4%)	3	30
39	MA	117/120 (98%)	91 (78%)	19 (16%)	7 (6%)	2	21
40	NA	97/100 (97%)	70 (72%)	18 (19%)	9 (9%)	1	11
41	OA	85/88 (97%)	59 (69%)	20 (24%)	6 (7%)	1	17
42	PA	75/78 (96%)	61 (81%)	11 (15%)	3 (4%)	4	33
43	QA	48/51 (94%)	37 (77%)	8 (17%)	3 (6%)	2	21
44	RA	50/128 (39%)	39 (78%)	5 (10%)	6 (12%)	0	6
45	SA	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	3	31
46	TA	103/106 (97%)	78 (76%)	19 (18%)	6 (6%)	2	23
47	UA	89/92 (97%)	74 (83%)	13 (15%)	2 (2%)	8	49
48	VA	187/312 (60%)	138 (74%)	32 (17%)	17 (9%)	1	11
49	WA	316/319 (99%)	230 (73%)	73 (23%)	13 (4%)	3	33
50	XA	204/252 (81%)	147 (72%)	42 (21%)	15 (7%)	1	16
51	YA	212/255 (83%)	150 (71%)	46 (22%)	16 (8%)	1	15
52	ZA	215/254 (85%)	160 (74%)	47 (22%)	8 (4%)	4	36
53	AB	221/240 (92%)	168 (76%)	40 (18%)	13 (6%)	2	22
54	BB	258/261 (99%)	183 (71%)	61 (24%)	14 (5%)	2	25
55	CB	204/225 (91%)	155 (76%)	39 (19%)	10 (5%)	3	27
56	DB	224/236 (95%)	172 (77%)	42 (19%)	10 (4%)	3	30
57	EB	182/190 (96%)	124 (68%)	39 (21%)	19 (10%)	1	8
58	FB	184/200 (92%)	136 (74%)	33 (18%)	15 (8%)	1	13
59	GB	183/197 (93%)	142 (78%)	28 (15%)	13 (7%)	1	17
60	HB	94/105 (90%)	66 (70%)	19 (20%)	9 (10%)	1	10
61	IB	153/156 (98%)	97 (63%)	42 (28%)	14 (9%)	1	11
62	JB	122/143 (85%)	80 (66%)	31 (25%)	11 (9%)	1	11
63	KB	148/151 (98%)	118 (80%)	23 (16%)	7 (5%)	3	29
64	LB	125/137 (91%)	85 (68%)	30 (24%)	10 (8%)	1	13
65	MB	120/142 (84%)	82 (68%)	21 (18%)	17 (14%)	0	4

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	NB	139/143 (97%)	109 (78%)	21 (15%)	9 (6%)	1	20
67	OB	115/136 (85%)	85 (74%)	23 (20%)	7 (6%)	2	21
68	PB	143/146 (98%)	111 (78%)	22 (15%)	10 (7%)	1	18
69	QB	141/144 (98%)	120 (85%)	15 (11%)	6 (4%)	3	31
70	RB	105/121 (87%)	79 (75%)	21 (20%)	5 (5%)	3	28
71	SB	85/87 (98%)	61 (72%)	17 (20%)	7 (8%)	1	13
72	TB	127/130 (98%)	92 (72%)	29 (23%)	6 (5%)	3	29
73	UB	142/145 (98%)	98 (69%)	29 (20%)	15 (11%)	0	8
74	VB	132/135 (98%)	100 (76%)	26 (20%)	6 (4%)	3	30
75	WB	68/108 (63%)	51 (75%)	7 (10%)	10 (15%)	0	4
76	XB	95/119 (80%)	56 (59%)	26 (27%)	13 (14%)	0	4
77	YB	79/82 (96%)	53 (67%)	22 (28%)	4 (5%)	2	26
78	ZB	61/67 (91%)	44 (72%)	15 (25%)	2 (3%)	5	39
79	AC	51/56 (91%)	44 (86%)	6 (12%)	1 (2%)	9	51
80	BC	58/63 (92%)	34 (59%)	18 (31%)	6 (10%)	1	9
81	CC	69/152 (45%)	44 (64%)	14 (20%)	11 (16%)	0	3
82	DC	819/842 (97%)	628 (77%)	144 (18%)	47 (6%)	2	23
All	All	12207/13416 (91%)	9156 (75%)	2296 (19%)	755 (6%)	4	21

5 of 755 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	2	SER
5	E	120	VAL
5	E	135	PRO
5	E	175	GLU
6	F	222	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	157/198 (79%)	129 (82%)	28 (18%)	2	13
6	F	194/196 (99%)	175 (90%)	19 (10%)	10	42
7	G	322/323 (100%)	297 (92%)	25 (8%)	16	53
8	H	288/289 (100%)	255 (88%)	33 (12%)	7	33
9	I	244/245 (100%)	220 (90%)	24 (10%)	10	42
10	J	152/153 (99%)	139 (91%)	13 (9%)	13	49
11	K	186/205 (91%)	170 (91%)	16 (9%)	13	49
12	L	191/208 (92%)	171 (90%)	20 (10%)	8	38
13	M	171/171 (100%)	157 (92%)	14 (8%)	14	51
14	N	180/187 (96%)	157 (87%)	23 (13%)	5	28
15	O	147/150 (98%)	134 (91%)	13 (9%)	12	48
16	P	81/136 (60%)	64 (79%)	17 (21%)	1	8
17	Q	154/159 (97%)	132 (86%)	22 (14%)	4	24
18	R	107/109 (98%)	96 (90%)	11 (10%)	9	40
19	S	175/176 (99%)	154 (88%)	21 (12%)	6	30
20	T	160/162 (99%)	152 (95%)	8 (5%)	30	69
21	U	145/146 (99%)	129 (89%)	16 (11%)	8	36
22	V	150/151 (99%)	142 (95%)	8 (5%)	28	67
23	W	153/154 (99%)	133 (87%)	20 (13%)	5	27
24	X	156/156 (100%)	133 (85%)	23 (15%)	4	22
25	Y	136/137 (99%)	120 (88%)	16 (12%)	6	31
26	Z	87/107 (81%)	82 (94%)	5 (6%)	25	66
27	AA	104/105 (99%)	90 (86%)	14 (14%)	5	26
28	BA	54/129 (42%)	49 (91%)	5 (9%)	11	45
29	CA	105/118 (89%)	90 (86%)	15 (14%)	4	24
30	DA	109/110 (99%)	97 (89%)	12 (11%)	8	36
31	EA	115/116 (99%)	97 (84%)	18 (16%)	3	19
32	FA	118/119 (99%)	106 (90%)	12 (10%)	9	40
33	GA	46/47 (98%)	44 (96%)	2 (4%)	35	74
34	HA	81/88 (92%)	70 (86%)	11 (14%)	5	26
35	IA	96/97 (99%)	88 (92%)	8 (8%)	14	50
36	JA	109/111 (98%)	99 (91%)	10 (9%)	11	45

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	KA	90/91 (99%)	87 (97%)	3 (3%)	45	79
38	LA	95/103 (92%)	82 (86%)	13 (14%)	4	25
39	MA	104/105 (99%)	90 (86%)	14 (14%)	5	26
40	NA	81/82 (99%)	75 (93%)	6 (7%)	17	56
41	OA	70/71 (99%)	64 (91%)	6 (9%)	13	49
42	PA	68/69 (99%)	65 (96%)	3 (4%)	35	73
43	QA	45/46 (98%)	42 (93%)	3 (7%)	20	61
44	RA	47/116 (40%)	44 (94%)	3 (6%)	22	62
45	SA	23/23 (100%)	18 (78%)	5 (22%)	1	7
46	TA	90/91 (99%)	88 (98%)	2 (2%)	60	85
47	UA	71/72 (99%)	63 (89%)	8 (11%)	7	34
48	VA	160/254 (63%)	133 (83%)	27 (17%)	2	15
49	WA	261/262 (100%)	243 (93%)	18 (7%)	19	59
50	XA	173/210 (82%)	153 (88%)	20 (12%)	7	33
52	ZA	176/205 (86%)	165 (94%)	11 (6%)	22	63
53	AB	182/195 (93%)	162 (89%)	20 (11%)	8	36
54	BB	221/222 (100%)	202 (91%)	19 (9%)	13	49
55	CB	173/191 (91%)	155 (90%)	18 (10%)	9	39
56	DB	193/201 (96%)	185 (96%)	8 (4%)	37	74
57	EB	165/170 (97%)	154 (93%)	11 (7%)	20	61
58	FB	150/161 (93%)	141 (94%)	9 (6%)	24	64
59	GB	158/166 (95%)	148 (94%)	10 (6%)	22	63
60	HB	89/98 (91%)	79 (89%)	10 (11%)	7	35
61	IB	136/137 (99%)	127 (93%)	9 (7%)	21	61
63	KB	127/128 (99%)	114 (90%)	13 (10%)	9	40
65	MB	103/118 (87%)	97 (94%)	6 (6%)	25	65
66	NB	117/119 (98%)	106 (91%)	11 (9%)	11	44
67	OB	82/124 (66%)	75 (92%)	7 (8%)	13	49
68	PB	128/129 (99%)	117 (91%)	11 (9%)	13	49
69	QB	115/116 (99%)	106 (92%)	9 (8%)	16	53
70	RB	100/114 (88%)	92 (92%)	8 (8%)	15	52

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	SB	74/74 (100%)	68 (92%)	6 (8%)	15	52
72	TB	110/111 (99%)	98 (89%)	12 (11%)	8	37
73	UB	119/120 (99%)	112 (94%)	7 (6%)	24	65
74	VB	112/113 (99%)	106 (95%)	6 (5%)	27	67
75	WB	61/89 (68%)	54 (88%)	7 (12%)	7	33
77	YB	70/71 (99%)	69 (99%)	1 (1%)	74	91
78	ZB	56/60 (93%)	52 (93%)	4 (7%)	18	58
79	AC	47/49 (96%)	42 (89%)	5 (11%)	8	38
80	BC	51/54 (94%)	45 (88%)	6 (12%)	6	31
82	DC	699/714 (98%)	621 (89%)	78 (11%)	7	35
All	All	9865/10602 (93%)	8910 (90%)	955 (10%)	15	42

5 of 955 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	DA	26	GLN
40	NA	52	PRO
82	DC	122	THR
31	EA	43	VAL
35	IA	13	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 251 such sidechains are listed below:

Mol	Chain	Res	Type
37	KA	42	GLN
50	XA	39	ASN
82	DC	91	GLN
38	LA	18	ASN
43	QA	32	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1682/1798 (93%)	330 (19%)	11 (0%)
2	B	3267/3396 (96%)	533 (16%)	31 (0%)
3	C	157/158 (99%)	26 (16%)	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	D	120/121 (99%)	11 (9%)	0
83	EC	187/201 (93%)	79 (42%)	5 (2%)
All	All	5413/5674 (95%)	979 (18%)	47 (0%)

5 of 979 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	45	U

5 of 47 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	1331	U
2	B	2101	C
83	EC	6876	A
2	B	1481	A
2	B	2197	C

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

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	1.90	3 (23%)	12,28,30	1.88	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 (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	DC	699	DDE	CD2-NE2	2.01	1.39	1.36
82	DC	699	DDE	OAG-CBI	2.08	1.27	1.23
82	DC	699	DDE	CBW-CBI	4.92	1.61	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	DC	699	DDE	CAU-CBW-CBI	-2.34	106.01	110.72
82	DC	699	DDE	OAG-CBI-NAD	2.27	126.82	123.06
82	DC	699	DDE	CAU-CAT-CE1	4.50	136.85	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	1.73	7 (29%)	26,47,47	1.93	7 (26%)
86	SO1	DC	903	-	36,39,39	2.61	18 (50%)	36,64,64	1.68	7 (19%)

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 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	DC	903	SO1	O56-C52	-3.73	1.32	1.41
86	DC	903	SO1	O56-C56	2.06	1.49	1.44
84	DC	901	GDP	O4'-C1'	2.06	1.44	1.41
86	DC	903	SO1	C7-C16	2.10	1.56	1.53
84	DC	901	GDP	PB-O3B	2.12	1.62	1.54

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	DC	901	GDP	N3-C2-N1	-4.90	120.89	127.56
84	DC	901	GDP	C5-C6-N1	-3.42	119.05	123.52
84	DC	901	GDP	C6-C5-C4	-2.98	117.46	120.86
86	DC	903	SO1	C61-C56-C55	-2.90	108.60	113.38
86	DC	903	SO1	C12-C6-C10	-2.68	103.05	107.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	DC	901	GDP	5	0
86	DC	903	SO1	3	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.