



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Sep 3, 2017 – 03:58 PM EDT

PDB ID : 5JUU
EMDB ID: : EMD-6647
Title : Saccharomyces cerevisiae 80S ribosome bound with elongation factor eEF2-GDP-sordarin and Taura Syndrome Virus IRES, Structure V (least rotated 40S subunit)
Authors : Abeyrathne, P.; Koh, C.S.; Grant, T.; Grigorieff, N.; Korostelev, A.A.
Deposited on : unknown
Resolution : 4.00 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

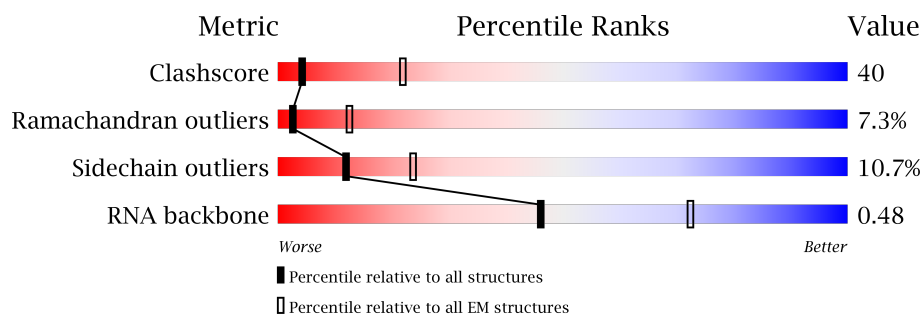
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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.




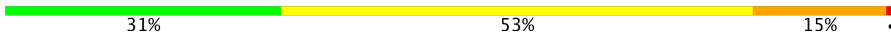
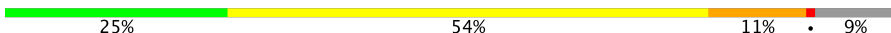


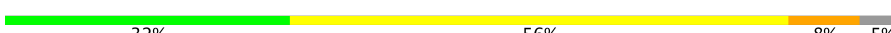
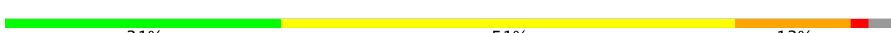




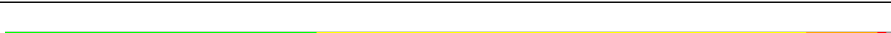









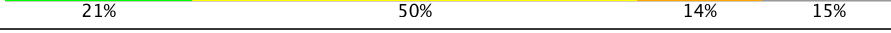



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	
2	B	3396	
3	C	158	
4	D	121	
5	E	217	
6	F	254	
7	G	387	
8	H	362	


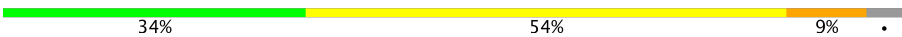



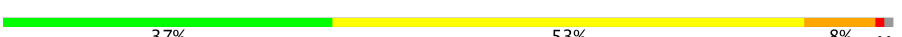

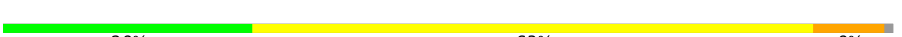
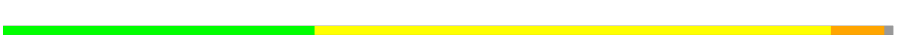


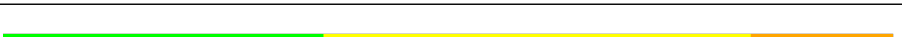

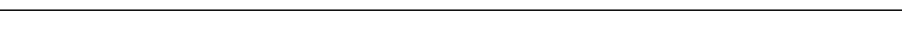
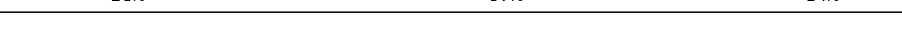
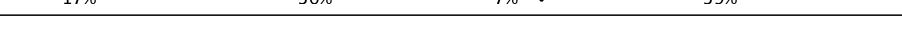

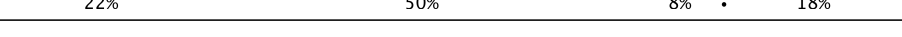
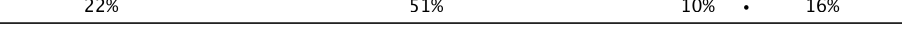
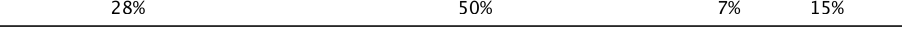


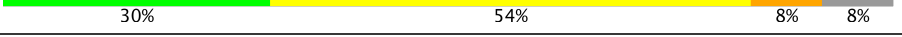


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Mol	Chain	Length	Quality of chain
9	I	297	
10	J	176	
11	K	244	
12	L	256	
13	M	191	
14	N	221	
15	O	174	
16	P	165	
17	Q	199	
18	R	138	
19	S	204	
20	T	199	
21	U	184	
22	V	186	
23	W	189	
24	X	172	
25	Y	160	
26	Z	121	
27	AA	137	
28	BA	155	
29	CA	142	
30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


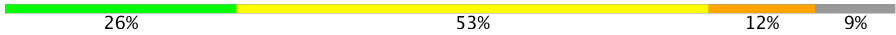


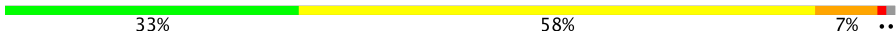
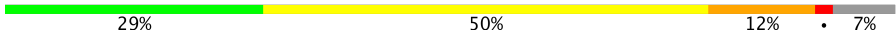
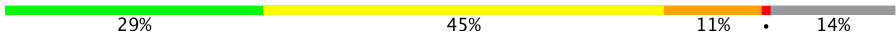
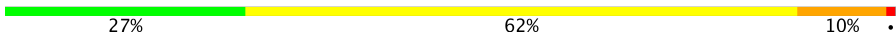
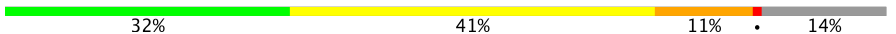
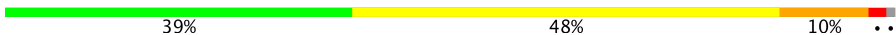
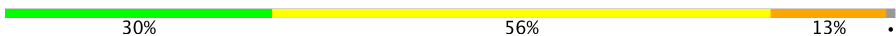
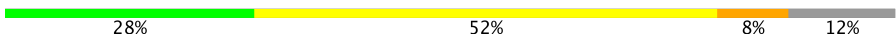
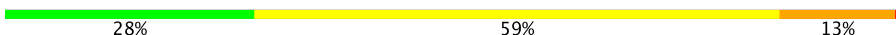
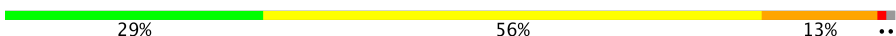



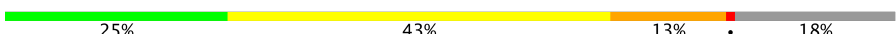







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Mol	Chain	Length	Quality of chain
34	HA	105	
35	IA	113	
36	JA	130	
37	KA	107	
38	LA	121	
39	MA	120	
40	NA	100	
41	OA	88	
42	PA	78	
43	QA	51	
44	RA	128	
45	SA	25	
46	TA	106	
47	UA	92	
48	VA	312	
49	WA	319	
50	XA	252	
51	YA	255	
52	ZA	254	
53	AB	240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

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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 215045 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
			37658	16811	6630	12436	1781		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	3307	Total	C	N	O	P	0	0
			70248	31336	12590	23015	3307		

- 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	S	0	0
			1709	1084	310	311	4		

- 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	S	0	0
			942	578	186	175	3		

- 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	S	0	0
			769	475	160	129	5		

- 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		

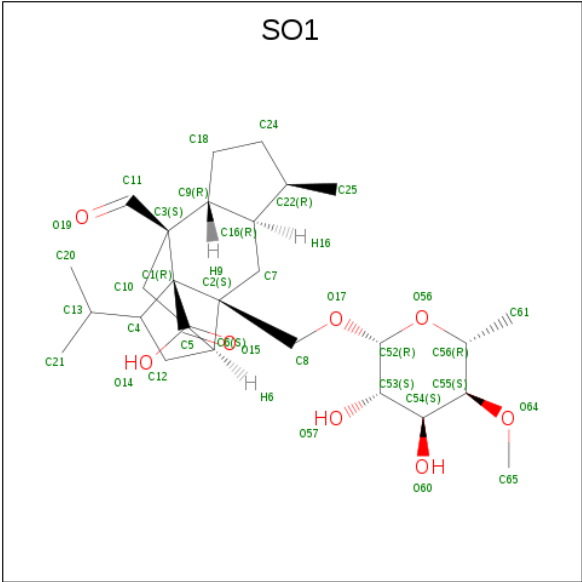
- Molecule 82 is a protein called yeast eEF2.

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
			3968	1753	669	1348	198		

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

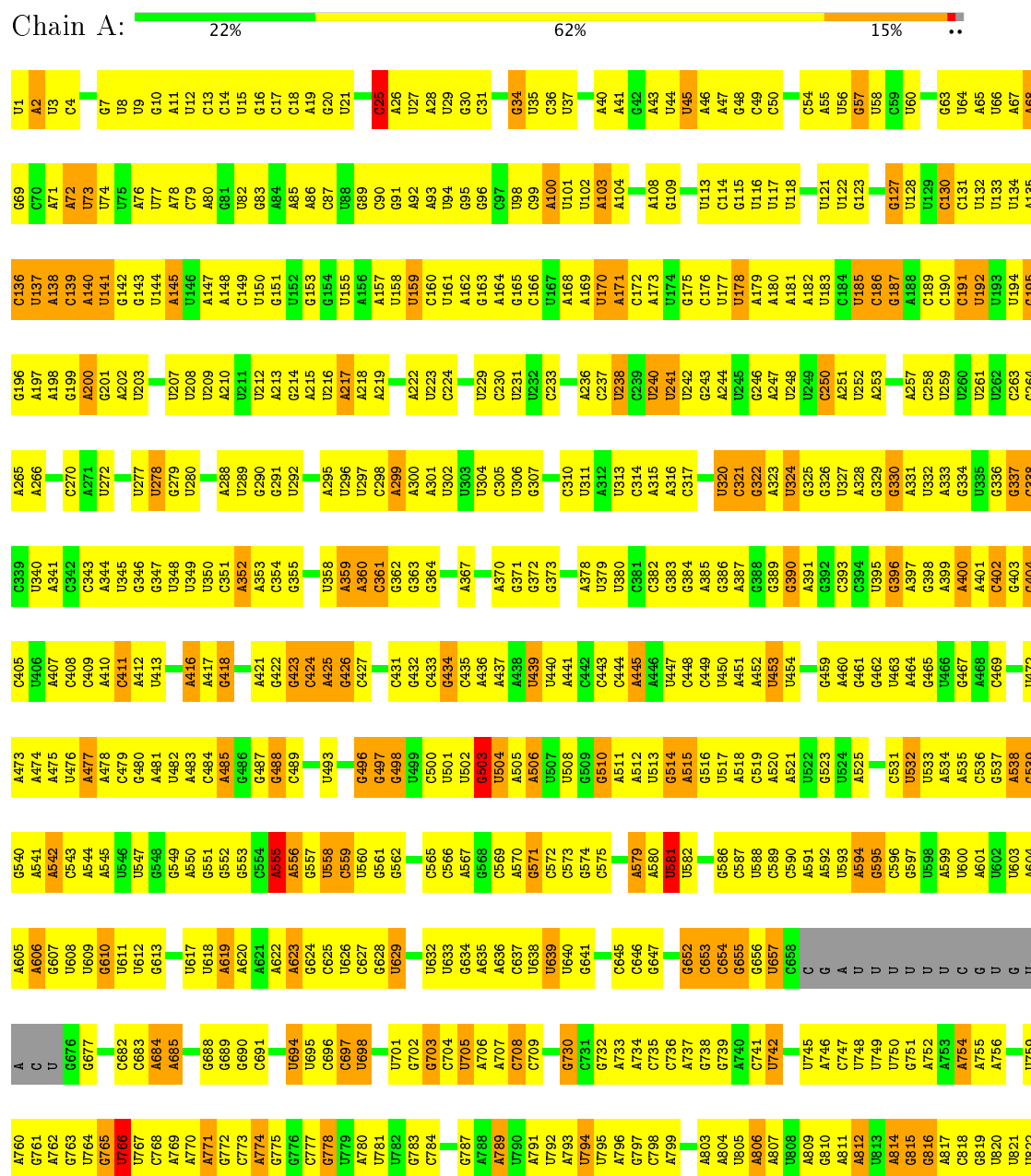


Mol	Chain	Residues	Atoms			AltConf
86	DC	1	Total	C	O	0
			35	27	8	

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 the various outlier classes 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.

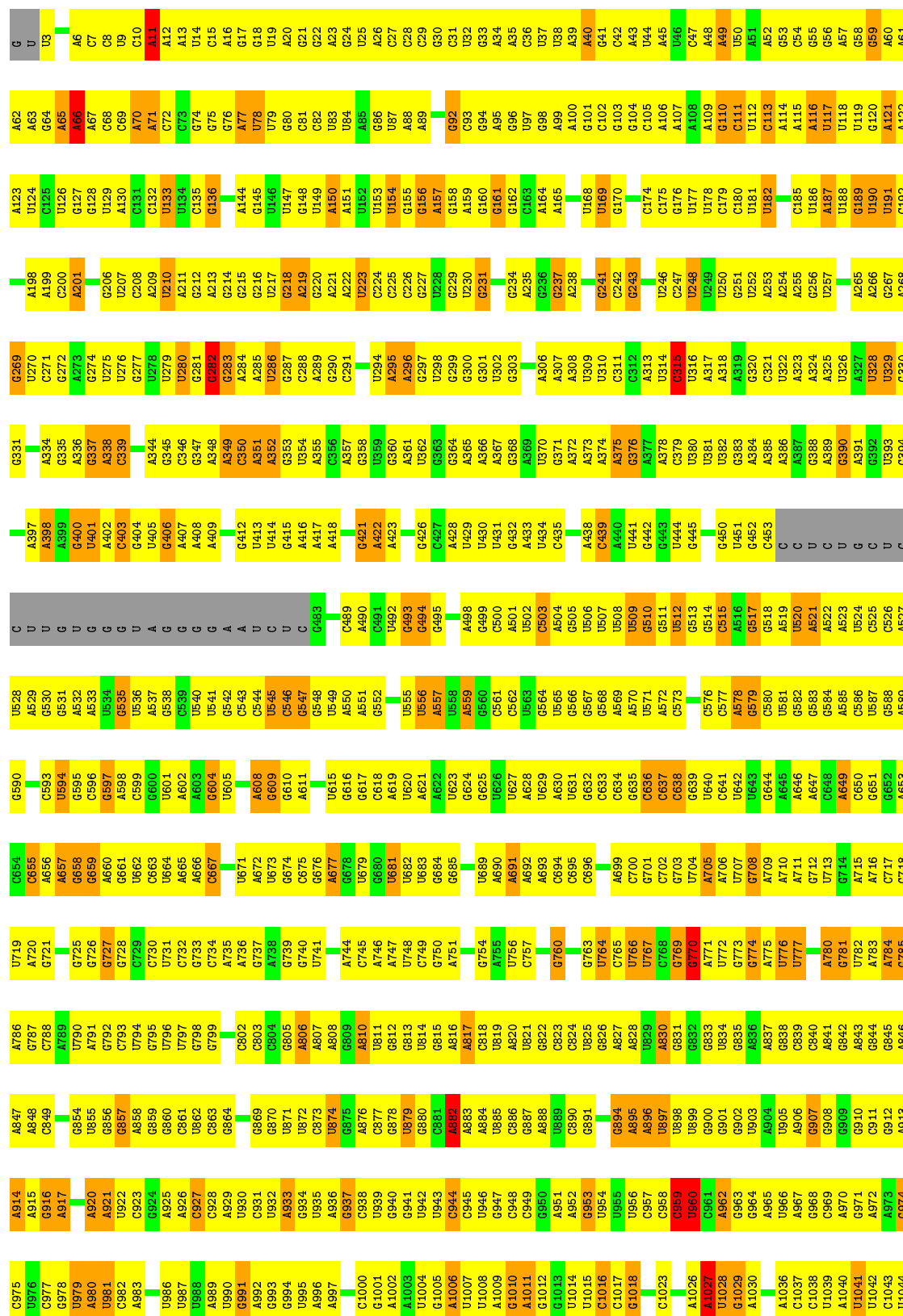
• Molecule 1: 18S ribosomal RNA



U1775	A1714	G1643	U1582	U1398	C1338	U1276	C1210	A1147	A1081	G1016	G954	A887	G823
A1776	G1715	U1643	A1583	C1399	C1339	G1277	U1214	C1143	C1082	U1017	A955	U888	G824
G1777	G1644	G1584	A1584	A1400	A1340	G1278	U1215	G1149	G1083	A1020	C956	U889	U825
G1778	G1645	A1585	A1524	A1401	A1341	C1279	C1216	G1150	A1084	G1021	C957	C890	
U1779	G1716	G1646	A1526	G1402	C1342	G1280	G1217	A1151	G1085	C1022	U958	U853	U828
G1780	A1717	C1527	C1527	U1407	C1343	G1281	G1218	A1152	A1086	U1029	U959	U833	A829
A1781	G1720	U1468	U1528	G1408	A1344	U1282	G1219	A1157	A1087	U1025	U960	U830	U830
A1782	C1649	A1469	C1529	G1409	A1345	U1283	U1219	C1158	A1088	A1026	U961	U831	U831
C1783	U1650	G1590	C1530	A1408	A1346	U1284	U1220	C1159	A1092	A1027	C962	U896	U832
C1784	G1591	G1531	A1471	A1410	A1347	U1285	U1225	A1160	A1093	G1028	A963	U897	U833
U1785	U1532	C1472	C1472	U1413	A1348	U1286	A1226	C1161	G1094	U1029	U965	A898	A834
G1786	C1533	U1473	U1473	U1414	U1350	G1287	A1227	C1162	G1095	A1030	A966	U836	U835
C1787	G1534	A1474	A1474	U1415	G1351	U1288	G1228	A1163	C1096	U1031	A967	G837	G837
G1788	U1535	A1475	A1475	U1416	G1352	U1289	G1229	G1164	U1097	G1032	U968	U838	U838
G1789	G1536	C1476	C1476	A1417	U1353	U1290	G1230	G1165	U1098	G1033	C969	U903	U839
A1790	C1537	G1477	G1477	A1418	G1354	G1291	U1231	A1166	U1099	C1034	A970	G904	U840
A1791	U1538	C1478	C1478	G1419	G1355	G1292	U1232	G1167	G1100	G1035	A971	A905	U841
G1792	G1539	G1479	G1479	G1420	U1356	U1293	G1233	U1168	G1101	A1036	G972	A906	U842
G1793	G1540	G1480	G1480	A1421	A1357	U1296	U1234	U1169	G1102	C1037	A973	U918	U843
A1794	G1541	C1481	C1481	A1422	G1358	G1297	A1235	G1170	U1103	U1038	A974	G913	U851
U1795	C1542	G1482	G1482	G1423	C1359	U1298	A1236	A1171	U1104	A1039	C975	G914	C852
C1796	A1543	A1483	A1483	A1424	A1360	U1299	G1237	G1172	C1105	G1040	G976	A915	G845
A1797	U1544	G1484	G1484	A1425	U1361	A1300	A1238	C1173	U1106	G1041	A977	U916	G846
U1798	A1545	C1485	C1485	A1426	U1362	U1301	U1239	C1174	G1107	G1042	A978	U917	A847
	G1546	G1486	G1486	A1427	U1363	U1302	U1240	U1175	G1108	A1043	A979	U918	C848
	A1547	A1487	A1487	A1428	G1364	U1303	G1241	G1176	G1109	G1046	G980	A919	U851
	G1548	G1488	G1488	G1429	C1365	G1304	A1242	G1177	U1110	G1047	U981	A920	C852
	C1549	A1489	A1489	U1430	U1366	U1305	G1243	G1178	G1111	G1048	U982	U921	G853
	A1550	C1490	C1490	A1431	G1367	C1306	A1244	G1179	G1112	U1049	G986	G922	U854
	U1551	U1491	U1491	U1432	U1368	U1307	G1245	C1180	A1113		G987	A923	A855
	G1552	A1492	A1492	U1433	U1369	G1308	G1246	U1181			A988	A924	A856
	C1553	A1493	A1493	G1434	U1370	C1309	U1247	U1182	A1116	G1053	A988	G925	U857
	U1554	U1494	U1494	A1435	A1371	U1310	C1248	A1183	U1117	U1054	U989	A926	G858
	A1555	G1436	G1436	A1436	U1372	U1311	U1249	A1184	G1118	U1055	C990	C927	A859
	A1556	U1437	U1437	U1437	C1373	A1312	U1250	U1185	U1119	U1056	G991		U860
	U1557	G1438	G1438	U1438	C1374	A1313	U1251	U1186	U1120	U1057	A992	A930	A863
	C1558	U1439	U1439	C1439	A1375	U1314	C1252	U1187	C1121	U1058	A993	C931	A864
	U1559	G1499	G1499	U1440	U1376	U1315	U1253	G1188	C1122	U1059	A994	U932	A865
	A1560	C1500	C1500	C1441	U1377	G1316	G1254	A1189	C1123	U1060	A995	A933	G866
	U1561	U1501	U1501	U1442	U1378	C1317	G1255	C1190	A1124	A1061	U996	U935	G867
	G1562	A1502	A1502	U1443	C1379	A1317	A1256	U1191	A1125	A1062	G997	A125	G868
	C1563	G1503	G1503	A1444	U1380	G1318	U1257	C1192	G1126	U1063	A998	G936	G869
	U1564	U1504	U1504	G1445	U1381		U1258	A1193	G1127	G1064	U999	C937	A869
	C1565	A1505	A1505	U1446	A1382	A1321	U1259	C1194	C1128	A1065	C1000	G938	C870
	U1566	G1506	G1506	A1447	U1383	A1322	U1260	A1194	U1129	C1066	A1001	A939	G871
	A1567	U1507	U1507	G1448	A1384	G1323	G1261	C1195	G1130	C1067	G1002	A940	G872
	C1568	C1508	C1508	U1449	G1385	G1324	U1262	A1196	A1131	C1068	A1003	A941	U873
	A1569	U1509	U1509	U1450	A1386	A1325	G1263	C1197	A1132	A1069	U1004	G942	C874
	C1570	G1510	G1510	U1451	G1387	A1326	G1264	G1198	A1133	C1070	A1005	C943	G875
	U1571	U1511	U1511	C1451	U1388	C1327	G1265	G1199	A1134	U1071	C1006	A944	G876
	G1572	G1512	G1512	U1452	A1389	G1328	U1266	G1200	C1134	U1072	C1007	U945	G877
	C1573	A1513	A1513	G1453	C1389	A1329	U1267	G1201	U1135	G1072	C1008	U946	C880
	U1574	G1514	G1514	U1454	U1390	A1331	G1267	A1202	G1073	U1074	U1009	U947	
	C1575	A1515	A1515	G1455	A1391	A1332		A1203	G1074	C1075	G1010	G948	A881
	U1576	U1516	U1516	G1456	U1392	C1332	G1270	G1141	G1141	A1076	G1011	C949	U882
	C1577	G1517	G1517	U1457	C1393	C1333	G1271	C1205	A1142	C1076	U1012	C950	C883
	U1578	A1518	A1518	G1458	G1394	U1334	U1272	U1206	A1143	C1077	U1013	A951	A884
	U1579	U1519	U1519	G1459	U1395	U1335	G1273	C1207	U1144	C1078	A1013	A952	G885
	C1580	U1520	U1520	A1460	G1396	A1336	C1274	A1208	U1145	U1079	G1014	G953	
	U1581	G1521	G1521	U1461	U1397	A1337	A1275	C1209	G1146	U1080	U1015		U886

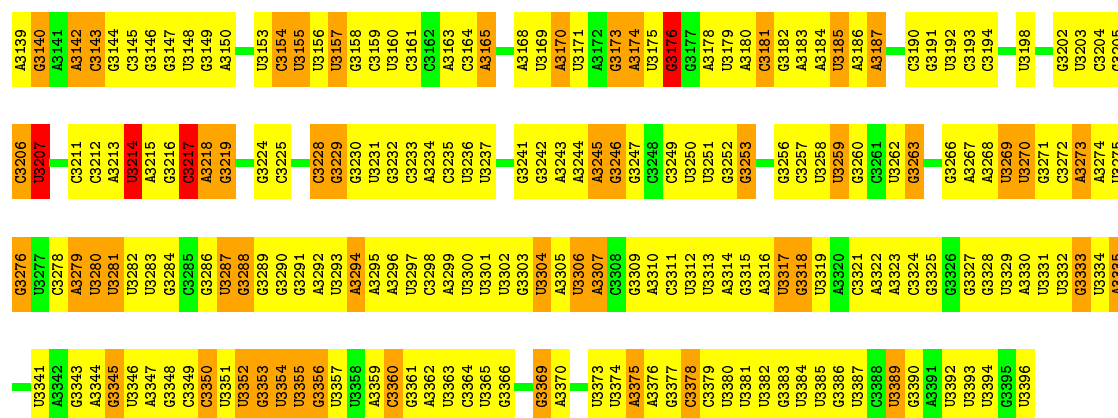
- Molecule 2: 25S ribosomal RNA

Chain B:  20% 62% 14% ..

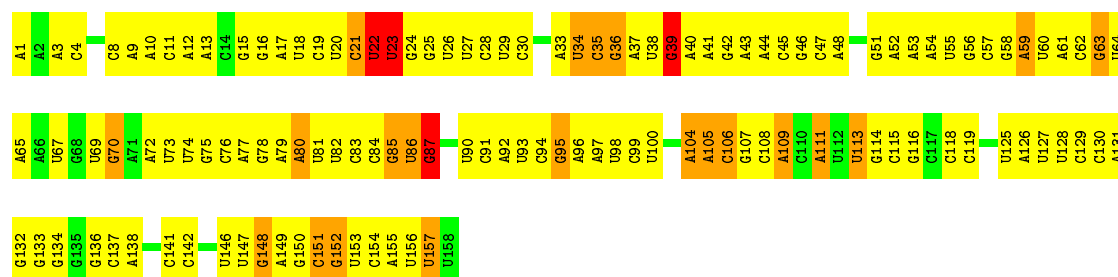


G	G1934	G1873	A1809	U1746	A1679	G1617	C1556	G1488	C1424	U1361	U1235	U1168	C1107	C1045
C	G1935	A1874	A1810	G1747	G1680	U1620	A1557	A1489	U1425	G1362	G1236	A1169	U1108	A1046
U	G1936	G1875	G1811	U1748	U1681	U1621	A1558	A1490	C1426	A1363	G1237	A1170	U1109	A1047
C	U1937	G1876	G1812	A1749	U1682	A1622	A1559	A1491	U1427	C1364	C1238	G1171	U1110	A1048
U	G1938	A1878	A1813	G1750	A1683	G1623	G1560	G1492	A1428	G1365	C1239	G1174	U1111	C1049
U	G1939	A1879	A1814	A1751	A1684	G1624	G1561	G1493	G1429	A1366	A1240	C1175	U1050	C1050
C	G1940	A1880	U1815	A1752	C1685	G1625	C1562	U1494	U1430	G1367	U1241	C1176	U1051	U1051
U	G1941	A1881	A1816	G1753	U1686	A1626	C1563	U1495	G1431	U1368	G1242	C1177	U1052	U1052
A	G1942	G1882	G1817	U1754	U1687	U1627	U1564	C1496	C1432	A1369	G1243	G1177	G1115	A1053
G	C1943	A1883	U1818	C1755	U1688	G1628	G1565	C1497	A1433	G1370	A1244	G1178	G1117	A1054
G	U1944	A1884	U1819	C1756	A1689	U1629	A1566	A1498	G1434	A1371	A1245	A1179	C1118	A1055
C	A1945	U1885	U1820	A1757	C1690	G1630	U1567	C1499	A1435	C1372	G1246	U1180	C1119	U1056
U	A1946	A1886	U1821	G1758	U1691	U1630	U1568	G1500	U1436	A1373	U1247	U1181	U1120	
G	G1947	C1759	C1822	C1759	U1692	C1631	U1569	U1501	C1437	G1374	C1248	A1182	U1121	G1059
A	G1948	A1760	A1632	C1502	C1693	A1632	U1570	C1502	U1438	U1378	G1249	C1183	U1122	U1060
C	G1949	C1761	U1694	A1571	U1694	C1633	A1571	A1503	U1439	G1379	G1250	A1184	U1123	A1061
U	U1950	U1763	G1825	U1572	C1695	G1634	U1572	A1504	G1440	G1379	A1251	C1185	U1124	A1062
A		A1891	C1826	G1573	A1696	G1635	G1573	C1505	G1441	G1380		C1186	U1125	G1063
C		U1764	C1827	C1574	A1697	U1636	C1574	A1506	U1442	A1381	G1254	C1187	G1126	A1064
U	G1954	U1765	A1828	A1575	U1697	A1637	A1575	C1507	G1443	G1382	C1255	U1188	G1127	A1065
U		G1766	G1829	G1576	U1703	A1638	G1576	C1508	U1444	G1383	G1256	U1189	G1128	G1066
U	G1957	U1766	U1830	U1577	A1704	C1639	G1577	A1509	U1445	U1384	C1257	A1190	A1129	U1067
G	U1958	A1895	U1831	G1578	U1705	G1640	C1578	G1510	A1446	C1385	U1258	U1191	A1130	C1068
G	G1959	A1896	A1696	U1579	C1706	U1641	C1579	U1511	G1447	A1386	A1259	C1192	G1131	C1069
G	A1960	U1767	A1697	C1580	C1708	A1643	C1581	G1514	U1448	G1387	A1260	A1193	C1132	U1070
U		U1768	A1697	C1582	C1709	A1644	C1582	A1515	A1449	U1388	G1261	G1194	A1133	U1071
G	U1967	C1774	C1775	C1583	C1710	G1645	A1583	C1516	G1450	G1389	G1262	A1195	A1134	G1072
G	G1968	G1776	G1776	C1584	C1711	A1646	U1584	G1517	C1451	A1390	A1263	C1196	A1135	G1073
U		G1777	G1777	C1585	G1712	G1647	C1585	G1520	A1452	C1328	G1264		A1136	U1074
U		C1779	G1713	G1586	G1713	A1648	C1586	G1521	U1455	C1329	U1265	A1200	C1137	U1075
U	G1970	U1780	A1649	A1587	A1715	G1649	A1587	C1522	A1456	A1393		C1201	U1138	G1076
U		C1781	A1715	A1588	G1650	U1651	A1588	C1521	U1457	A1394	G1268	A1202	G1139	U1077
U	G1972	U1782	G1651	A1589	U1523	G1652	A1589	C1522	U1458	A1396	U1269	A1203	G1140	U1078
U	G1973	U1783	G1652	G1590	A1524	C1653	G1590	C1524	C1459	C1397	A1271	A1204	G1141	A1079
C	U1974	G1784	G1653	G1591	U1525	A1460	C1591	C1525	A1461	U1398	C1272	G1206	G1142	A1080
C	G1975	U1785	G1654	G1592	U1526	A1461	C1592	C1526	A1462	A1399	A1273	G1207	A1143	U1081
U	G1976	G1786	G1655	A1593	C1527	A1462	A1593	C1527	U1463	G1400	U1274	U1208	U1144	U1082
U		U1787	A1656	A1594	G1528	U1463	A1594	A1401	U1463	A1401	C1275	G1209	G1145	G1083
U	G1978	C1788	C1657	U1595	A1529	G1464	U1595	C1402	C1339	C1338	U1276	U1210	C1146	A1084
G	G1979	U1722	G1658	C1596	A1529	A1465	C1596	C1403	C1340	C1340	C1277	U1211	G1147	A1085
G	U1980	A1723	U1659	C1597	U1533	G1466	C1597	G1404	U1341	A1278	U1278	A1212	G1148	U1088
U	C1725	C1724	C1660	G1598	U1534	A1467	G1598	G1405	C1342	C1279	C1279	G1213	G1149	G1089
U		G1661	G1661	G1598	A1534			U1405	A1343	U1214	U1151	U1151	A1150	G1090
U		G1662	G1662	U1601	A1535					U1215	G1152	C1092	A1091	A1091
U	G1728	C1663	A1602	A1603	G1536	U1470	A1602	C1408	G1346	C1216	A1153	A1154	A1093	C1093
U	A1729	G1664	A1603	A1604	A1537	U1471	A1603	G1409	U1347	C1217	A1154	C1155	U1094	U1094
U	G1730	G1665	G1604	G1604	A1539	U1472	G1604	U1410	U1348	C1284	C1156	G1157	U1095	U1095
C	A1731	G1666	A1605	A1606	U1540	G1473	A1605	G1412	G1349	G1285			U1096	U1096
U	U1732	G1667	U1606	U1607	G1541	A1475	U1606	G1413	A1360	A1286	G1223	A1158	G1097	G1097
U	G1733	G1668	U1607	C1608	A1546			G1414	U1351	U1287	A1223	A1159	A1098	A1098
U		G1669	C1608	C1609	A1549	C1478	C1609	U1415	A1352	U1288	C1224	A1160	A1099	A1099
U	U1737	U1670	U1609	U1610	U1549	U1479	U1609	G1416	C1353	G1289	A1225	C1160	U1100	U1100
U	C1738	G1671	G1610	G1611	A1481	G1480	G1610	G1417	G1354	A1290		G1161	G1101	G1101
G	U1739	G1672	G1611	A1612	A1482	A1481	A1611	A1419	A1355	A1291	G1229	A1162	A1102	A1102
G	U1740	G1673	A1612	C1551	A1482	A1481	A1612	A1419	U1356	C1292	G1230	A1163	G1164	A1103
G	A1741	G1674	A1613	C1552	G1483	C1420	A1613	C1420	G1357	U1293	A1231	G1165	G1165	G1104
U	U1742	G1675	C1614	U1553	U1484	G1421	C1614	G1421	A1294	A1294	C1232	A1166	G1166	A1105
U	G1743	A1676	C1615	U1554	U1484	G1421	C1615	G1421	C1359	G1233	G1234	U1167	G1167	G1106

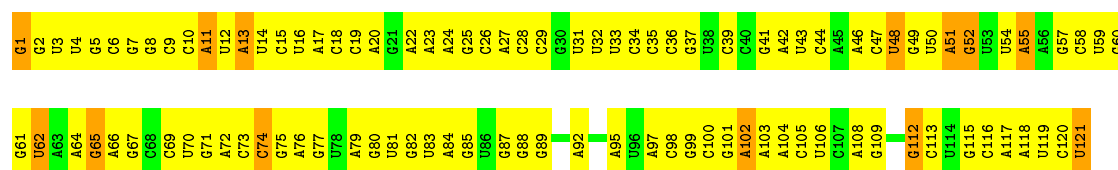


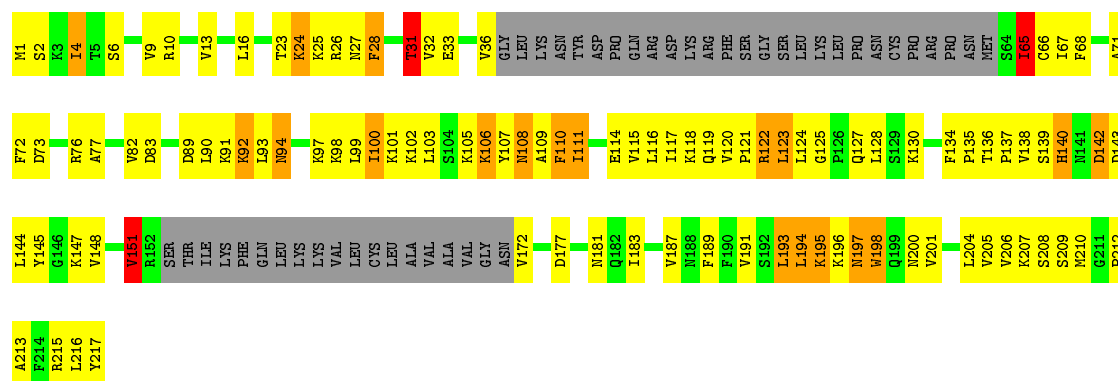
• Molecule 3: 5.8S ribosomal RNA



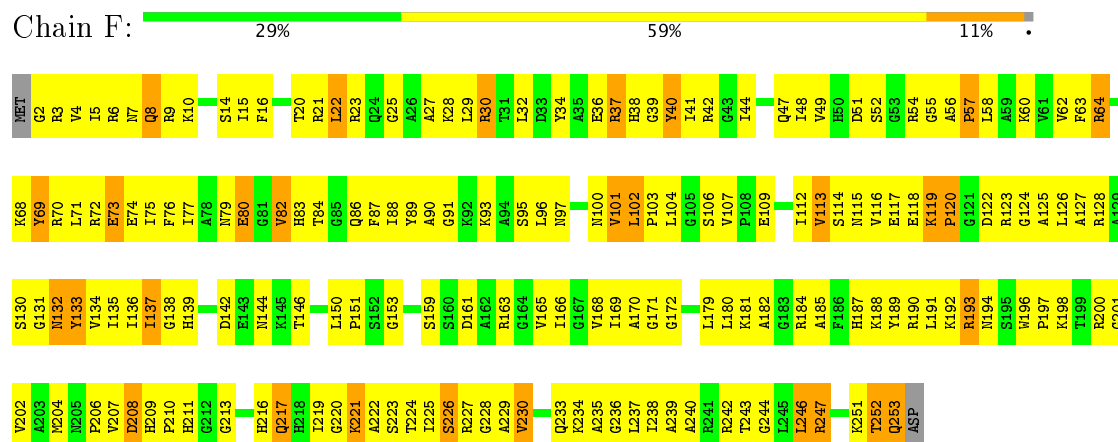
• Molecule 4: 5S ribosomal RNA



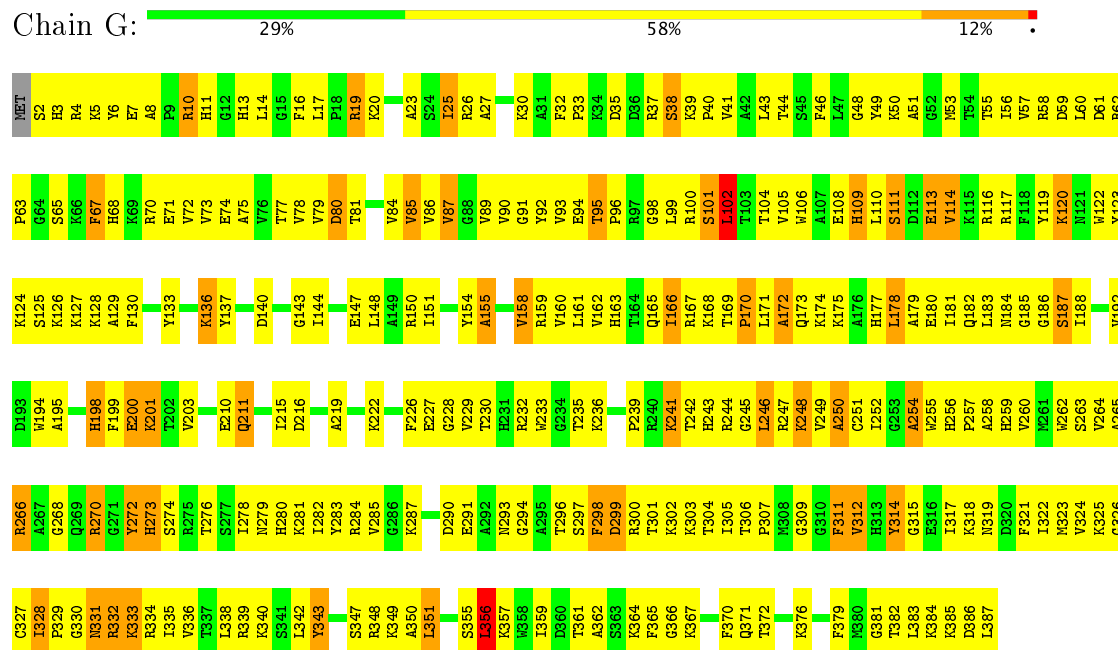
• Molecule 5: uL1 (yeast L1)



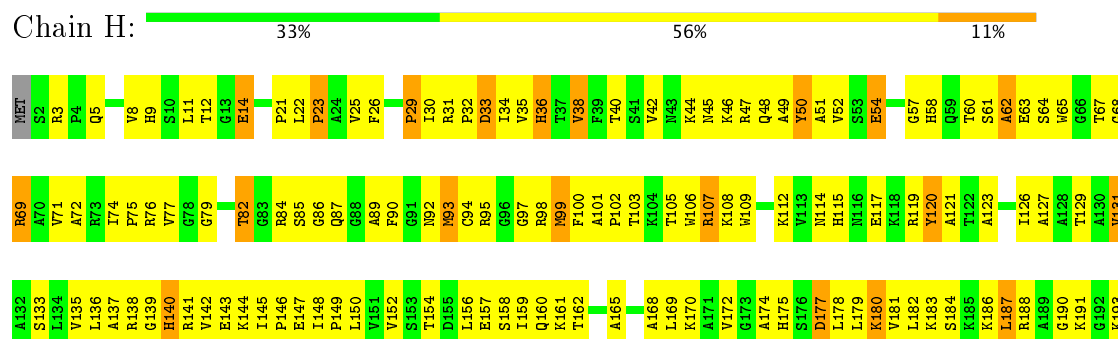
- Molecule 6: uL2 (yeast L2)



- Molecule 7: uL3 (yeast L3)

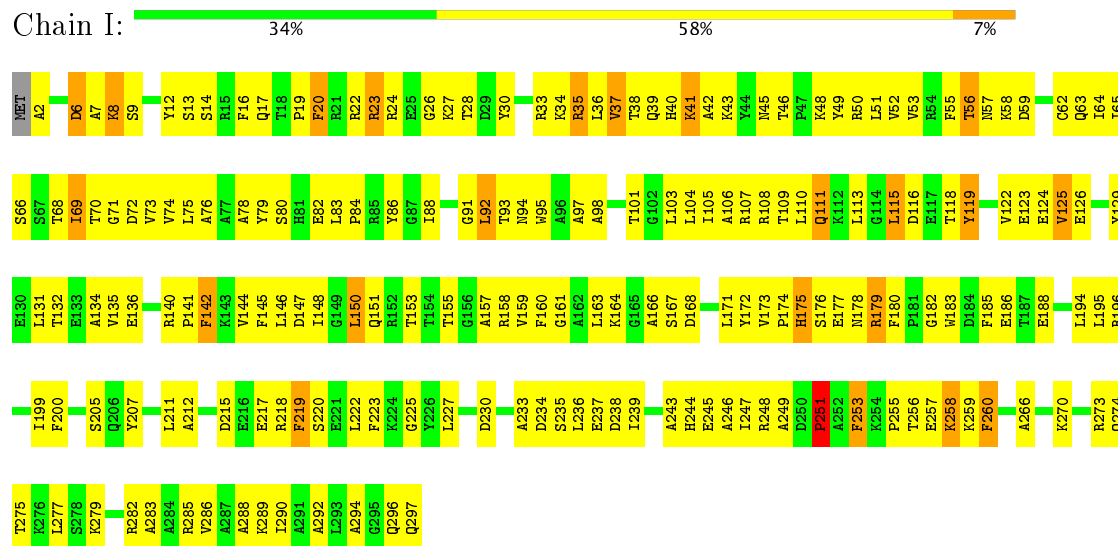


- Molecule 8: uL4 (yeast L4)

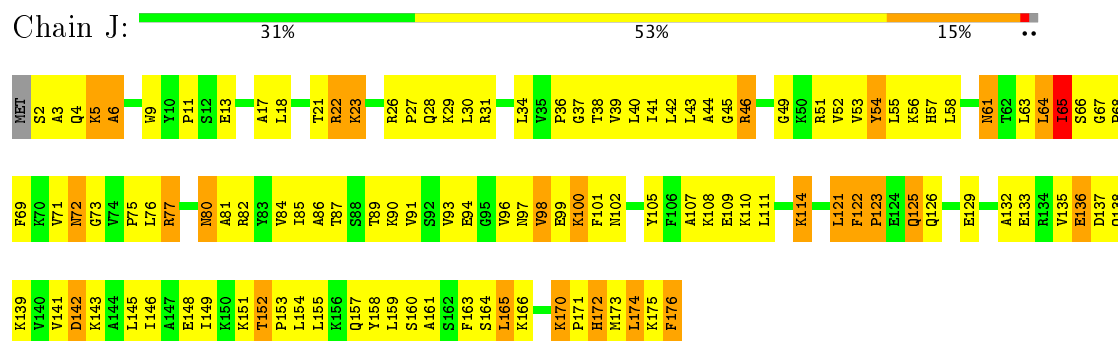




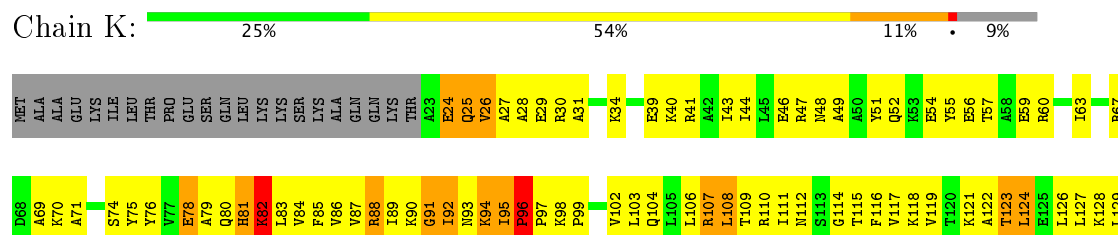
• Molecule 9: uL18 (yeast L5)

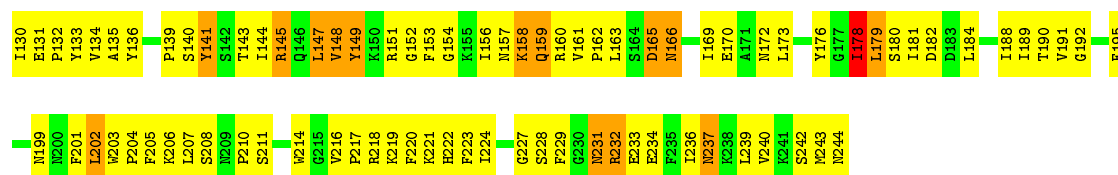


• Molecule 10: eL6 (yeast L6)



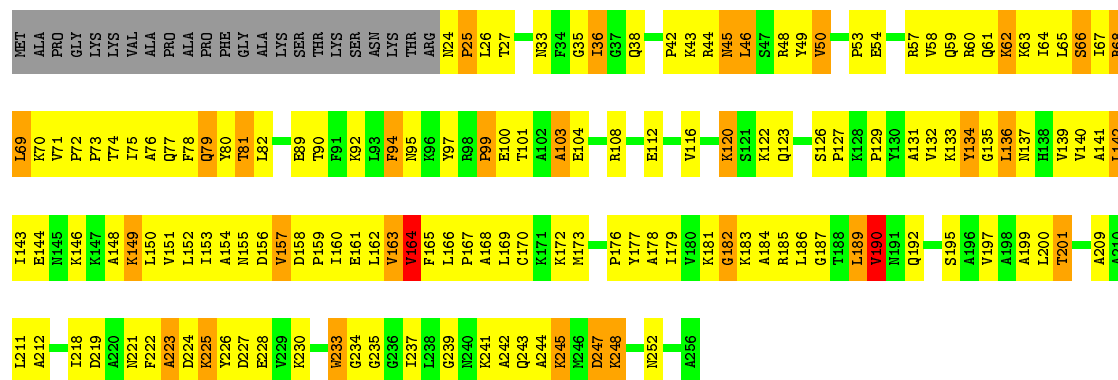
• Molecule 11: uL30 (yeast L7)





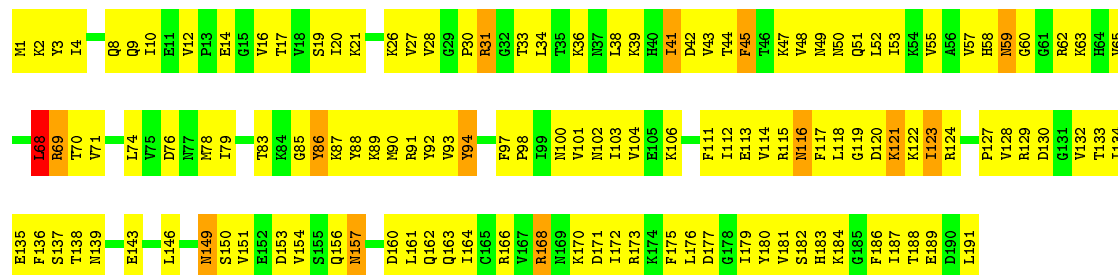
• Molecule 12: eL8 (yeast L8)

Chain L: 33% 46% 12% 9%



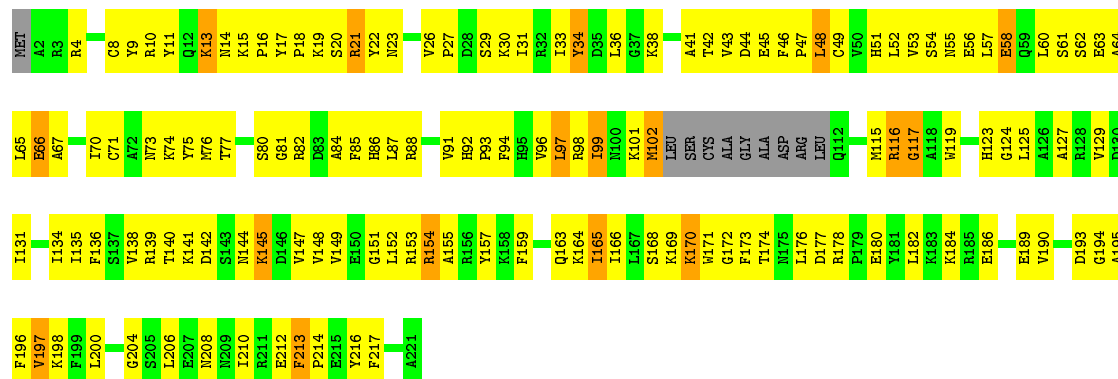
• Molecule 13: uL6 (yeast L9)

Chain M: 31% 61% 7%

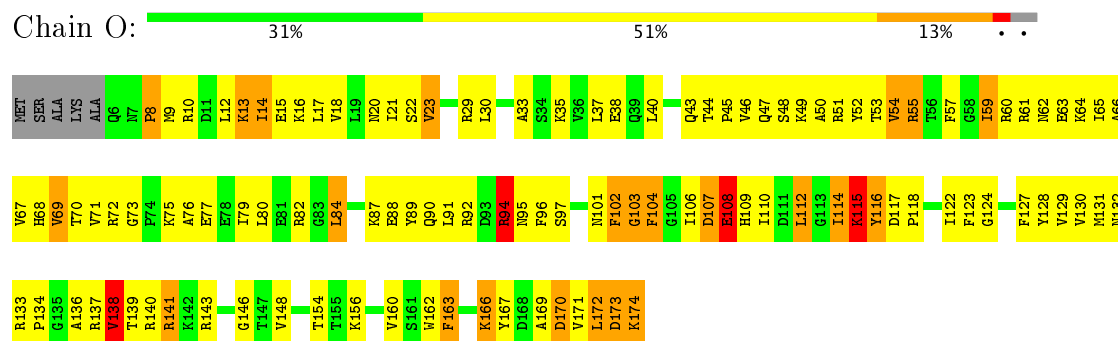


• Molecule 14: uL16 (yeast L10)

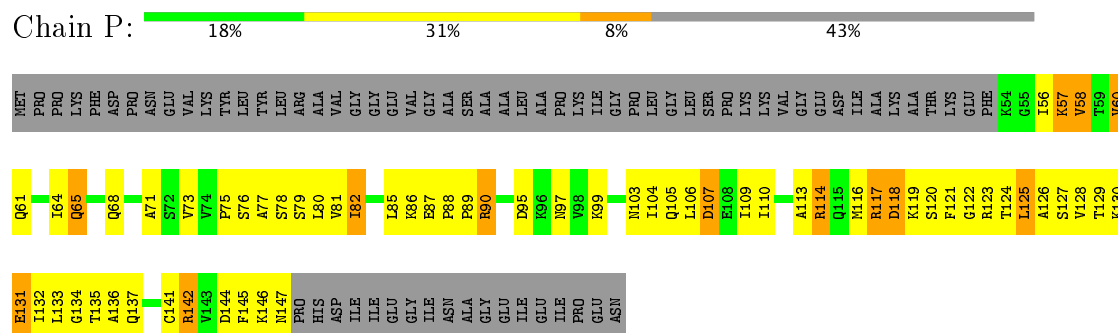
Chain N: 32% 56% 8% 5%



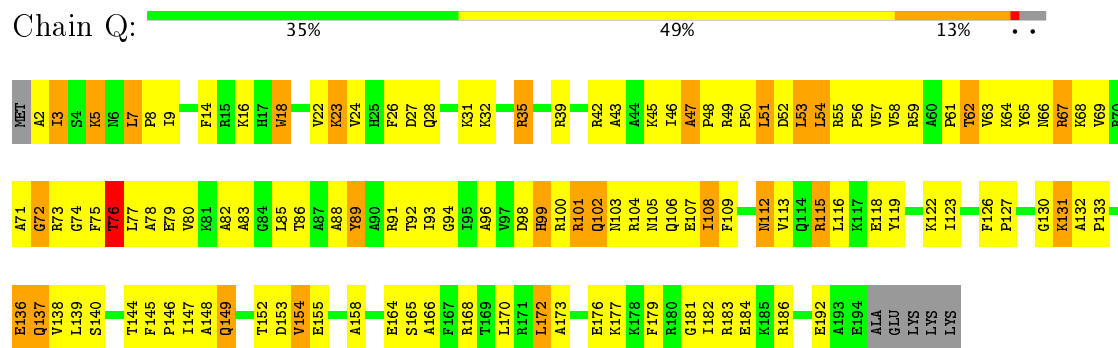
• Molecule 15: uL5 (yeast L11)



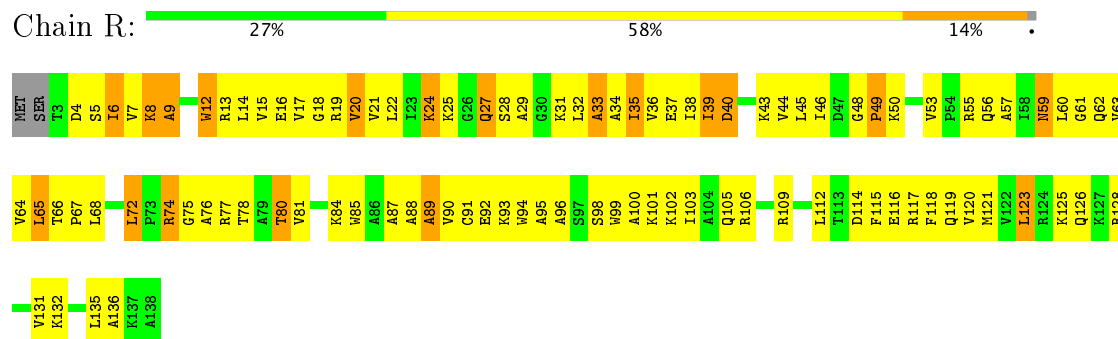
• Molecule 16: uL11 (yeast L12)



• Molecule 17: eL13 (yeast L13)



• Molecule 18: eL14 (yeast L14)

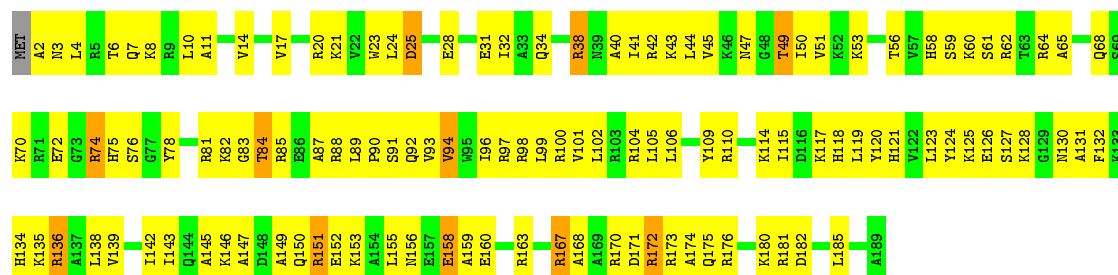


• Molecule 19: eL15 (yeast L15)



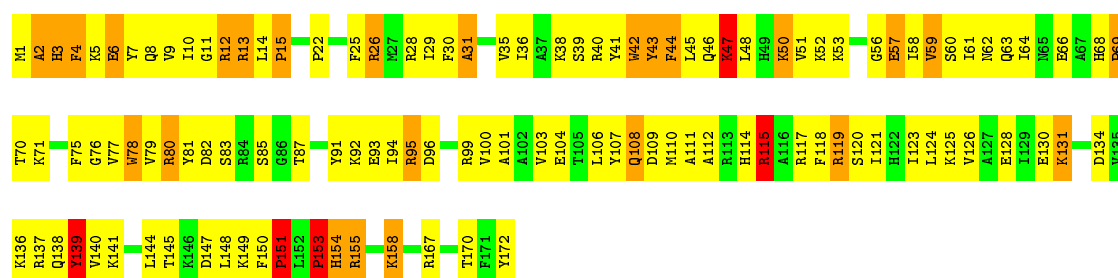
• Molecule 23: eL19 (yeast L19)

Chain W: 35% 58% 6%



• Molecule 24: eL20 (yeast L20)

Chain X: 32% 51% 15%



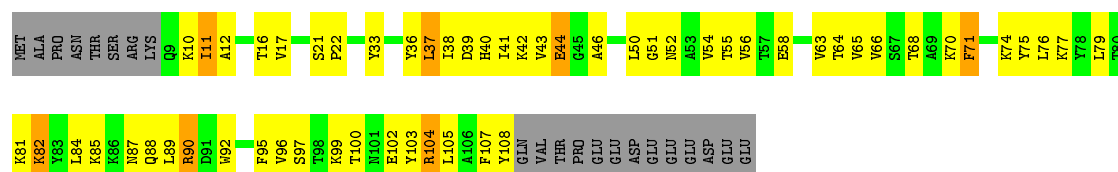
• Molecule 25: eL21 (yeast L21)

Chain Y: 32% 53% 14%

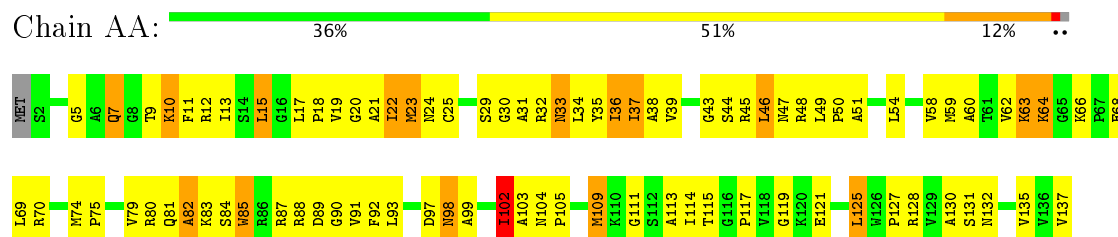


• Molecule 26: eL22 (yeast L22)

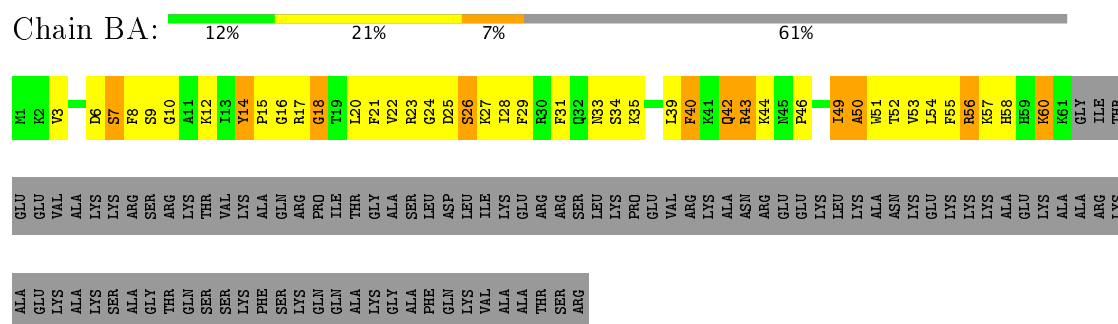
Chain Z: 36% 41% 6% 17%



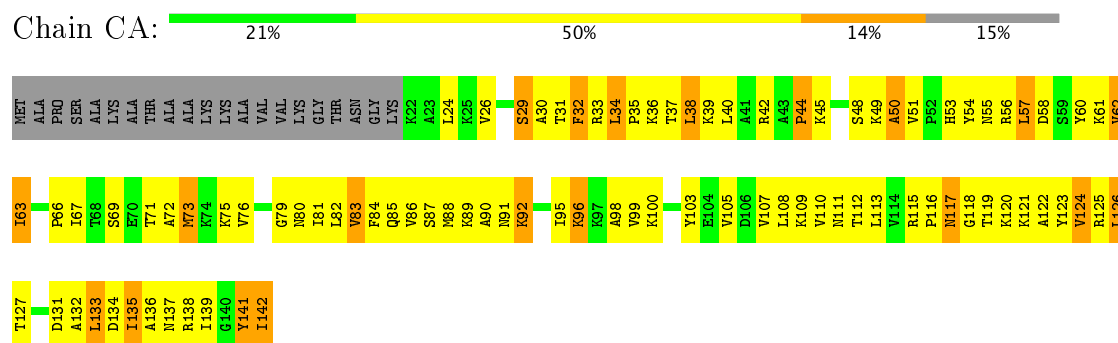
- Molecule 27: uL14 (yeast L23)



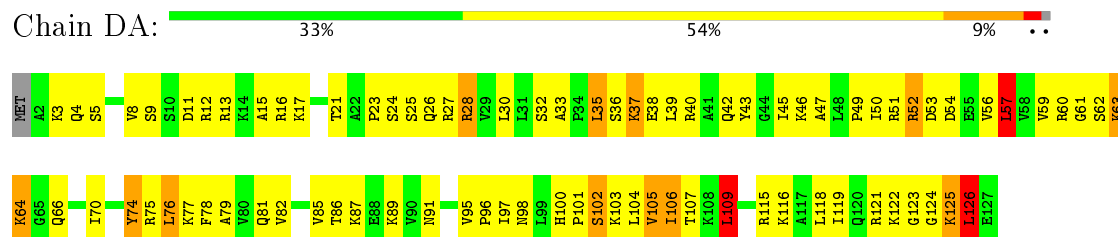
- Molecule 28: eL24 (yeast L24)



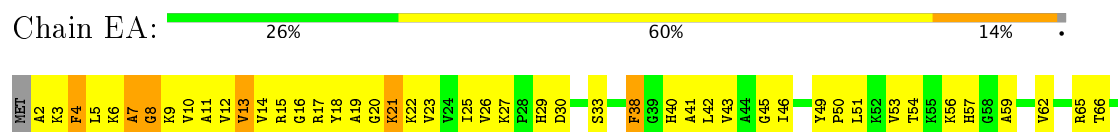
- Molecule 29: uL23 (yeast L25)

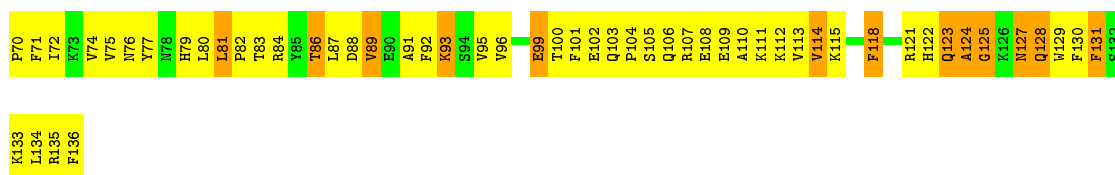


- Molecule 30: uL24 (yeast L26)



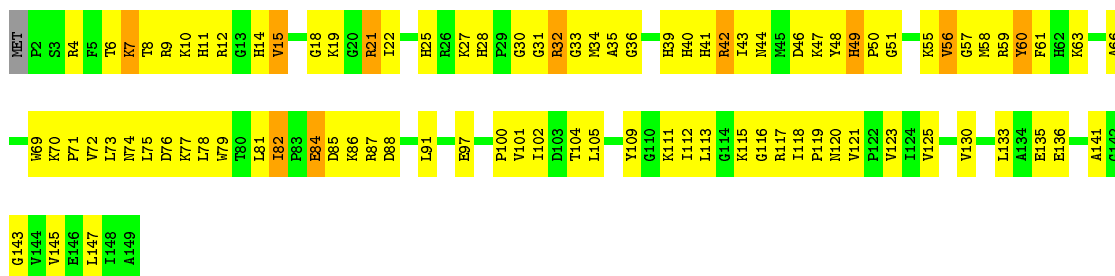
- Molecule 31: eL27 (yeast L27)





• Molecule 32: uL15 (yeast L28)

Chain FA: 38% 54% 7% .



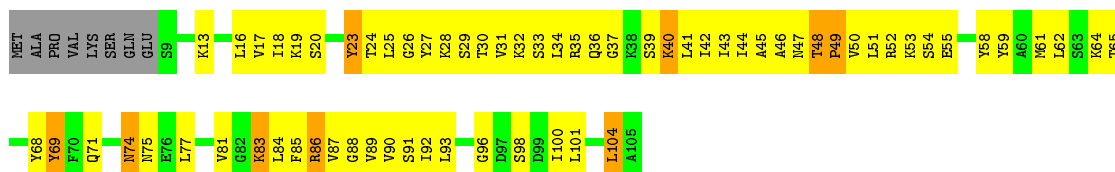
• Molecule 33: eL29 (yeast L29)

Chain GA: 46% 42% 10% .



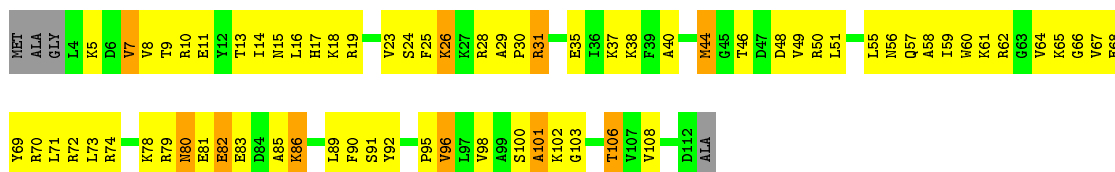
• Molecule 34: eL30 (yeast L30)

Chain HA: 29% 55% 9% 8% .



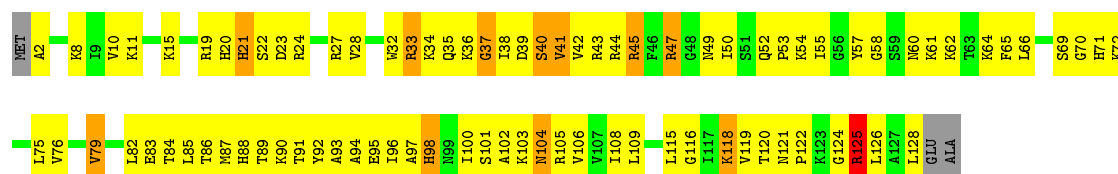
• Molecule 35: eL31 (yeast L31)

Chain IA: 34% 54% 9% .



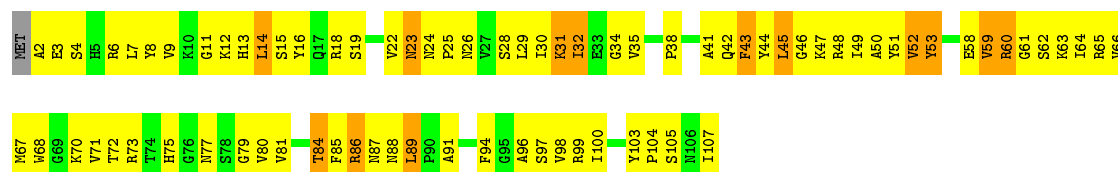
• Molecule 36: eL32 (yeast L32)

Chain JA: 32% 57% 8% ..



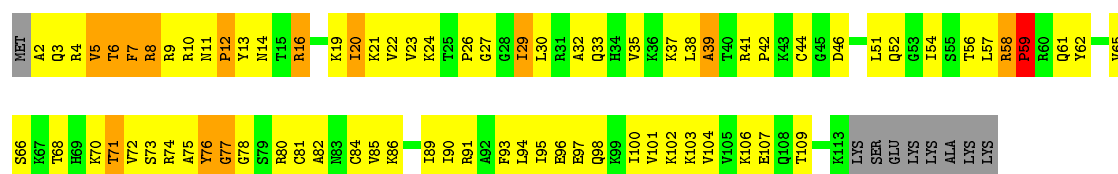
• Molecule 37: eL33 (yeast L33)

Chain KA: 26% 61% 12%



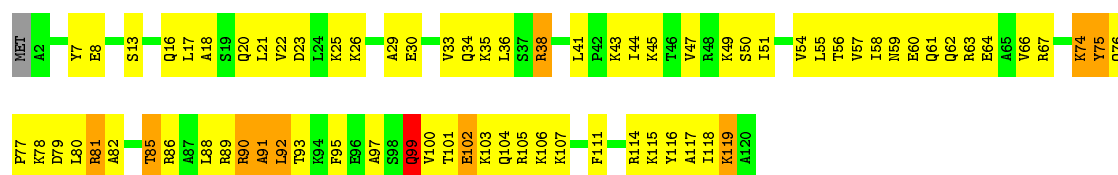
• Molecule 38: eL34 (yeast L34)

Chain LA: 28% 53% 11% 7%



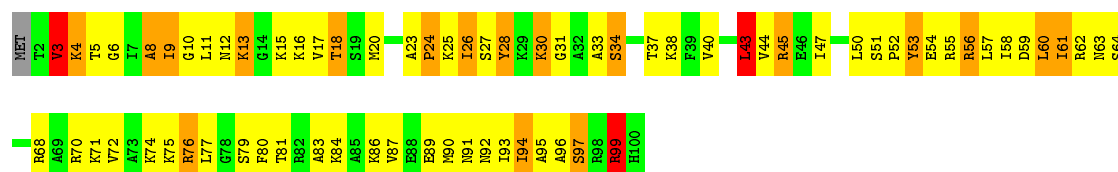
• Molecule 39: uL29 (yeast L35)

Chain MA: 37% 53% 8% ..



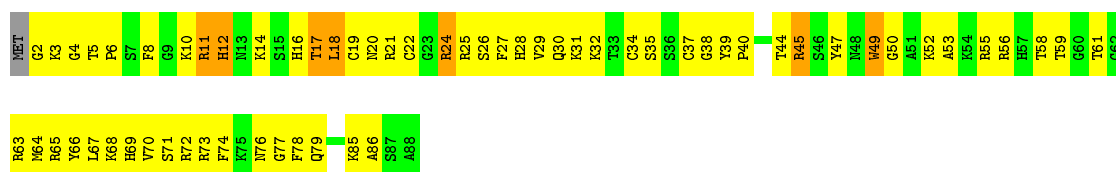
• Molecule 40: eL36 (yeast L36)

Chain NA: 27% 51% 18% ..



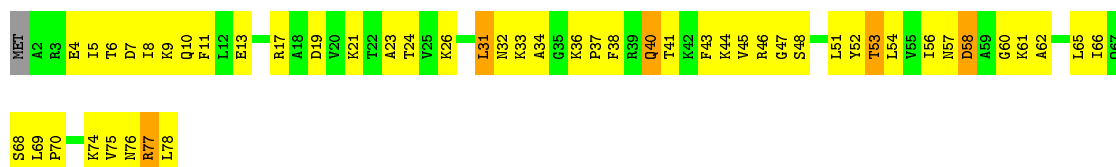
• Molecule 41: eL37 (yeast L37)

Chain OA: 28% 63% 8%



• Molecule 42: eL38 (yeast L38)

Chain PA: 35% 58% 6%



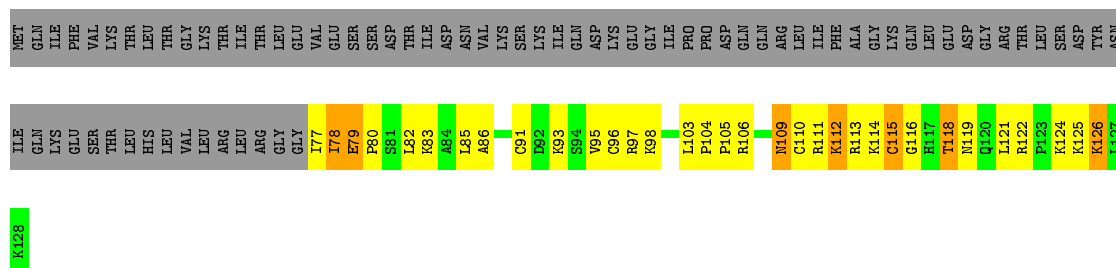
• Molecule 43: eL39 (yeast L39)

Chain QA: 24% 51% 22%



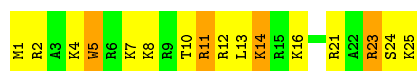
• Molecule 44: eL40 (yeast L40)

Chain RA: 15% 20% 5% 59%



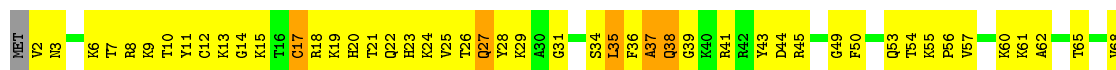
• Molecule 45: eL41 (yeast L41)

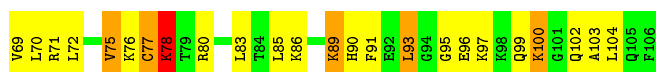
Chain SA: 36% 48% 16%



• Molecule 46: eL42 (yeast L42)

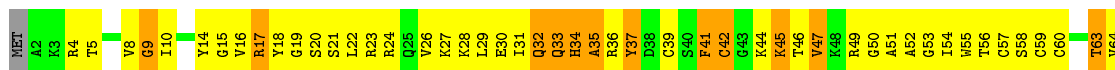
Chain TA: 31% 58% 9%





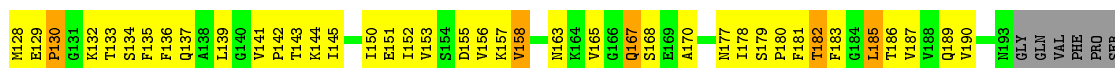
• Molecule 47: eL43 (yeast L43)

Chain UA: 28% 57% 14%



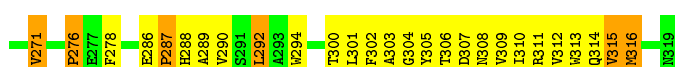
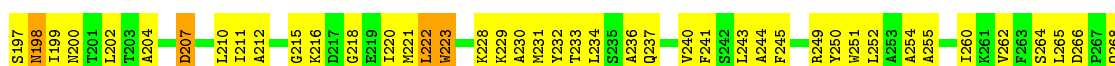
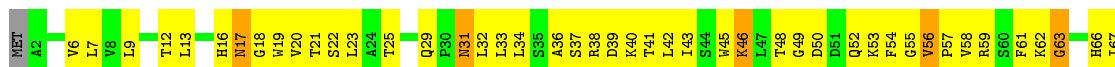
• Molecule 48: uL10 (yeast P0)

Chain VA: 17% 36% 7% 39%



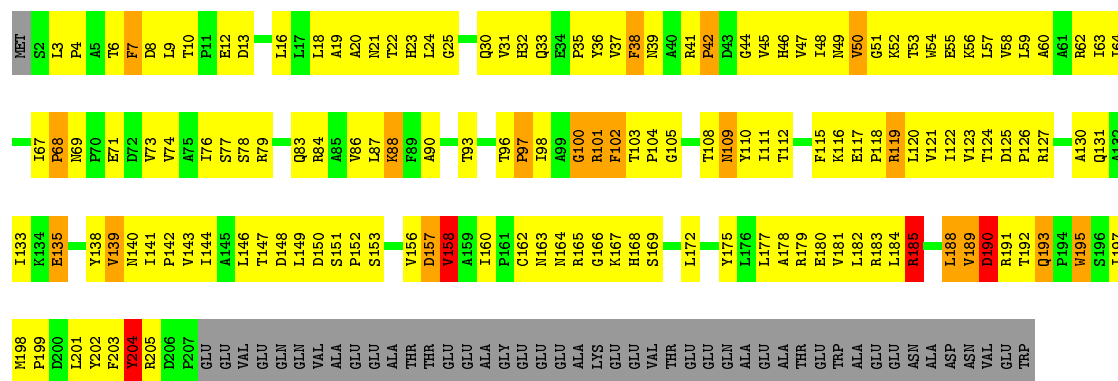
• Molecule 49: RACK1 (yeast Asc1)

Chain WA: 35% 55% 9%

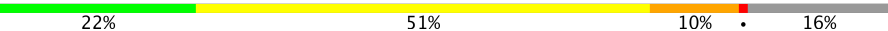


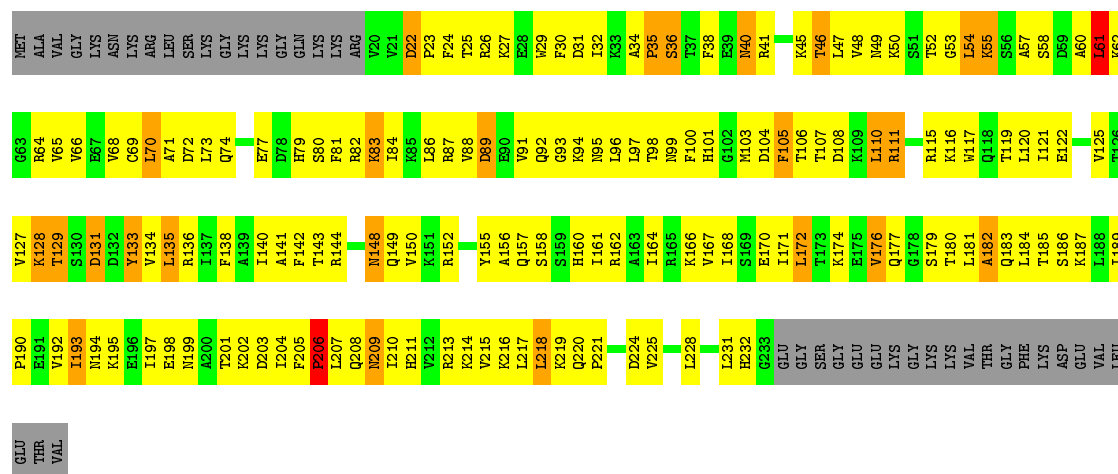
• Molecule 50: uS2 (yeast S0)

Chain XA:  22% 50% 8% 18%



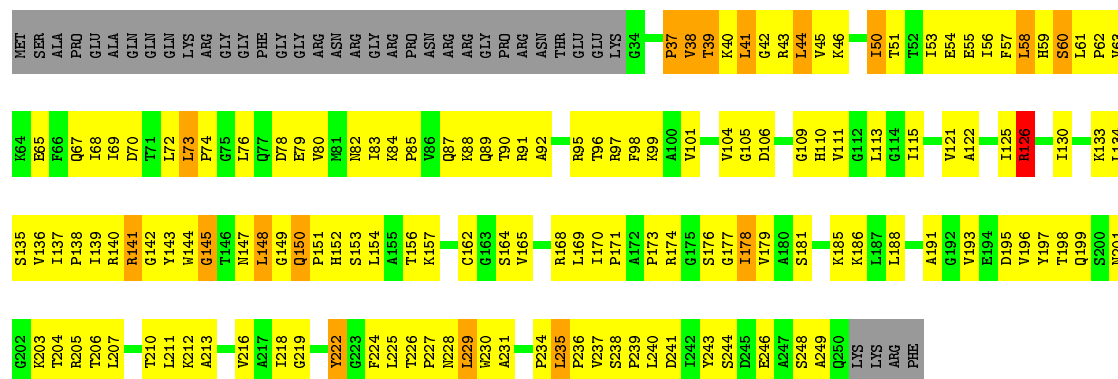
• Molecule 51: eS1 (yeast S1)

Chain YA:  22% 51% 10% 16%



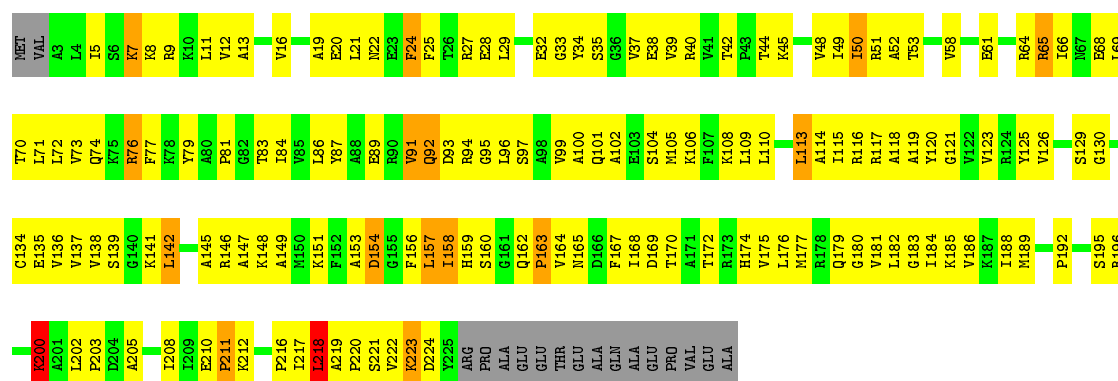
• Molecule 52: uS5 (yeast S2)

Chain ZA:  28% 50% 7% 15%

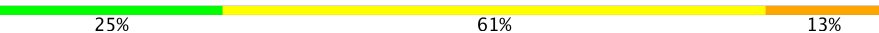


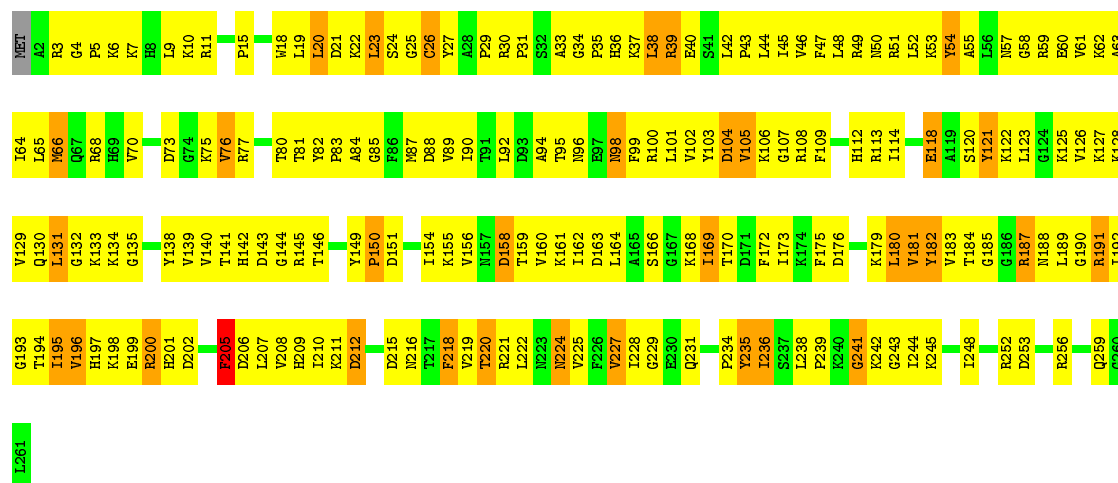
• Molecule 53: uS3 (yeast S3)

Chain AB: 



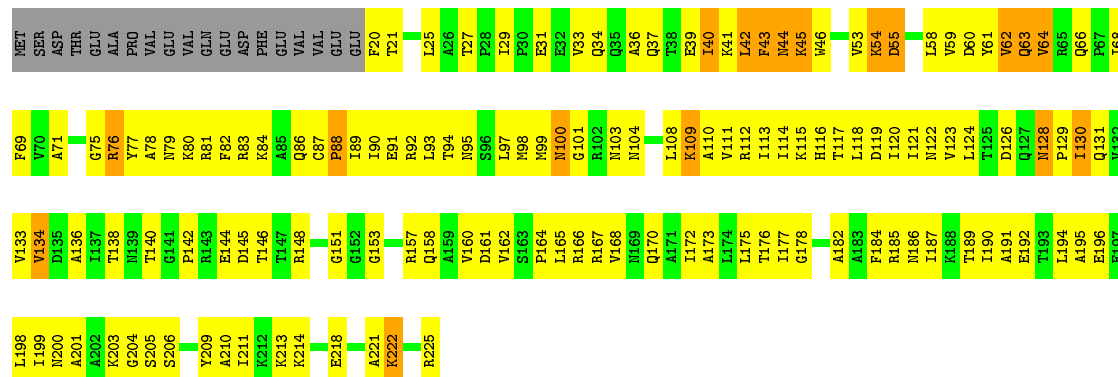
• Molecule 54: eS4 (yeast S4)

Chain BB: 

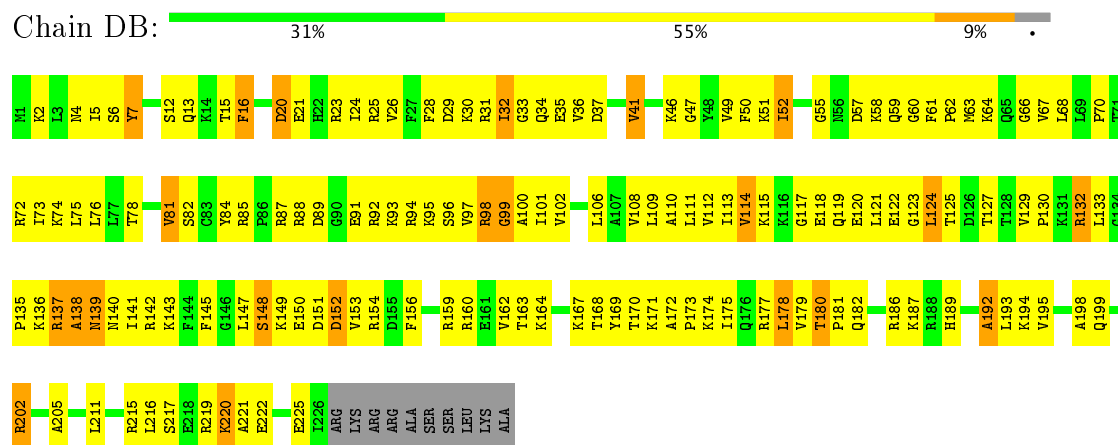


• Molecule 55: uS7 (yeast S5)

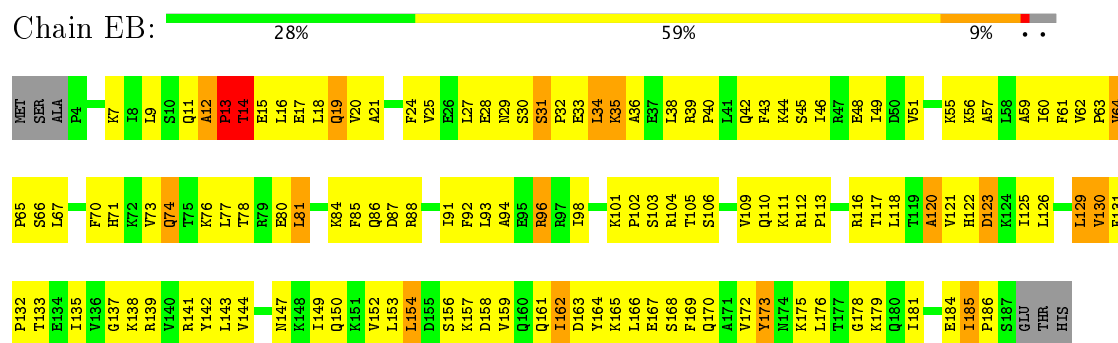
Chain CB: 



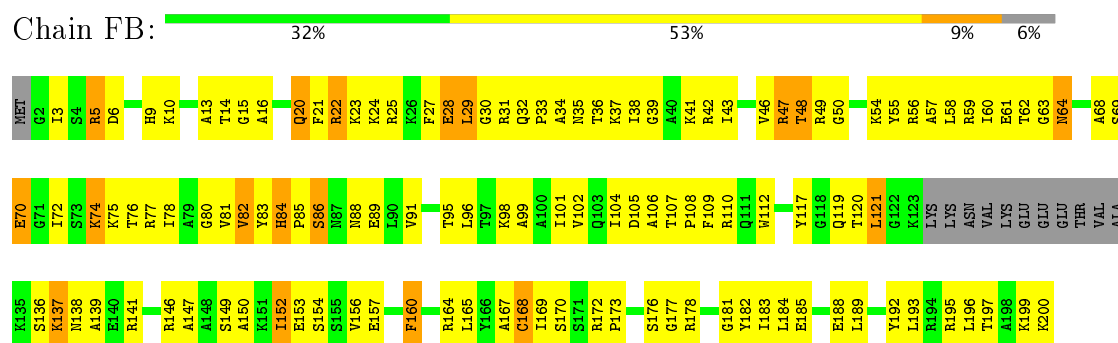
• Molecule 56: eS6 (yeast S6)



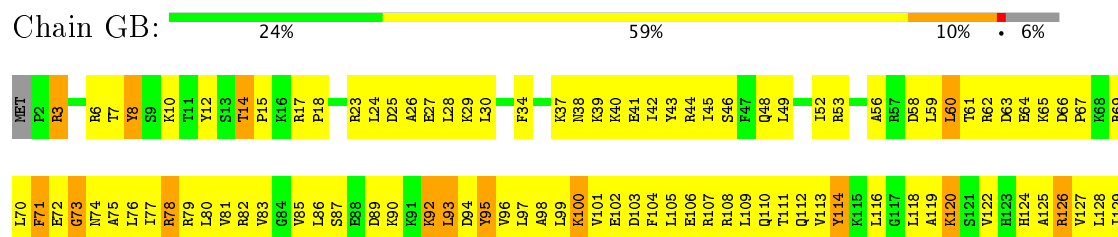
• Molecule 57: eS7 (yeast S7)



• Molecule 58: eS8 (yeast S8)



• Molecule 59: uS4 (yeast S9)





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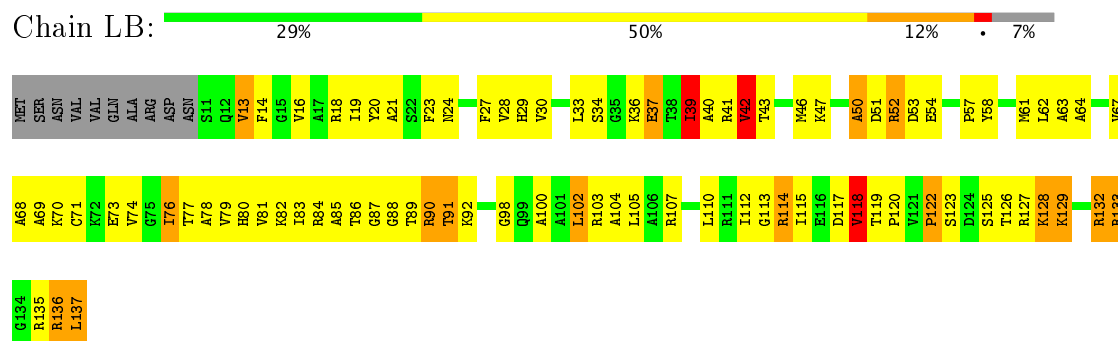
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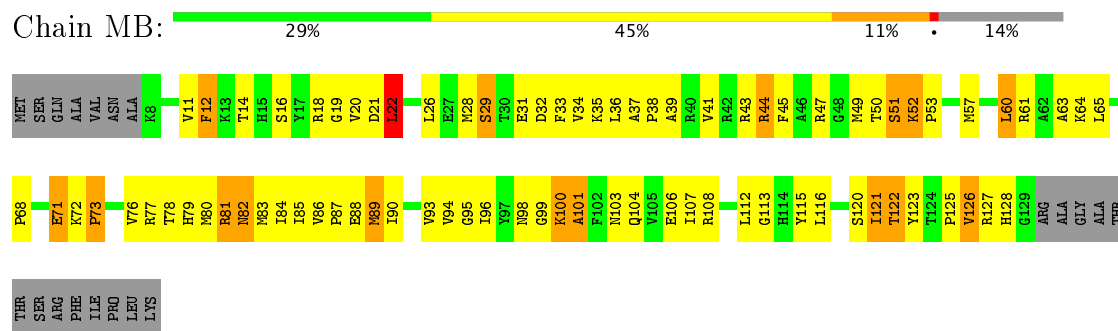
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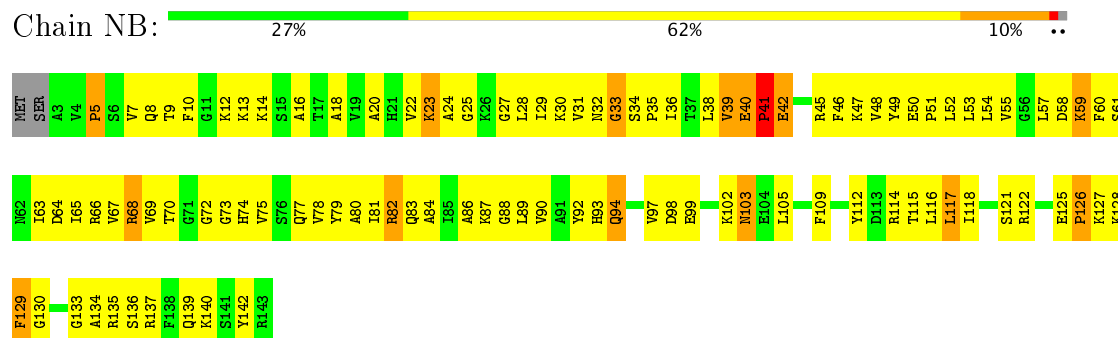
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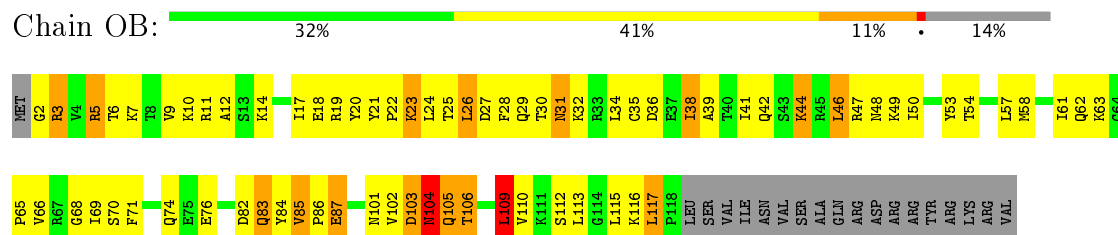
• Molecule 65: uS19 (yeast S15)



• Molecule 66: uS9 (yeast S16)

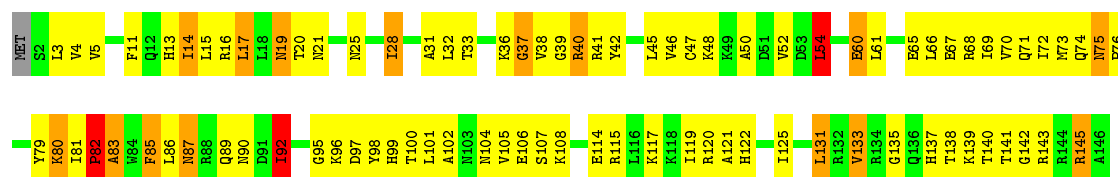


• Molecule 67: eS17 (yeast S17)



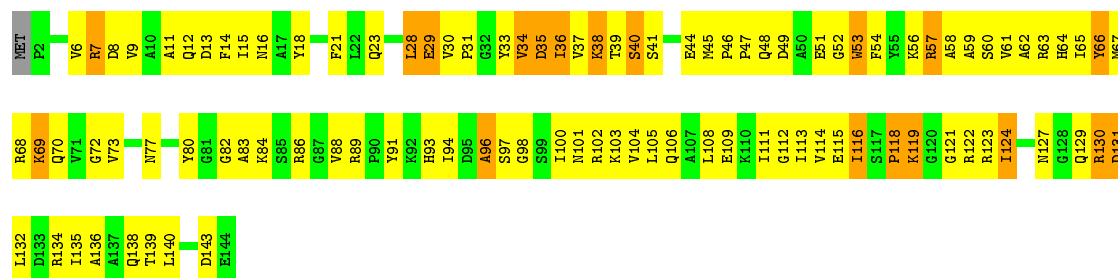
• Molecule 68: uS13 (yeast S18)





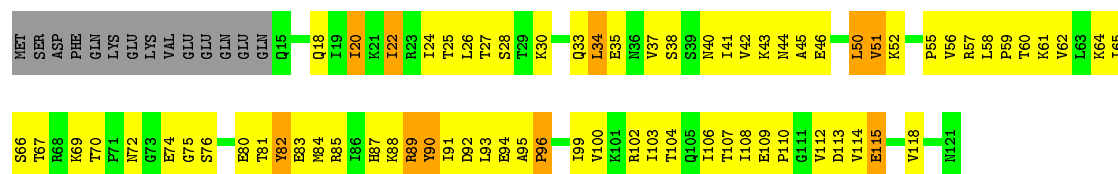
• Molecule 69: eS19 (yeast S19)

Chain QB: 30% 56% 13%



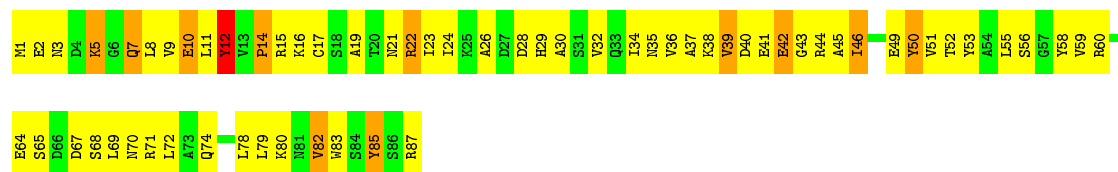
• Molecule 70: uS10 (yeast S20)

Chain RB: 28% 52% 8% 12%



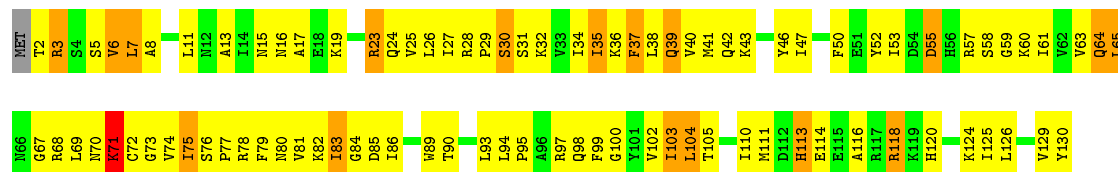
• Molecule 71: eS21 (yeast S21)

Chain SB: 28% 59% 13%

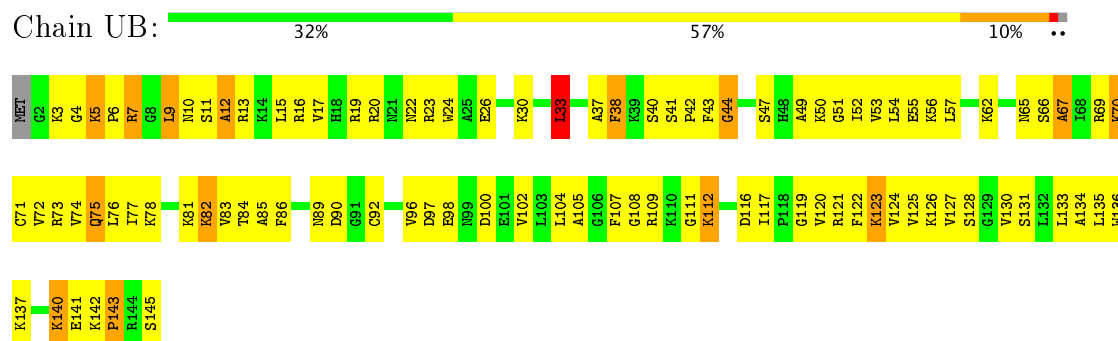


• Molecule 72: uS8 (yeast S22)

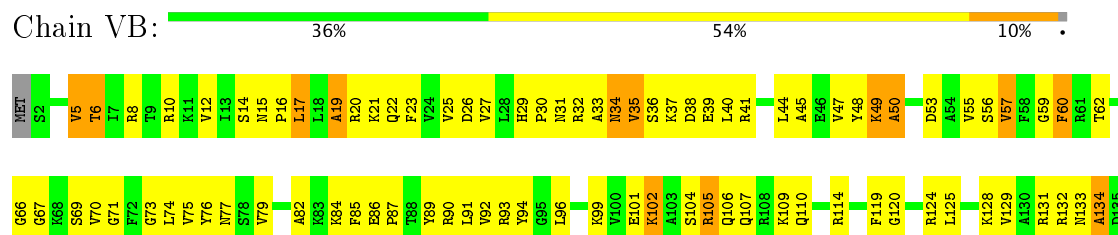
Chain TB: 29% 56% 13%



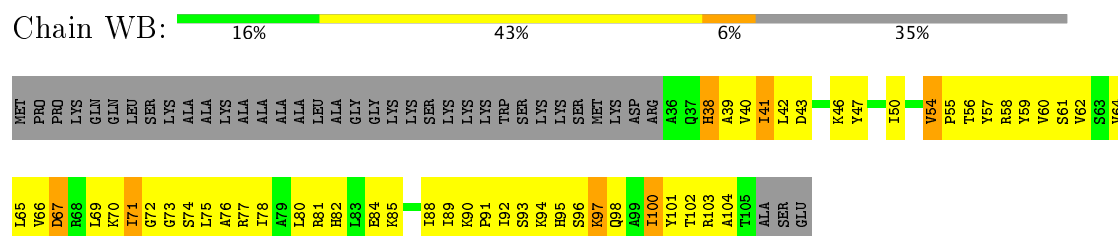
• Molecule 73: uS12 (yeast S23)



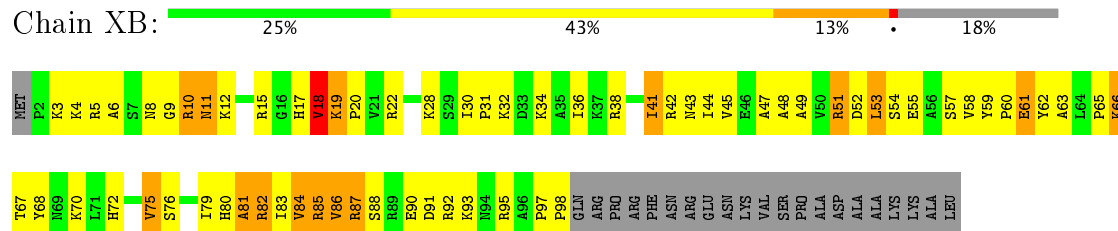
- Molecule 74: eS24 (yeast S24)



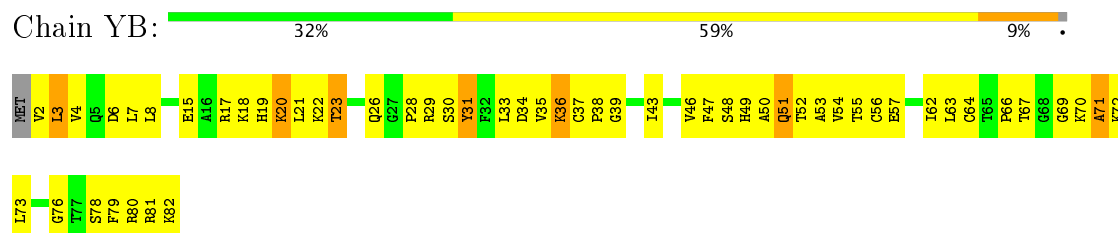
- Molecule 75: eS25 (yeast S25)



- Molecule 76: eS26 (yeast S26)



- Molecule 77: eS27 (yeast S27)



- Molecule 78: eS28 (yeast S28)

Met	ASP	ASU	TS	T5		L9		A10	K11	V12	I13	K14	V15	L16	G17	R18	T19		R22	G23	G24	V25	T26	T27	V28	R29	E30	E31	F32	L33		T36	S37	R38		M43	V44	K45	G46		R49	E50	N51	D52	I53	L54	V55	L56	M57	E58	S59	E60	R61	E62	A63	R64	R65	L66	a67
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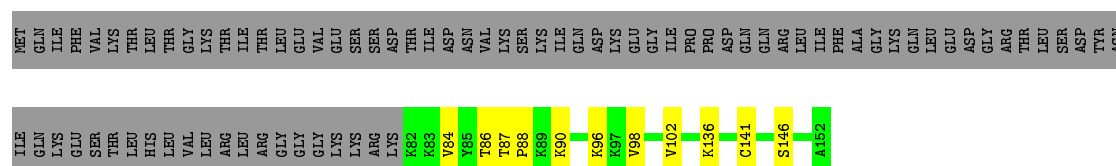
- Chain AC: 25% 63% 7% 5%



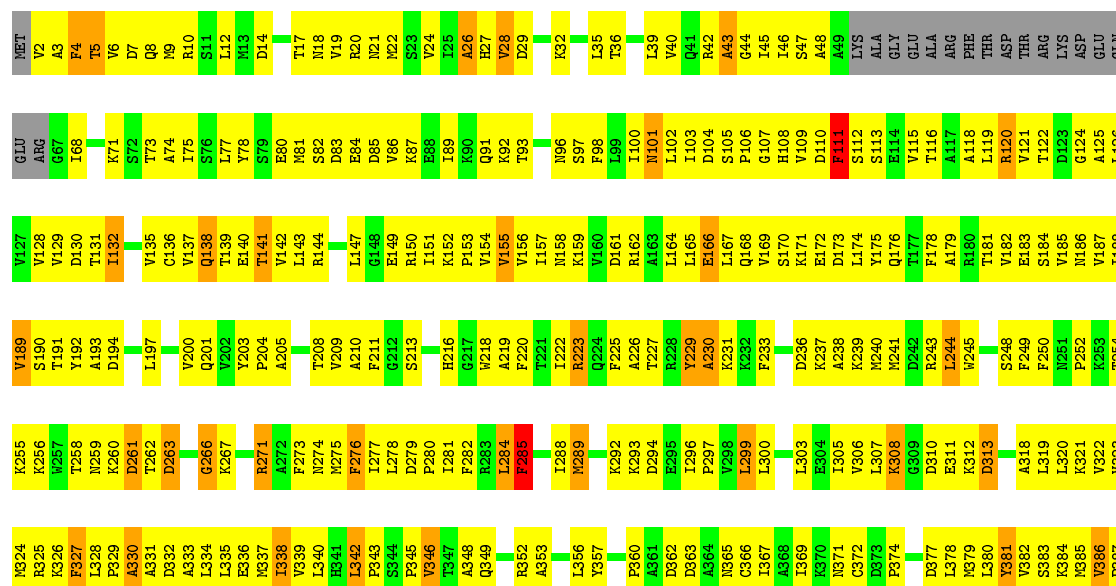
- Chain BC:

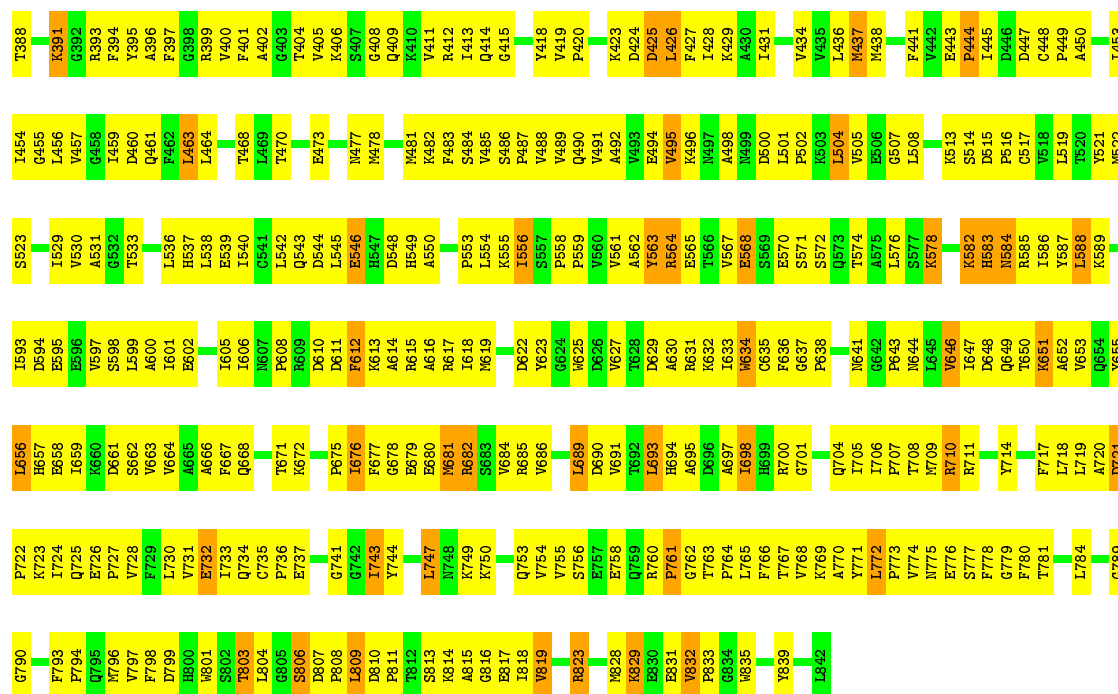


- Chain CC: 



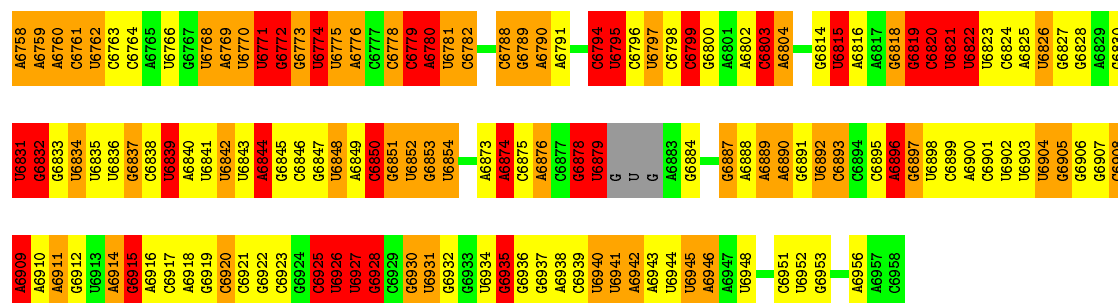
- Chain DC: 





● Molecule 83: IRES

Chain EC: 28% 31% 24% 15%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	35045	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.4	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	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	0.85	1/42096 (0.0%)	0.75	16/65570 (0.0%)
10	J	1.09	0/1425	0.76	1/1912 (0.1%)
11	K	1.13	0/1822	0.68	0/2451
12	L	0.95	0/1850	0.64	0/2495
13	M	1.05	0/1540	0.67	1/2073 (0.0%)
14	N	1.09	0/1754	0.64	0/2350
15	O	0.87	0/1375	0.63	0/1842
16	P	1.81	0/728	0.79	0/975
17	Q	1.03	0/1568	0.68	0/2106
18	R	1.16	0/1069	0.67	0/1438
19	S	1.13	0/1758	0.68	0/2354
2	B	1.16	20/78587 (0.0%)	0.77	40/122484 (0.0%)
20	T	1.11	0/1586	0.65	0/2128
21	U	1.12	0/1466	0.65	0/1968
22	V	1.09	0/1466	0.68	0/1965
23	W	0.90	0/1539	0.62	0/2050
24	X	1.18	0/1482	0.69	0/1990
25	Y	1.17	0/1301	0.68	0/1743
26	Z	0.82	0/812	0.58	0/1099
27	AA	1.04	0/1019	0.67	0/1369
28	BA	1.17	0/521	0.68	0/691
29	CA	1.06	0/984	0.66	0/1325
3	C	1.17	3/3747 (0.1%)	0.76	3/5832 (0.1%)
30	DA	1.09	0/1005	0.67	2/1341 (0.1%)
31	EA	0.85	0/1119	0.59	0/1497
32	FA	1.04	0/1205	0.65	0/1612
33	GA	1.02	0/474	0.66	0/629
34	HA	0.83	0/751	0.65	0/1008
35	IA	0.95	0/904	0.64	0/1213
36	JA	1.15	0/1041	0.62	0/1394
37	KA	1.14	0/869	0.69	0/1168
38	LA	0.98	0/891	0.67	0/1191

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	MA	1.02	0/979	0.66	0/1301
4	D	1.08	1/2884 (0.0%)	0.73	1/4491 (0.0%)
40	NA	0.94	0/779	0.70	1/1034 (0.1%)
41	OA	1.20	0/697	0.69	0/923
42	PA	0.92	0/619	0.61	0/826
43	QA	1.16	0/444	0.71	0/588
44	RA	1.11	0/424	0.65	0/562
45	SA	0.96	0/235	0.62	0/300
46	TA	1.04	0/861	0.66	0/1136
47	UA	1.02	0/702	0.65	0/934
48	VA	1.72	0/1498	0.83	1/2025 (0.0%)
49	WA	0.83	0/2498	0.58	0/3398
5	E	1.90	2/1377 (0.1%)	0.82	1/1844 (0.1%)
50	XA	0.67	0/1653	0.64	1/2261 (0.0%)
51	YA	0.71	0/1735	0.59	0/2335
52	ZA	0.71	0/1665	0.58	0/2263
53	AB	0.84	0/1759	0.60	0/2368
54	BB	0.72	0/2110	0.63	0/2839
55	CB	0.74	0/1630	0.61	0/2202
56	DB	0.74	0/1844	0.61	0/2464
57	EB	0.81	0/1506	0.61	0/2028
58	FB	0.86	0/1515	0.59	0/2021
59	GB	0.70	0/1519	0.61	0/2035
6	F	1.03	0/1952	0.71	0/2622
60	HB	0.98	0/837	0.59	0/1131
61	IB	0.92	0/1273	0.61	0/1712
62	JB	1.10	0/495	0.56	0/617
63	KB	0.80	0/1216	0.62	0/1638
64	LB	0.64	0/953	0.60	0/1279
65	MB	1.05	0/996	0.64	0/1335
66	NB	0.80	0/1126	0.60	0/1510
67	OB	0.77	0/844	0.76	1/1120 (0.1%)
68	PB	0.86	0/1212	0.62	0/1628
69	QB	0.79	0/1131	0.57	0/1517
7	G	1.00	0/3153	0.65	0/4239
70	RB	0.86	0/866	0.60	0/1169
71	SB	0.68	0/694	0.56	0/935
72	TB	0.75	0/1039	0.62	0/1395
73	UB	0.87	0/1140	0.65	1/1518 (0.1%)
74	VB	0.71	0/1088	0.59	0/1449
75	WB	0.80	0/571	0.60	0/768
76	XB	0.69	0/782	0.60	0/1047
77	YB	0.74	0/621	0.62	0/838

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
78	ZB	0.72	0/500	0.59	0/670
79	AC	0.94	0/454	0.58	0/602
8	H	1.11	0/2802	0.70	1/3792 (0.0%)
80	BC	0.83	0/483	0.57	0/643
81	CC	1.05	0/283	0.63	0/352
82	DC	1.41	0/6521	0.71	2/8830 (0.0%)
83	EC	2.21	71/4413 (1.6%)	1.02	23/6849 (0.3%)
9	I	0.93	0/2426	0.65	0/3271
All	All	1.08	98/230558 (0.0%)	0.73	96/337917 (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	19
2	B	0	65
3	C	0	4
4	D	0	1
83	EC	0	8
All	All	0	97

The worst 5 of 98 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	EC	6875	C	N1-C2	7.27	1.47	1.40
83	EC	6831	U	N1-C2	7.18	1.45	1.38
83	EC	6879	U	N1-C2	7.00	1.44	1.38
83	EC	6843	U	N1-C2	6.99	1.44	1.38
83	EC	6775	U	N1-C2	6.94	1.44	1.38

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	EC	6799	C	N1-C1'-C2'	8.09	124.52	114.00
48	VA	182	THR	N-CA-C	7.73	131.88	111.00
10	J	126	GLN	N-CA-C	-7.47	90.83	111.00
83	EC	6774	U	N1-C1'-C2'	7.36	123.57	114.00
2	B	3360	C	N1-C1'-C2'	7.26	123.44	114.00

There are no chirality outliers.

5 of 97 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	313	U	Sidechain
1	A	322	G	Sidechain
1	A	324	U	Sidechain
1	A	330	G	Sidechain
1	A	396	G	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	37658	0	18908	1739	0
2	B	70248	0	35241	3748	0
3	C	3354	0	1695	184	0
4	D	2580	0	1304	123	0
5	E	1359	0	1425	113	0
6	F	1918	0	1987	279	0
7	G	3082	0	3165	364	0
8	H	2750	0	2863	343	0
9	I	2376	0	2325	266	0
10	J	1401	0	1501	161	0
11	K	1785	0	1862	230	0
12	L	1818	0	1908	203	0
13	M	1519	0	1587	161	0
14	N	1718	0	1754	166	0
15	O	1354	0	1383	182	0
16	P	723	0	774	107	0
17	Q	1543	0	1608	188	0
18	R	1054	0	1149	174	0
19	S	1721	0	1779	243	0
20	T	1556	0	1659	150	0
21	U	1443	0	1485	166	0
22	V	1442	0	1543	200	0
23	W	1522	0	1617	164	0
24	X	1446	0	1487	179	0
25	Y	1277	0	1323	152	0
26	Z	796	0	812	60	0
27	AA	1004	0	1048	113	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	BA	509	0	537	51	0
29	CA	969	0	1036	133	0
30	DA	994	0	1081	124	0
31	EA	1093	0	1155	140	0
32	FA	1174	0	1215	132	0
33	GA	463	0	491	41	0
34	HA	743	0	797	90	0
35	IA	890	0	938	84	0
36	JA	1020	0	1090	89	0
37	KA	851	0	880	121	0
38	LA	881	0	949	128	0
39	MA	970	0	1078	122	0
40	NA	772	0	849	109	0
41	OA	682	0	687	83	0
42	PA	613	0	682	52	0
43	QA	437	0	475	72	0
44	RA	418	0	459	43	0
45	SA	234	0	284	20	0
46	TA	848	0	918	69	0
47	UA	695	0	738	87	0
48	VA	1473	0	1514	176	0
49	WA	2445	0	2401	191	0
50	XA	1612	0	1623	176	0
51	YA	1709	0	1784	217	0
52	ZA	1635	0	1723	207	0
53	AB	1734	0	1817	169	0
54	BB	2069	0	2154	255	0
55	CB	1610	0	1675	180	0
56	DB	1820	0	1918	158	0
57	EB	1481	0	1572	152	0
58	FB	1490	0	1525	155	0
59	GB	1494	0	1573	181	0
60	HB	817	0	804	72	0
61	IB	1245	0	1314	123	0
62	JB	496	0	141	0	0
63	KB	1193	0	1255	126	0
64	LB	942	0	979	148	0
65	MB	975	0	1017	91	0
66	NB	1106	0	1166	141	0
67	OB	836	0	827	75	0
68	PB	1193	0	1222	100	0
69	QB	1113	0	1124	140	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	RB	856	0	917	97	0
71	SB	685	0	672	107	0
72	TB	1022	0	1060	133	0
73	UB	1122	0	1196	121	0
74	VB	1074	0	1132	119	0
75	WB	563	0	603	85	0
76	XB	769	0	818	104	0
77	YB	611	0	633	76	0
78	ZB	498	0	535	56	0
79	AC	444	0	436	61	0
80	BC	475	0	525	38	0
81	CC	284	0	76	0	0
82	DC	6419	0	6493	727	0
83	EC	3968	0	1973	103	0
84	DC	28	0	12	2	0
85	DC	1	0	0	0	0
86	DC	35	0	40	6	0
All	All	215045	0	159780	14774	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 40.

The worst 5 of 14774 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)
2:B:509:U:H2'	2:B:510:G:H5''	1.22	1.20
56:DB:64:LYS:HE3	56:DB:81:VAL:HG21	1.24	1.19
2:B:1948:G:H5'	23:W:101:VAL:HG11	1.25	1.17
19:S:73:ARG:HE	19:S:92:LEU:HD21	1.11	1.15
18:R:21:VAL:HG12	18:R:65:LEU:HA	1.27	1.15

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%)	114 (69%)	40 (24%)	11 (7%)	1	22
6	F	250/254 (98%)	165 (66%)	71 (28%)	14 (6%)	2	26
7	G	384/387 (99%)	277 (72%)	79 (21%)	28 (7%)	1	20
8	H	359/362 (99%)	253 (70%)	76 (21%)	30 (8%)	1	15
9	I	294/297 (99%)	221 (75%)	57 (19%)	16 (5%)	2	27
10	J	173/176 (98%)	117 (68%)	40 (23%)	16 (9%)	1	14
11	K	220/244 (90%)	173 (79%)	30 (14%)	17 (8%)	1	18
12	L	231/256 (90%)	165 (71%)	43 (19%)	23 (10%)	1	12
13	M	189/191 (99%)	146 (77%)	37 (20%)	6 (3%)	5	39
14	N	207/221 (94%)	157 (76%)	42 (20%)	8 (4%)	3	34
15	O	167/174 (96%)	125 (75%)	28 (17%)	14 (8%)	1	15
16	P	92/165 (56%)	63 (68%)	18 (20%)	11 (12%)	0	7
17	Q	191/199 (96%)	140 (73%)	38 (20%)	13 (7%)	1	22
18	R	134/138 (97%)	101 (75%)	24 (18%)	9 (7%)	1	22
19	S	201/204 (98%)	155 (77%)	33 (16%)	13 (6%)	1	23
20	T	195/199 (98%)	158 (81%)	30 (15%)	7 (4%)	4	37
21	U	181/184 (98%)	135 (75%)	35 (19%)	11 (6%)	2	24
22	V	183/186 (98%)	135 (74%)	34 (19%)	14 (8%)	1	18
23	W	186/189 (98%)	151 (81%)	30 (16%)	5 (3%)	6	43
24	X	170/172 (99%)	126 (74%)	25 (15%)	19 (11%)	0	9
25	Y	157/160 (98%)	102 (65%)	41 (26%)	14 (9%)	1	15
26	Z	98/121 (81%)	68 (69%)	22 (22%)	8 (8%)	1	16
27	AA	134/137 (98%)	95 (71%)	32 (24%)	7 (5%)	2	28
28	BA	59/155 (38%)	44 (75%)	8 (14%)	7 (12%)	0	7
29	CA	119/142 (84%)	90 (76%)	18 (15%)	11 (9%)	1	14
30	DA	124/127 (98%)	93 (75%)	21 (17%)	10 (8%)	1	17
31	EA	133/136 (98%)	93 (70%)	28 (21%)	12 (9%)	1	15
32	FA	146/149 (98%)	108 (74%)	31 (21%)	7 (5%)	2	29
33	GA	56/59 (95%)	45 (80%)	9 (16%)	2 (4%)	4	37
34	HA	95/105 (90%)	74 (78%)	16 (17%)	5 (5%)	2	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	IA	107/113 (95%)	84 (78%)	17 (16%)	6 (6%)	2	26
36	JA	125/130 (96%)	89 (71%)	27 (22%)	9 (7%)	1	20
37	KA	104/107 (97%)	82 (79%)	20 (19%)	2 (2%)	9	50
38	LA	110/121 (91%)	79 (72%)	23 (21%)	8 (7%)	1	20
39	MA	117/120 (98%)	89 (76%)	21 (18%)	7 (6%)	2	25
40	NA	97/100 (97%)	70 (72%)	13 (13%)	14 (14%)	0	5
41	OA	85/88 (97%)	65 (76%)	17 (20%)	3 (4%)	4	38
42	PA	75/78 (96%)	61 (81%)	14 (19%)	0	100	100
43	QA	48/51 (94%)	38 (79%)	6 (12%)	4 (8%)	1	16
44	RA	50/128 (39%)	32 (64%)	13 (26%)	5 (10%)	1	12
45	SA	23/25 (92%)	20 (87%)	3 (13%)	0	100	100
46	TA	103/106 (97%)	73 (71%)	19 (18%)	11 (11%)	0	10
47	UA	89/92 (97%)	55 (62%)	22 (25%)	12 (14%)	0	5
48	VA	187/312 (60%)	128 (68%)	42 (22%)	17 (9%)	1	14
49	WA	316/319 (99%)	229 (72%)	72 (23%)	15 (5%)	3	30
50	XA	204/252 (81%)	136 (67%)	49 (24%)	19 (9%)	1	14
51	YA	212/255 (83%)	146 (69%)	48 (23%)	18 (8%)	1	15
52	ZA	215/254 (85%)	165 (77%)	36 (17%)	14 (6%)	1	23
53	AB	221/240 (92%)	167 (76%)	39 (18%)	15 (7%)	1	22
54	BB	258/261 (99%)	178 (69%)	59 (23%)	21 (8%)	1	17
55	CB	204/225 (91%)	155 (76%)	31 (15%)	18 (9%)	1	15
56	DB	224/236 (95%)	167 (75%)	39 (17%)	18 (8%)	1	17
57	EB	182/190 (96%)	127 (70%)	40 (22%)	15 (8%)	1	16
58	FB	184/200 (92%)	149 (81%)	26 (14%)	9 (5%)	2	29
59	GB	183/197 (93%)	129 (70%)	35 (19%)	19 (10%)	0	10
60	HB	94/105 (90%)	67 (71%)	15 (16%)	12 (13%)	0	6
61	IB	153/156 (98%)	107 (70%)	34 (22%)	12 (8%)	1	18
62	JB	122/143 (85%)	74 (61%)	35 (29%)	13 (11%)	0	10
63	KB	148/151 (98%)	119 (80%)	21 (14%)	8 (5%)	2	27
64	LB	125/137 (91%)	83 (66%)	35 (28%)	7 (6%)	2	26
65	MB	120/142 (84%)	82 (68%)	25 (21%)	13 (11%)	0	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	NB	139/143 (97%)	104 (75%)	26 (19%)	9 (6%)	1	23
67	OB	115/136 (85%)	84 (73%)	21 (18%)	10 (9%)	1	15
68	PB	143/146 (98%)	109 (76%)	20 (14%)	14 (10%)	1	12
69	QB	141/144 (98%)	104 (74%)	23 (16%)	14 (10%)	1	12
70	RB	105/121 (87%)	73 (70%)	28 (27%)	4 (4%)	4	35
71	SB	85/87 (98%)	61 (72%)	14 (16%)	10 (12%)	0	8
72	TB	127/130 (98%)	93 (73%)	27 (21%)	7 (6%)	2	27
73	UB	142/145 (98%)	97 (68%)	36 (25%)	9 (6%)	1	24
74	VB	132/135 (98%)	94 (71%)	26 (20%)	12 (9%)	1	14
75	WB	68/108 (63%)	41 (60%)	21 (31%)	6 (9%)	1	15
76	XB	95/119 (80%)	52 (55%)	26 (27%)	17 (18%)	0	3
77	YB	79/82 (96%)	53 (67%)	21 (27%)	5 (6%)	1	24
78	ZB	61/67 (91%)	46 (75%)	10 (16%)	5 (8%)	1	16
79	AC	51/56 (91%)	37 (72%)	12 (24%)	2 (4%)	3	34
80	BC	58/63 (92%)	38 (66%)	15 (26%)	5 (9%)	1	15
81	CC	69/152 (45%)	41 (59%)	17 (25%)	11 (16%)	0	4
82	DC	819/842 (97%)	620 (76%)	154 (19%)	45 (6%)	2	27
All	All	12207/13416 (91%)	8881 (73%)	2429 (20%)	897 (7%)	2	20

5 of 897 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	138	VAL
5	E	151	VAL
6	F	57	PRO
6	F	125	ALA
6	F	217	GLN

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%)	130 (83%)	27 (17%)	2	17
6	F	194/196 (99%)	169 (87%)	25 (13%)	5	28
7	G	322/323 (100%)	283 (88%)	39 (12%)	6	30
8	H	288/289 (100%)	263 (91%)	25 (9%)	12	45
9	I	244/245 (100%)	220 (90%)	24 (10%)	9	39
10	J	152/153 (99%)	131 (86%)	21 (14%)	4	27
11	K	186/205 (91%)	165 (89%)	21 (11%)	7	34
12	L	191/208 (92%)	177 (93%)	14 (7%)	16	52
13	M	171/171 (100%)	152 (89%)	19 (11%)	7	34
14	N	180/187 (96%)	165 (92%)	15 (8%)	13	47
15	O	147/150 (98%)	126 (86%)	21 (14%)	4	25
16	P	81/136 (60%)	69 (85%)	12 (15%)	3	23
17	Q	154/159 (97%)	132 (86%)	22 (14%)	4	25
18	R	107/109 (98%)	94 (88%)	13 (12%)	6	30
19	S	175/176 (99%)	156 (89%)	19 (11%)	7	35
20	T	160/162 (99%)	144 (90%)	16 (10%)	9	38
21	U	145/146 (99%)	125 (86%)	20 (14%)	4	27
22	V	150/151 (99%)	140 (93%)	10 (7%)	19	55
23	W	153/154 (99%)	139 (91%)	14 (9%)	11	42
24	X	156/156 (100%)	136 (87%)	20 (13%)	5	29
25	Y	136/137 (99%)	109 (80%)	27 (20%)	1	12
26	Z	87/107 (81%)	83 (95%)	4 (5%)	31	66
27	AA	104/105 (99%)	88 (85%)	16 (15%)	3	22
28	BA	54/129 (42%)	48 (89%)	6 (11%)	7	34
29	CA	105/118 (89%)	88 (84%)	17 (16%)	3	20
30	DA	109/110 (99%)	98 (90%)	11 (10%)	9	38
31	EA	115/116 (99%)	103 (90%)	12 (10%)	8	37
32	FA	118/119 (99%)	110 (93%)	8 (7%)	18	55
33	GA	46/47 (98%)	39 (85%)	7 (15%)	3	22
34	HA	81/88 (92%)	72 (89%)	9 (11%)	7	34
35	IA	96/97 (99%)	90 (94%)	6 (6%)	21	57
36	JA	109/111 (98%)	95 (87%)	14 (13%)	5	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	KA	90/91 (99%)	77 (86%)	13 (14%)	4	25
38	LA	95/103 (92%)	85 (90%)	10 (10%)	8	36
39	MA	104/105 (99%)	95 (91%)	9 (9%)	12	45
40	NA	81/82 (99%)	66 (82%)	15 (18%)	2	14
41	OA	70/71 (99%)	61 (87%)	9 (13%)	5	28
42	PA	68/69 (99%)	60 (88%)	8 (12%)	6	32
43	QA	45/46 (98%)	36 (80%)	9 (20%)	1	12
44	RA	47/116 (40%)	41 (87%)	6 (13%)	5	29
45	SA	23/23 (100%)	19 (83%)	4 (17%)	2	16
46	TA	90/91 (99%)	80 (89%)	10 (11%)	7	34
47	UA	71/72 (99%)	64 (90%)	7 (10%)	9	39
48	VA	160/254 (63%)	145 (91%)	15 (9%)	10	41
49	WA	261/262 (100%)	233 (89%)	28 (11%)	8	36
50	XA	173/210 (82%)	153 (88%)	20 (12%)	6	33
51	YA	191/224 (85%)	174 (91%)	17 (9%)	11	44
52	ZA	176/205 (86%)	169 (96%)	7 (4%)	36	69
53	AB	182/195 (93%)	164 (90%)	18 (10%)	9	39
54	BB	221/222 (100%)	197 (89%)	24 (11%)	7	35
55	CB	173/191 (91%)	162 (94%)	11 (6%)	20	57
56	DB	193/201 (96%)	177 (92%)	16 (8%)	13	47
57	EB	165/170 (97%)	154 (93%)	11 (7%)	19	55
58	FB	150/161 (93%)	135 (90%)	15 (10%)	9	38
59	GB	158/166 (95%)	140 (89%)	18 (11%)	7	33
60	HB	89/98 (91%)	79 (89%)	10 (11%)	7	34
61	IB	136/137 (99%)	121 (89%)	15 (11%)	7	35
63	KB	127/128 (99%)	118 (93%)	9 (7%)	17	53
64	LB	96/105 (91%)	79 (82%)	17 (18%)	2	16
65	MB	103/118 (87%)	95 (92%)	8 (8%)	15	50
66	NB	117/119 (98%)	107 (92%)	10 (8%)	12	47
67	OB	82/124 (66%)	65 (79%)	17 (21%)	1	10
68	PB	128/129 (99%)	112 (88%)	16 (12%)	5	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	QB	115/116 (99%)	105 (91%)	10 (9%)	12	45
70	RB	100/114 (88%)	91 (91%)	9 (9%)	11	43
71	SB	74/74 (100%)	69 (93%)	5 (7%)	18	55
72	TB	110/111 (99%)	96 (87%)	14 (13%)	5	29
73	UB	119/120 (99%)	109 (92%)	10 (8%)	13	47
74	VB	112/113 (99%)	105 (94%)	7 (6%)	21	57
75	WB	61/89 (68%)	57 (93%)	4 (7%)	19	56
76	XB	83/101 (82%)	76 (92%)	7 (8%)	13	47
77	YB	70/71 (99%)	65 (93%)	5 (7%)	17	53
78	ZB	56/60 (93%)	53 (95%)	3 (5%)	26	62
79	AC	47/49 (96%)	44 (94%)	3 (6%)	20	57
80	BC	51/54 (94%)	49 (96%)	2 (4%)	37	70
82	DC	699/714 (98%)	622 (89%)	77 (11%)	7	35
All	All	10235/11032 (93%)	9143 (89%)	1092 (11%)	12	36

5 of 1092 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	FA	46	ASP
44	RA	115	CYS
78	ZB	52	ASP
34	HA	69	TYR
38	LA	58	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 315 such sidechains are listed below:

Mol	Chain	Res	Type
36	JA	49	ASN
49	WA	147	HIS
82	DC	21	ASN
37	KA	39	GLN
41	OA	76	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1755/1798 (97%)	359 (20%)	19 (1%)
2	B	3265/3396 (96%)	569 (17%)	29 (0%)
3	C	157/158 (99%)	25 (15%)	2 (1%)
4	D	120/121 (99%)	17 (14%)	0
83	EC	176/201 (87%)	70 (39%)	4 (2%)
All	All	5473/5674 (96%)	1040 (19%)	54 (0%)

5 of 1040 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	4	C
1	A	25	C
1	A	26	A
1	A	34	G

5 of 54 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	658	G
2	B	1481	A
3	C	85	G
2	B	780	A
2	B	1307	G

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	15,20,21	2.17	4 (26%)	15,28,30	2.09	5 (33%)

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 (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	DC	699	DDE	OAG-CBI	2.14	1.27	1.23
82	DC	699	DDE	CAT-CE1	2.94	1.53	1.50
82	DC	699	DDE	CBW-CBI	4.07	1.59	1.53
82	DC	699	DDE	CA-C	5.38	1.57	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	DC	699	DDE	CAU-CBW-CBI	-4.74	101.78	111.12
82	DC	699	DDE	OAG-CBI-CBW	-3.92	115.81	120.64
82	DC	699	DDE	CG-CD2-NE2	-2.08	104.98	109.25
82	DC	699	DDE	CAC-NCB-CBW	2.19	116.07	110.51
82	DC	699	DDE	OAG-CBI-NAD	2.73	127.25	123.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	25,30,30	2.21	10 (40%)	26,47,47	2.53	9 (34%)
86	SO1	DC	903	-	34,39,39	2.56	19 (55%)	35,64,64	2.07	9 (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
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 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	DC	903	SO1	O56-C52	-4.52	1.30	1.41
84	DC	901	GDP	C8-N7	-2.16	1.30	1.34
86	DC	903	SO1	C24-C22	2.00	1.60	1.53
84	DC	901	GDP	PB-O3B	2.03	1.63	1.54
84	DC	901	GDP	C2-N1	2.03	1.39	1.35

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	DC	903	SO1	C12-C6-C10	-7.11	102.20	107.70
84	DC	901	GDP	N3-C2-N1	-6.21	118.40	127.46
84	DC	901	GDP	C5-C6-N1	-4.50	117.08	123.48
84	DC	901	GDP	C6-C5-C4	-3.26	117.60	120.84
86	DC	903	SO1	C7-C2-C8	-3.01	104.60	110.09

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	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	DC	903	SO1	6	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.