wwPDB EM Validation Summary Report ⓘ

Mar 27, 2023 – 06:55 PM EDT

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

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

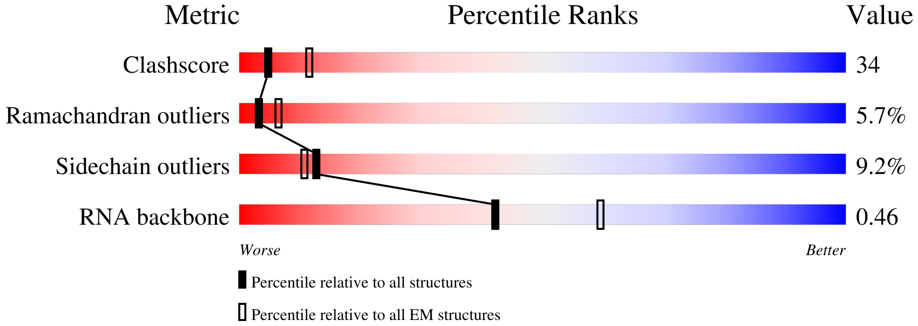
EMDB validation analysis	:	0.0.1.dev50
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.32.2

1 Overall quality at a glance ⓘ

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

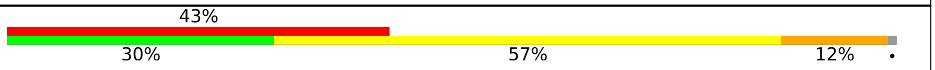
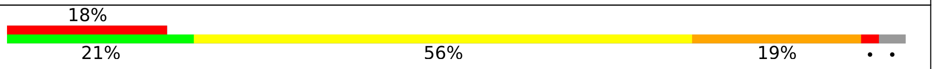
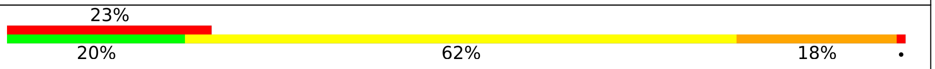
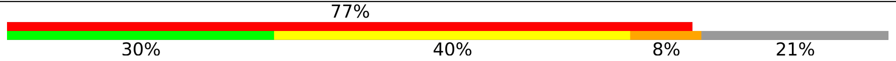
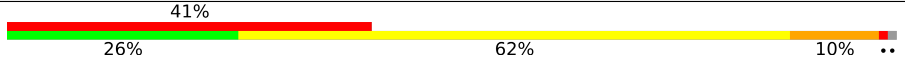
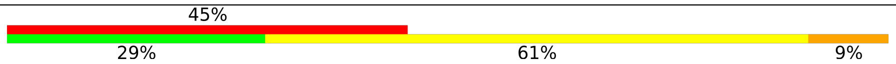
The reported resolution of this entry is 4.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A	1798	
2	B	3396	
3	C	158	
4	D	121	
5	E	217	
6	F	254	
7	G	387	

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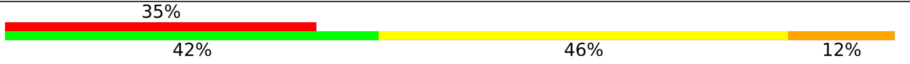
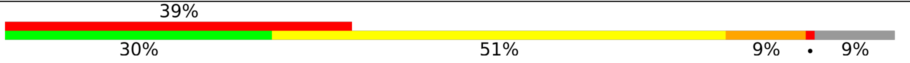
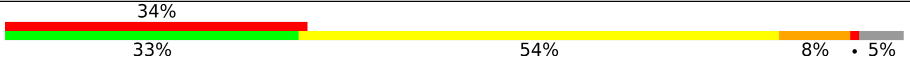
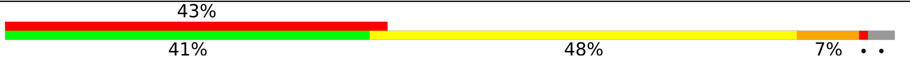
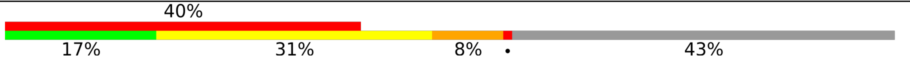
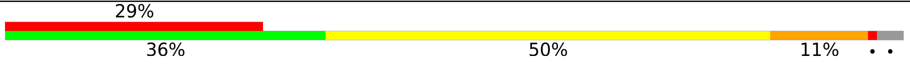
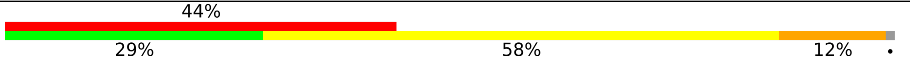
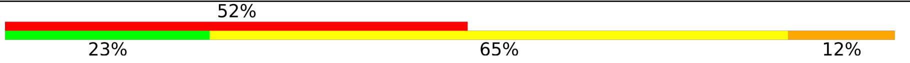
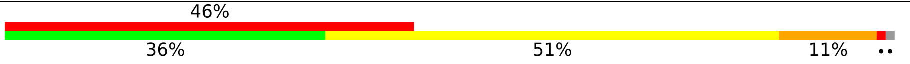
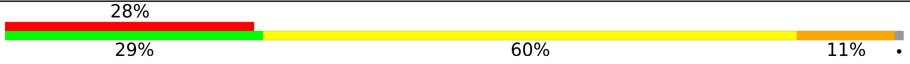
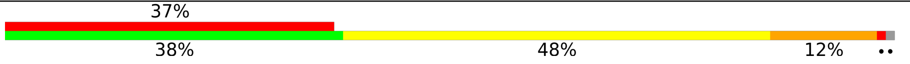
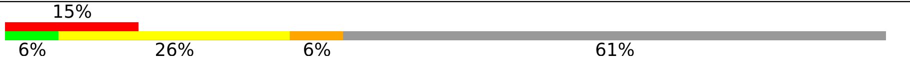
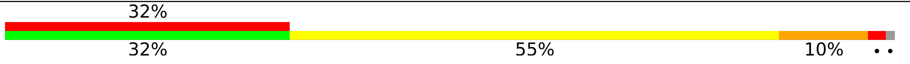
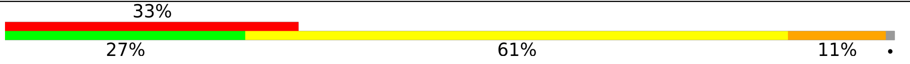
Mol	Chain	Length	Quality of chain
8	H	362	
9	I	297	
10	J	176	
11	K	244	
12	L	256	
13	M	191	
14	N	221	
15	O	174	
16	P	165	
17	Q	199	
18	R	138	
19	S	204	
20	T	199	
21	U	184	
22	V	186	
23	W	189	
24	X	172	
25	Y	160	
26	Z	121	
27	AA	137	
28	BA	155	
29	CA	142	
30	DA	127	
31	EA	136	
32	FA	149	

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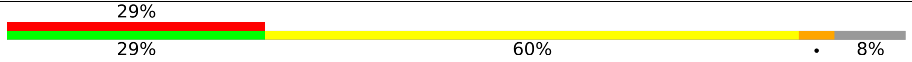
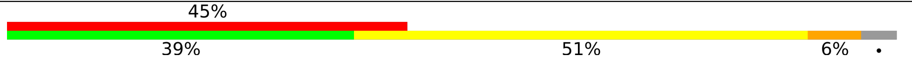
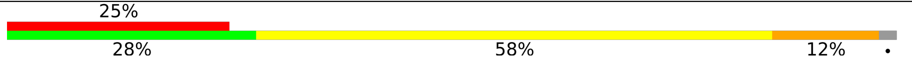
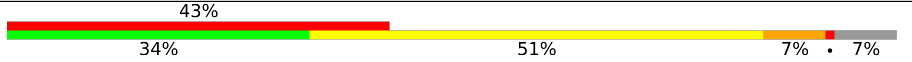
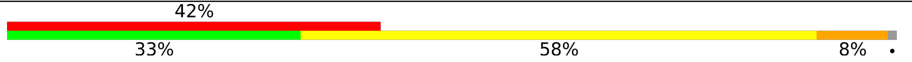
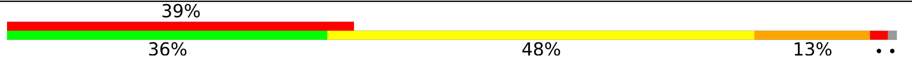
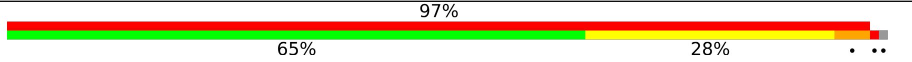
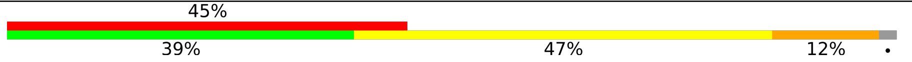
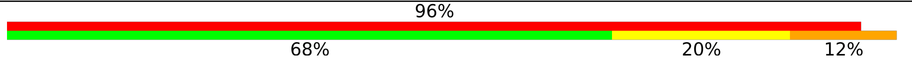
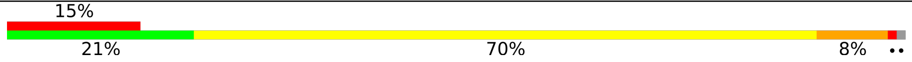
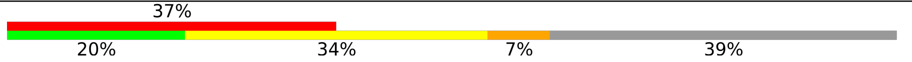
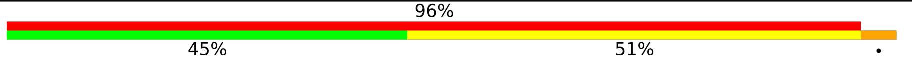
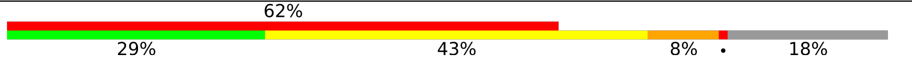
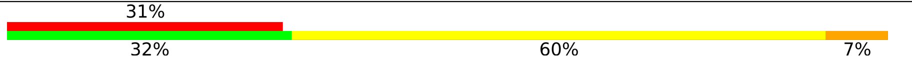
Mol	Chain	Length	Quality of chain
33	GA	59	 34% 49% 46% • •
34	HA	105	 29% 29% 60% • 8%
35	IA	113	 45% 39% 51% 6% •
36	JA	130	 25% 28% 58% 12% •
37	KA	107	 65% 33% 59% 7% •
38	LA	121	 43% 34% 51% 7% • 7%
39	MA	120	 65% 36% 58% 5% ••
40	NA	100	 42% 33% 58% 8% •
41	OA	88	 39% 36% 48% 13% ••
42	PA	78	 97% 65% 28% • ••
43	QA	51	 45% 39% 47% 12% •
44	RA	128	 8% 15% 21% • • 59%
45	SA	25	 96% 68% 20% 12%
46	TA	106	 15% 21% 70% 8% ••
47	UA	92	 49% 36% 52% 10% ••
48	VA	312	 37% 20% 34% 7% 39%
49	WA	319	 96% 45% 51% •
50	XA	252	 62% 29% 43% 8% • 18%
51	YA	255	 84% 76% 7% 16%
52	ZA	254	 57% 38% 44% • 15%
53	AB	240	 65% 45% 42% 5% 7%
54	BB	261	 31% 32% 60% 7%
55	CB	225	 79% 31% 52% 8% 8%
56	DB	236	 73% 44% 48% • •
57	EB	190	 88% 41% 46% 11% •

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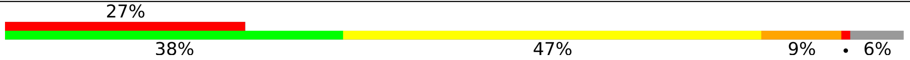
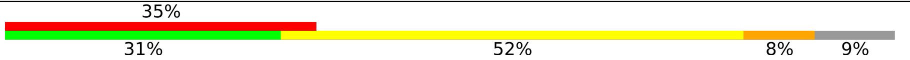
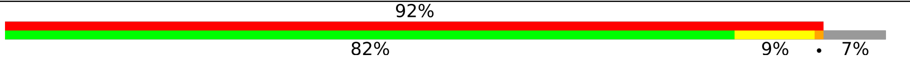
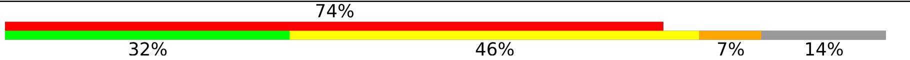
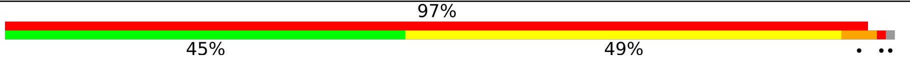
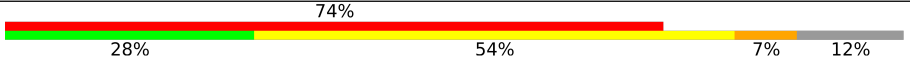
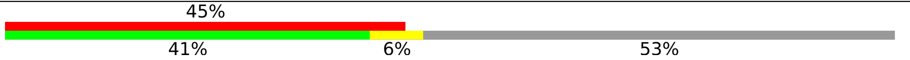
Mol	Chain	Length	Quality of chain
58	FB	200	
59	GB	197	
60	HB	105	
61	IB	156	
62	JB	143	
63	KB	151	
64	LB	137	
65	MB	142	
66	NB	143	
67	OB	136	
68	PB	146	
69	QB	144	
70	RB	121	
71	SB	87	
72	TB	130	
73	UB	145	
74	VB	135	
75	WB	108	
76	XB	119	
77	YB	82	
78	ZB	67	
79	AC	56	
80	BC	63	
81	CC	152	
82	DC	842	

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Mol	Chain	Length	Quality of chain
83	EC	201	

2 Entry composition (i)

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
28	BA	61	509	328	100	80	1	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O		
42	PA	77	613	391	115	107	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

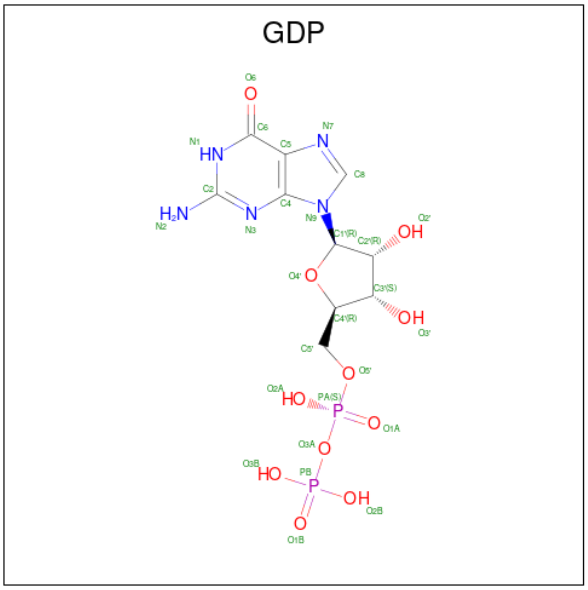
- Molecule 82 is a protein called yeast eEF2.

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

- Molecule 83 is a RNA chain called IRES.

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

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

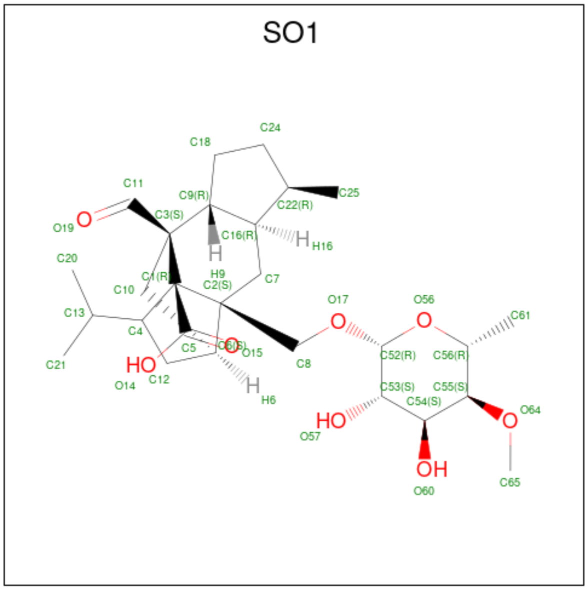


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
84	DC	1	28	10	5	11	2	0

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

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
85	DC	1	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: $C_{27}H_{42}O_8$).

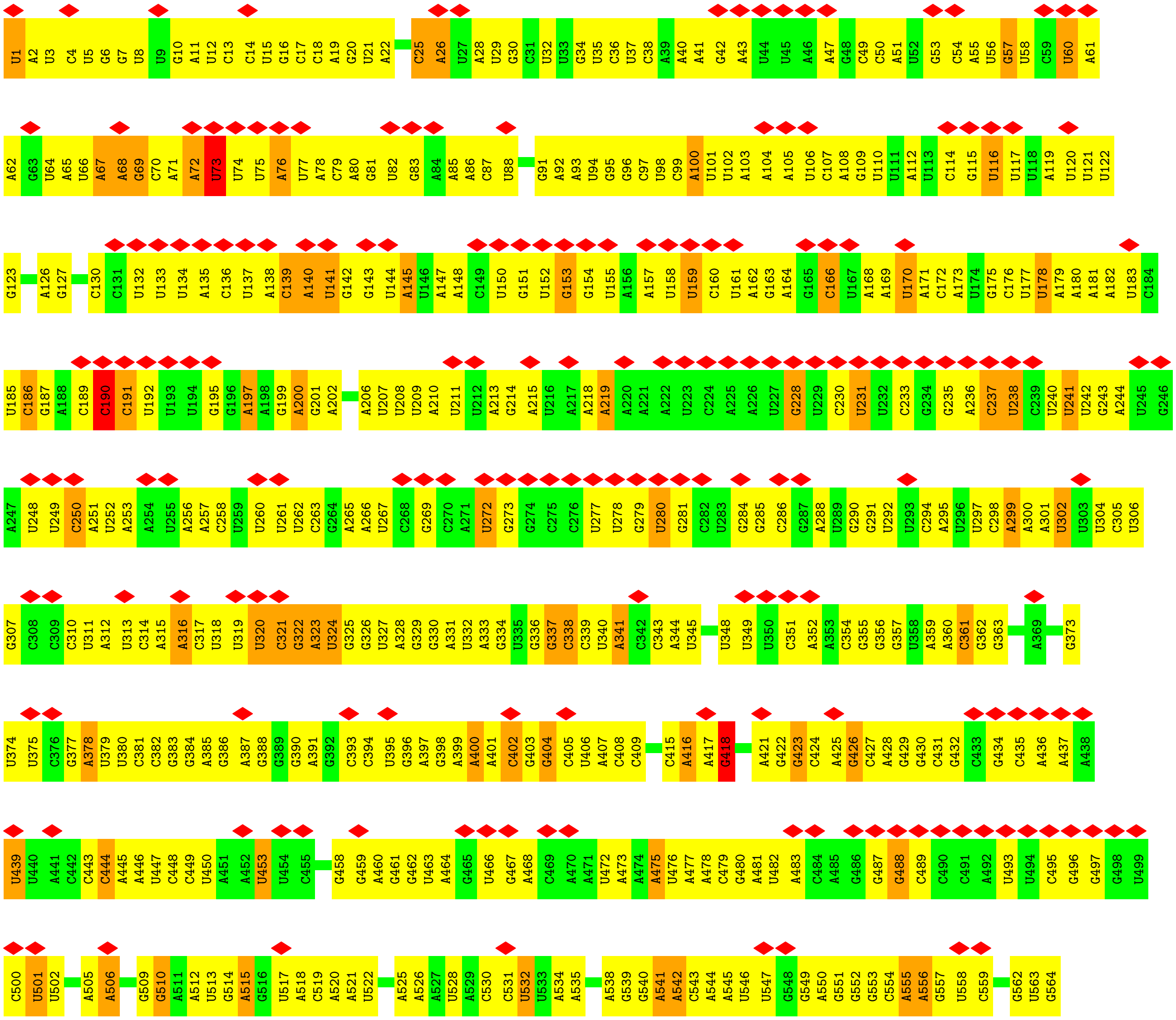


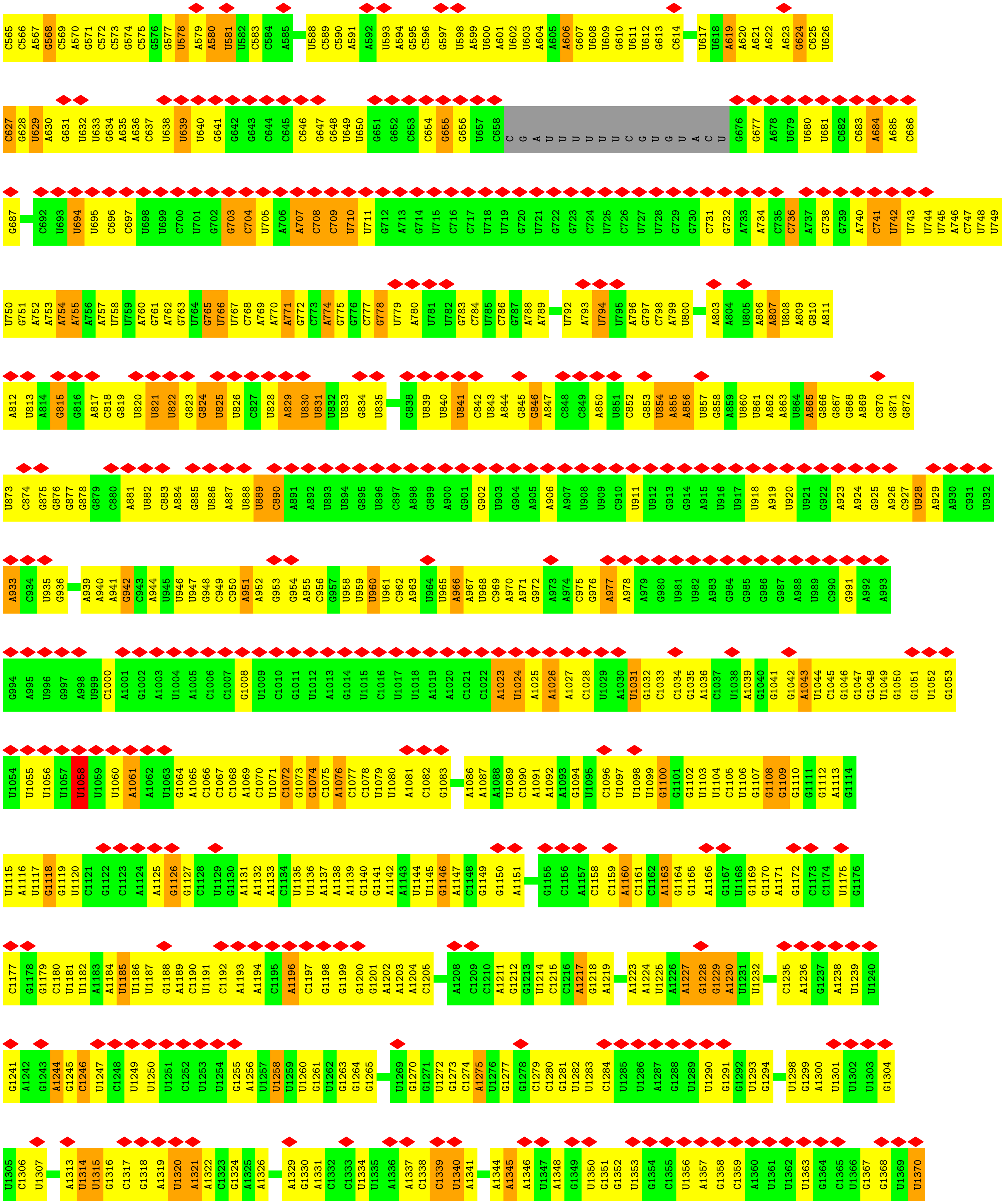
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
86	DC	1	35	27	8	0

3 Residue-property plots ⓘ

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

- Molecule 1: 18S ribosomal RNA

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A812 U813 A814 G815 G816 A817 C818 G819 U820 U821 U822 G823 G824 U825 U826 C827 U828 A829 U830 U831 U832 U833 G834 U835 G838 U839 U840 U841 C842 U843 A844 G845 G846 A847 C848 C849 A850 U851 C852 G853 U854 A855 A856 U857 G858 A859 U860 U861 A862 A863 U864 A865 C866 G867 C868 A869 C870 G871 G872
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A933 C934 U935 G936 A939 A940 A941 G942 C943 A944 U945 U946 U947 G948 C949 C950 A951 A952 G953 G954 A955 C956 G957 U958 U959 U960 U961 C962 A963 U964 U965 A966 A967 U968 C969 A970 A971 G972 A973 A974 C975 G976 A977 A978 A979 G980 U981 U982 A983 G984 G985 G986 G987 A988 U989 C990 G991 A992 A993
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U1115 A1116 U1117 G1118 G1119 U1120 C1121 G1122 C1123 A1124 A1125 G1126 G1127 C1128 U1129 G1130 A1131 A1132 A1133 C1134 U1135 U1136 A1137 A1138 A1139 G1140 G1141 A1142 A1143 U1144 U1145 G1146 A1147 C1148 G1149 G1150 A1151 G1155 C1156 A1157 C1158 C1159 A1160 C1161 C1162 A1163 G1164 G1165 A1166 G1167 U1168 G1169 G1170 A1171 G1172 C1173 C1174 U1175 G1176
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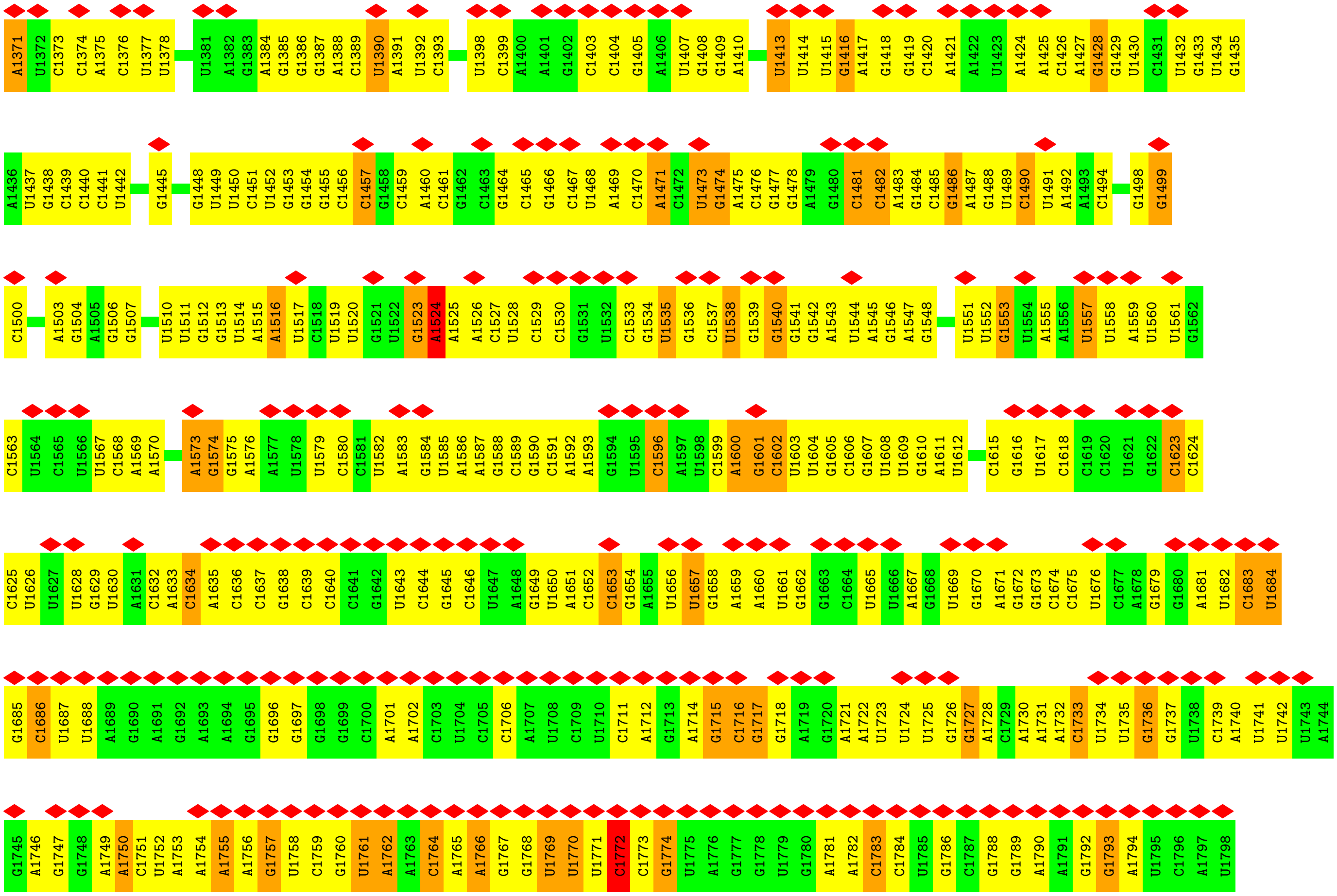
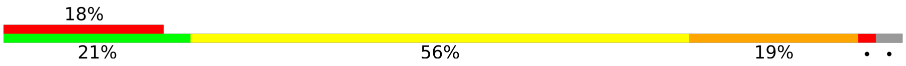
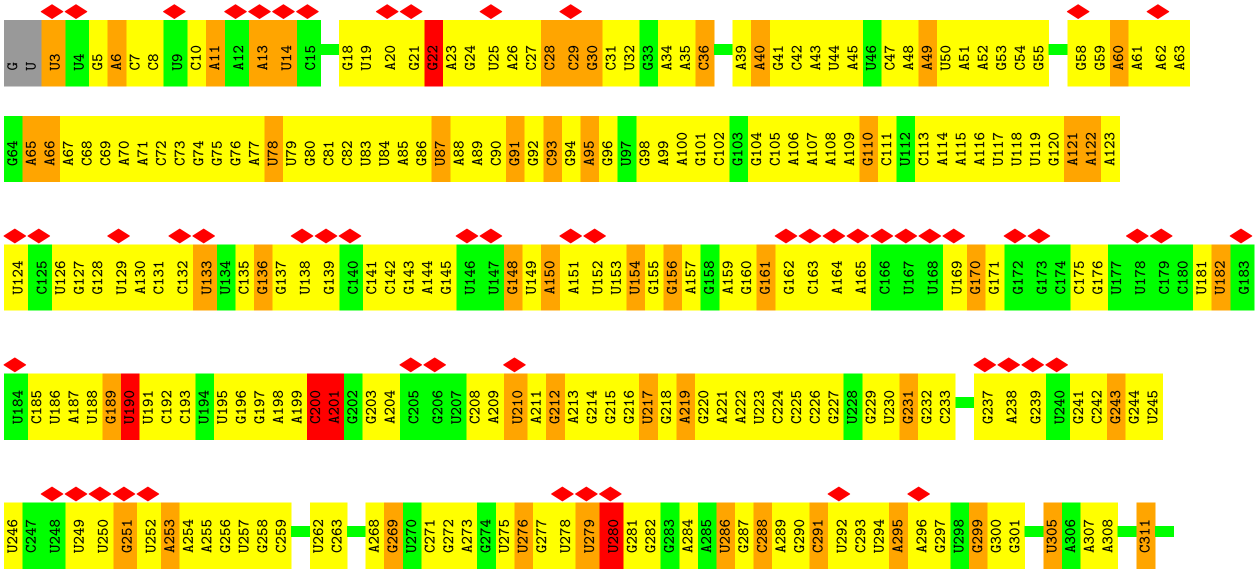
G1241 A1242 G1243 A1244 G1245 C1246 U1247 C1248 U1249 U1250 U1251 C1252 U1253 U1254 G1255 A1256 U1257 U1258 U1259 U1260 G1261 U1262 G1263 G1264 G1265 U1269 G1270 G1271 U1272 U1273 C1274 A1275 U1276 G1277 G1278 C1279 C1280 G1281 U1282 U1283 C1284 U1285 U1286 A1287 G1288 U1289 U1290 G1291 G1292 U1293 G1294 U1298 G1299 A1300 U1301 U1302 U1303 G1304
U1305 C1306 U1307 A1313 U1314 U1315 G1316 C1317 G1318 A1319 U1320 A1321 A1322 C1323 G1324 A1325 A1326 A1329 G1330 A1331 C1332 C1333 U1334 U1335 A1336 A1337 C1338 C1339 U1340 A1341 A1344 A1345 A1346 U1347 A1348 G1349 U1350 G1351 G1352 U1353 G1354 C1355 U1356 A1357 G1358 C1359 A1360 U1361 U1362 U1363 G1364 C1365 U1366 G1367 G1368 U1369 U1370

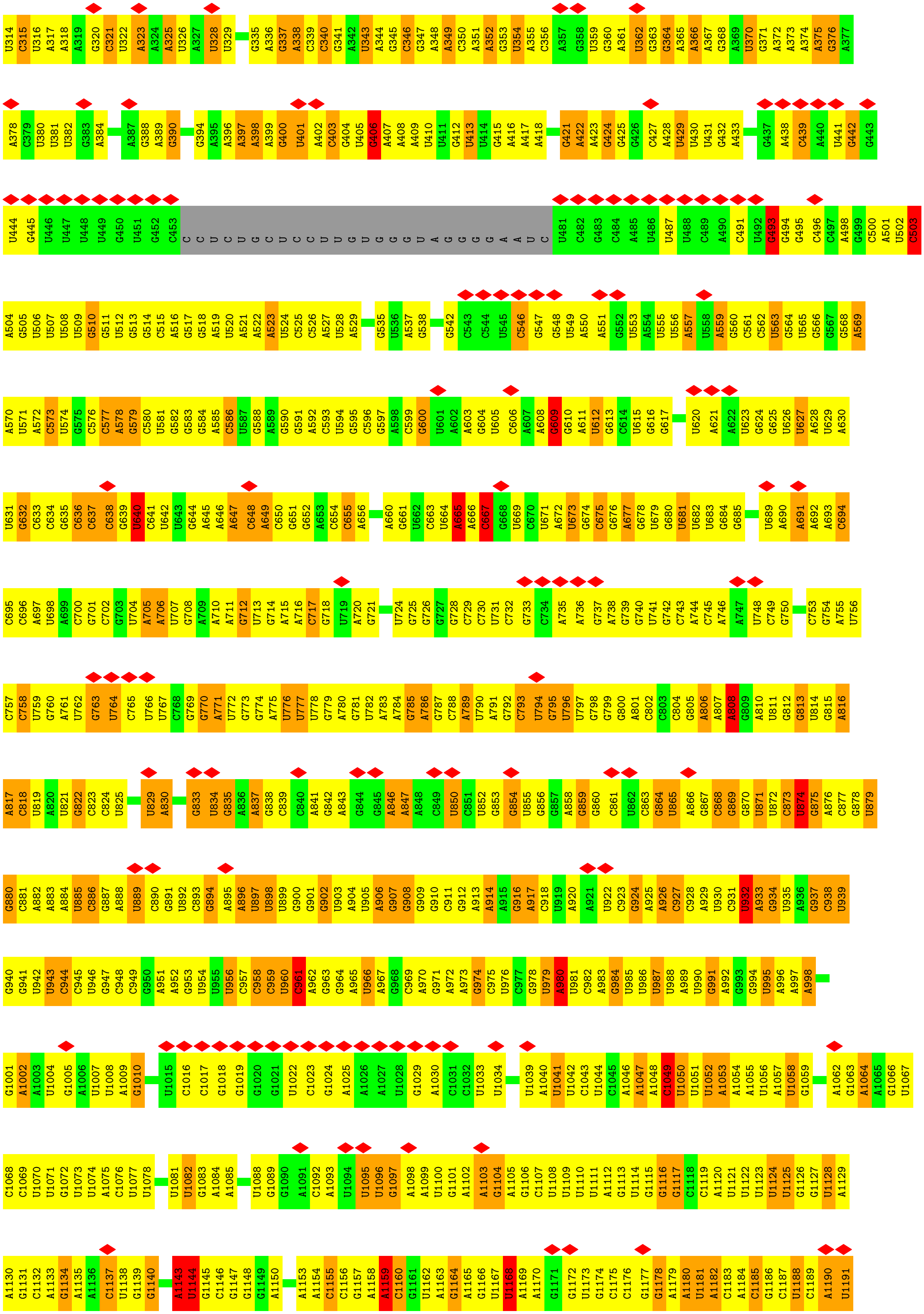


- Molecule 2: 25S ribosomal RNA

Chain B:



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A378 C379 U380 U381 U382 G383 A384 A387 G388 A389 G390 G394 A395 A396 A397 A398 A399 G400 U401 A402 C403 G404 U405 G406 A407 A408 A409 U410 U411 G412 U413 U414 G415 A416 A417 A418 G421 A422 A423 G424 G425 G426 C427 A428 U429 U430 U431 G432 A433 G437 A438 C439 A440 U441 G442 G443
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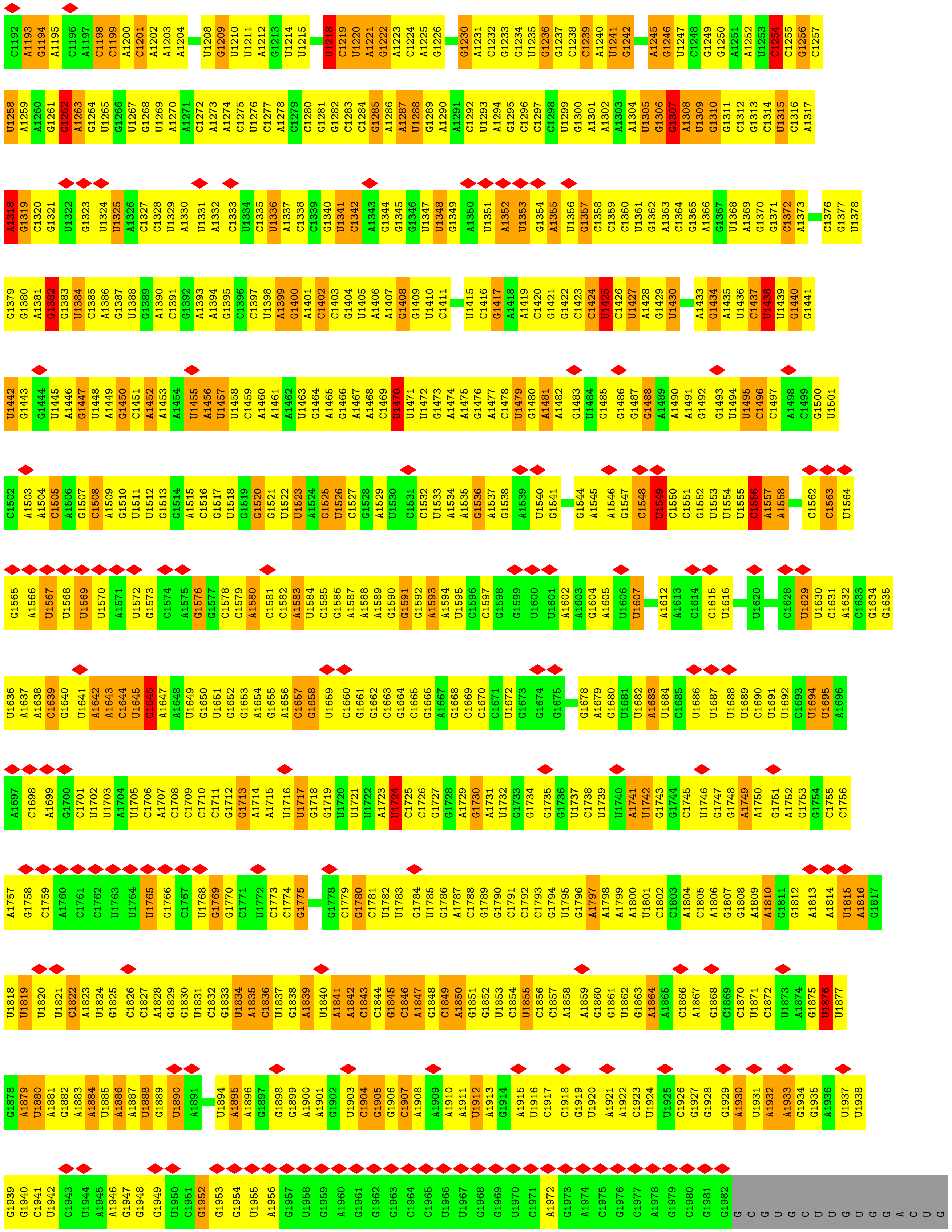
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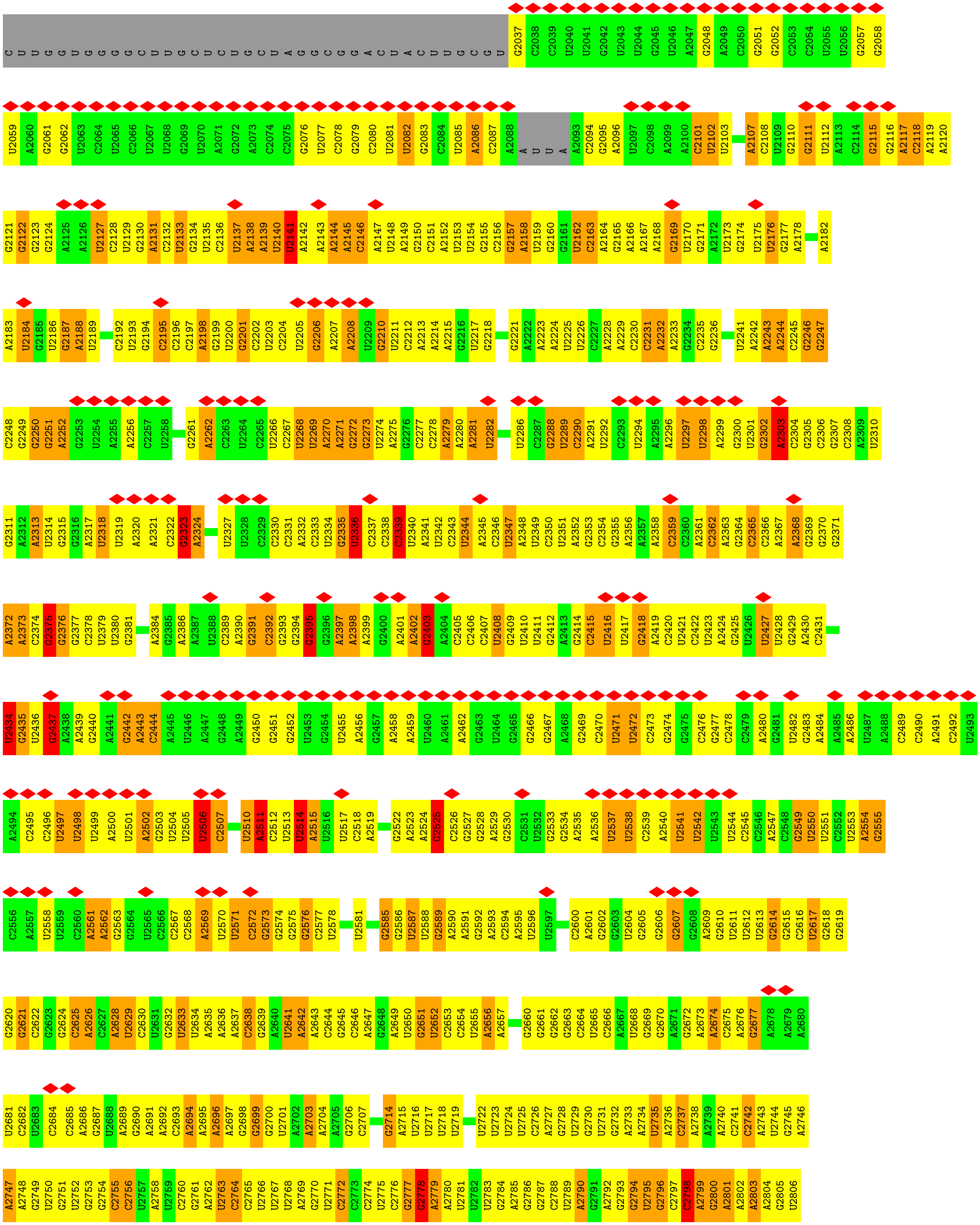
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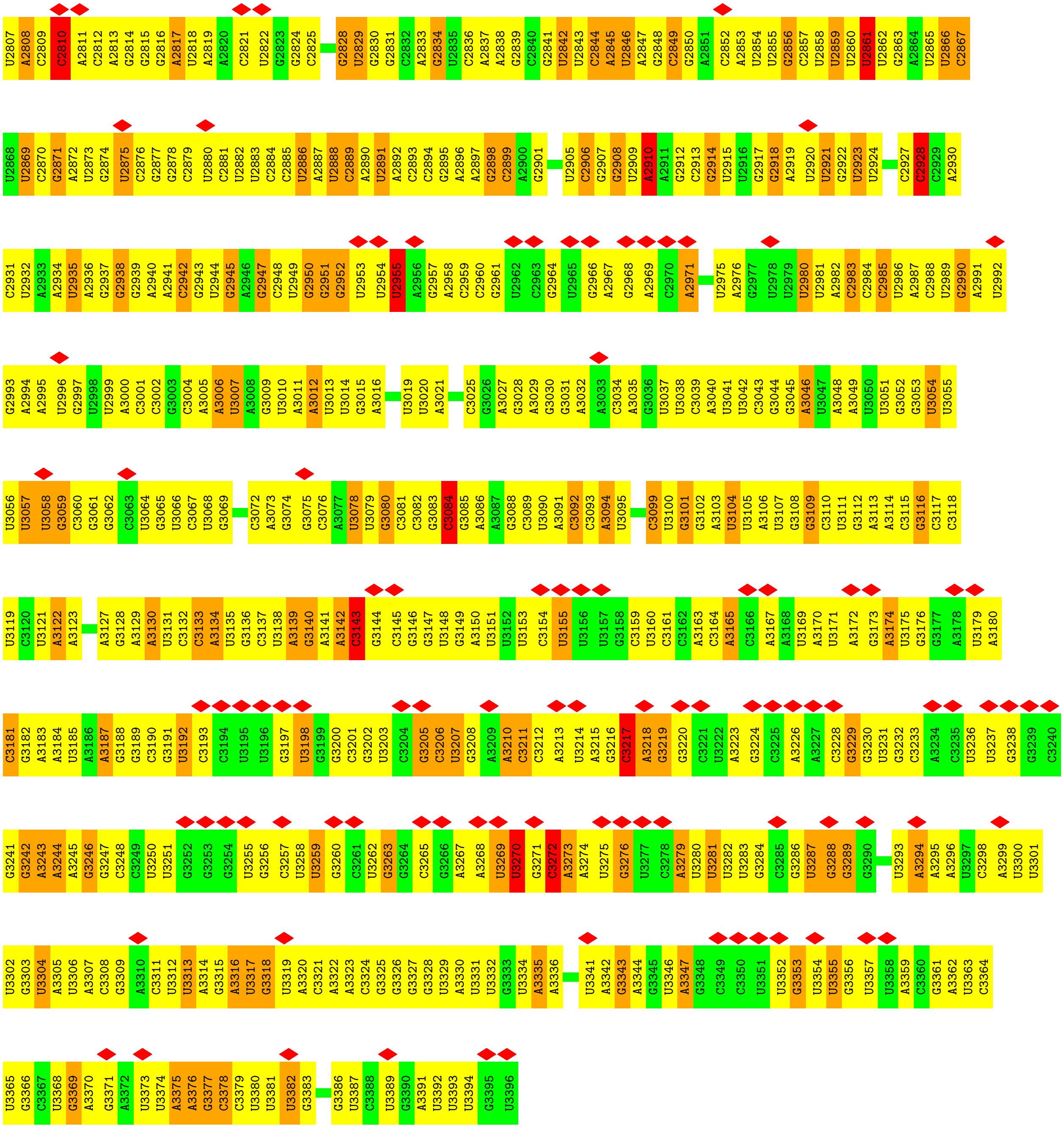

• Molecule 3: 5.8S ribosomal RNA

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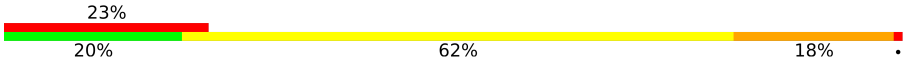

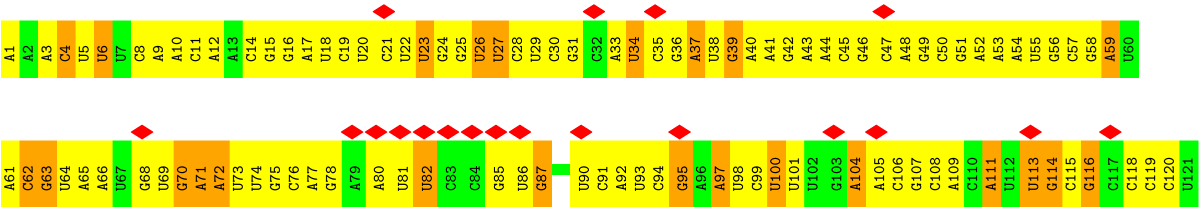

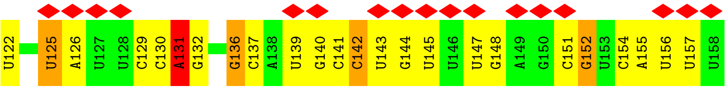

- Molecule 4: 5S ribosomal RNA

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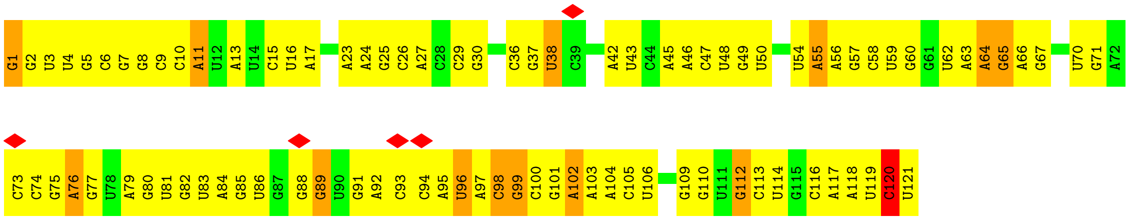

- Molecule 5: uL1 (yeast L1)

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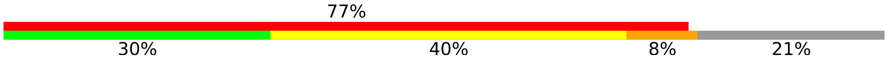

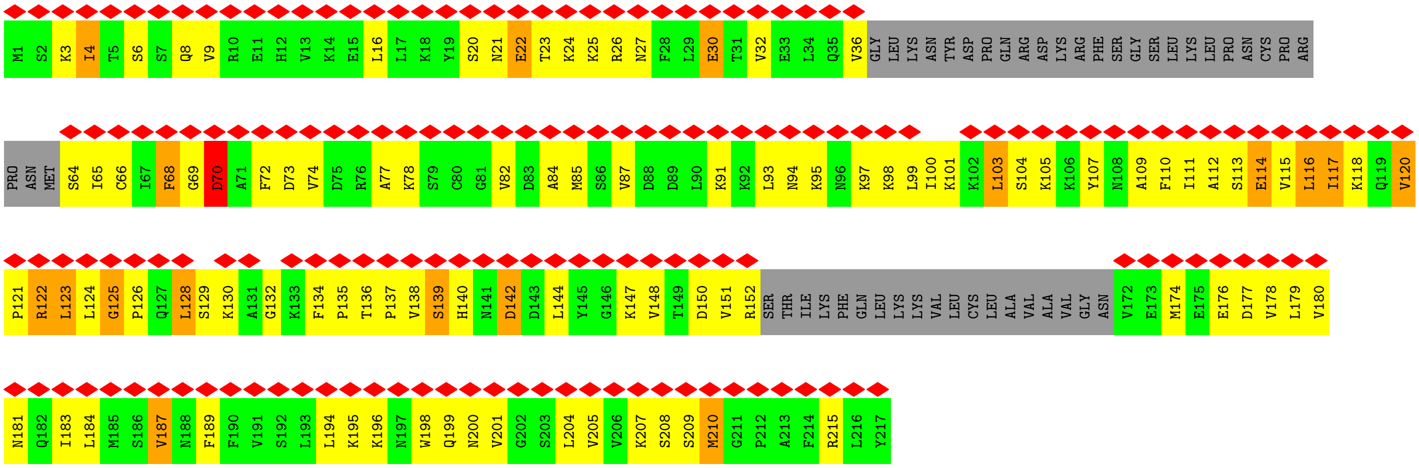

- Molecule 6: uL2 (yeast L2)

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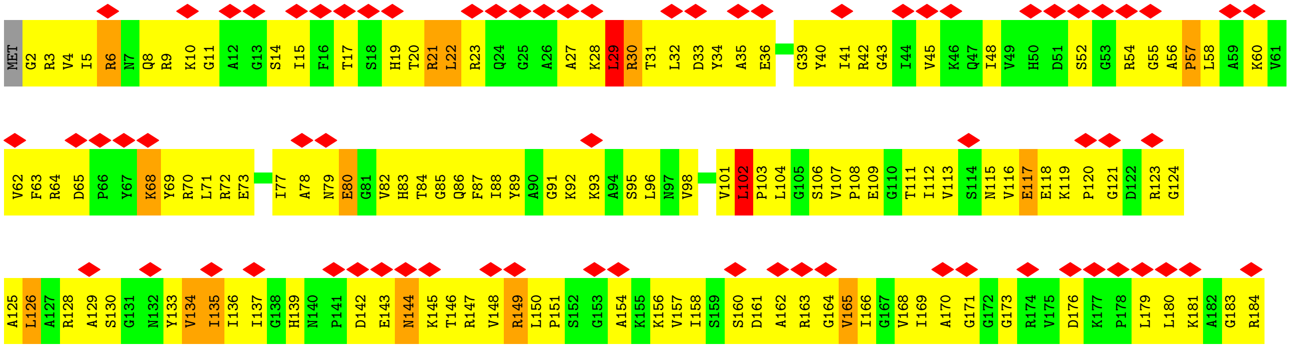

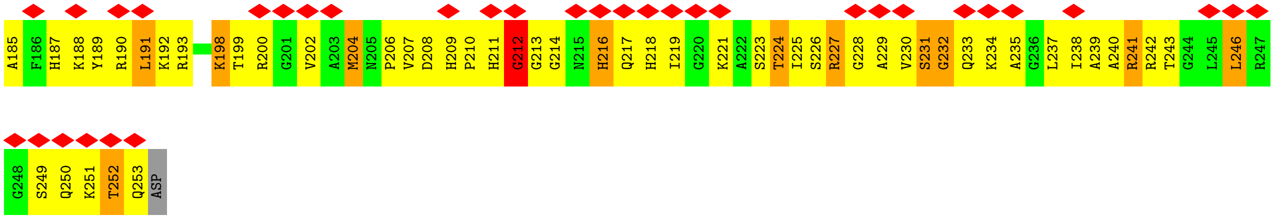

- Molecule 7: uL3 (yeast L3)

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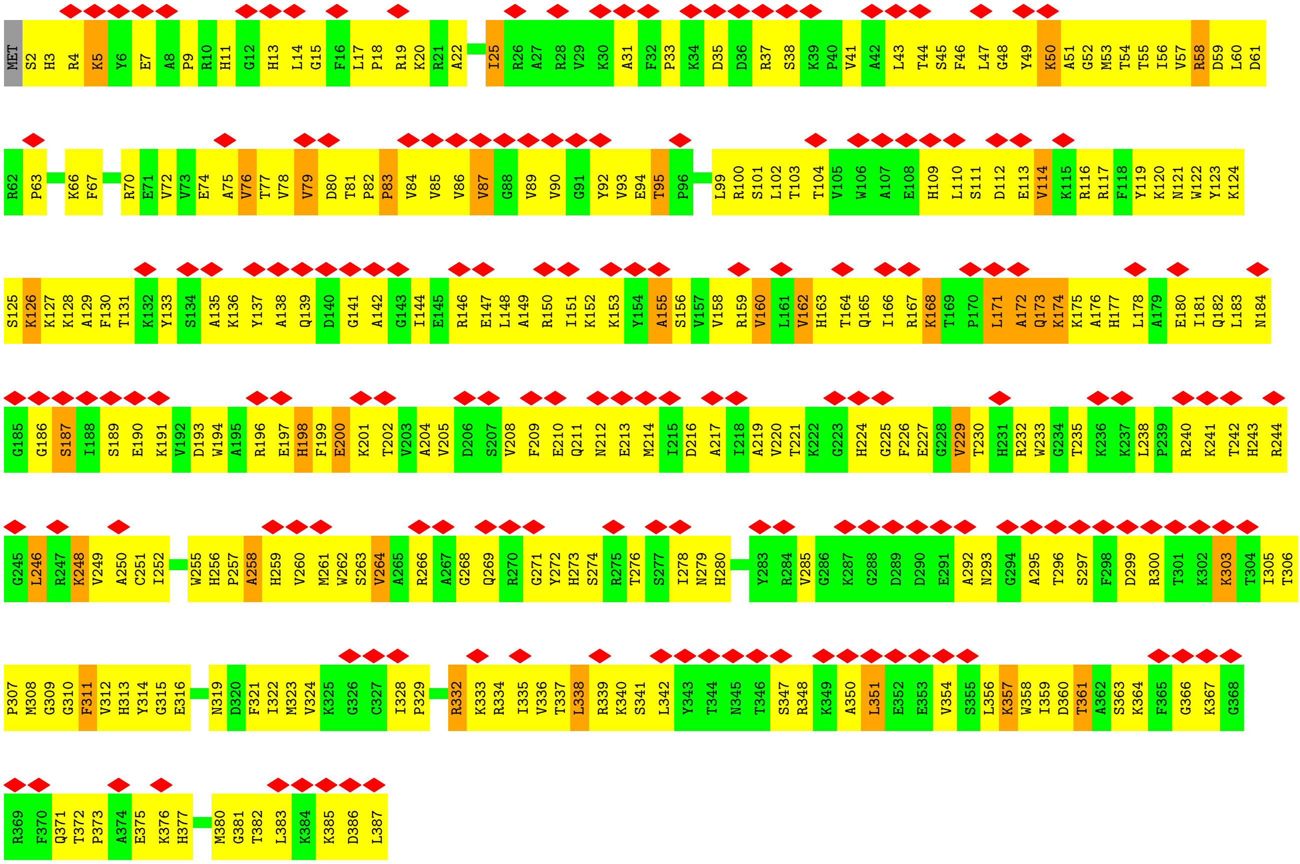

- Molecule 8: uL4 (yeast L4)

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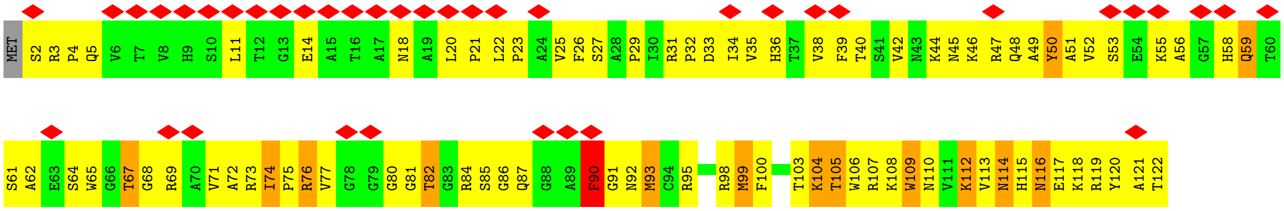

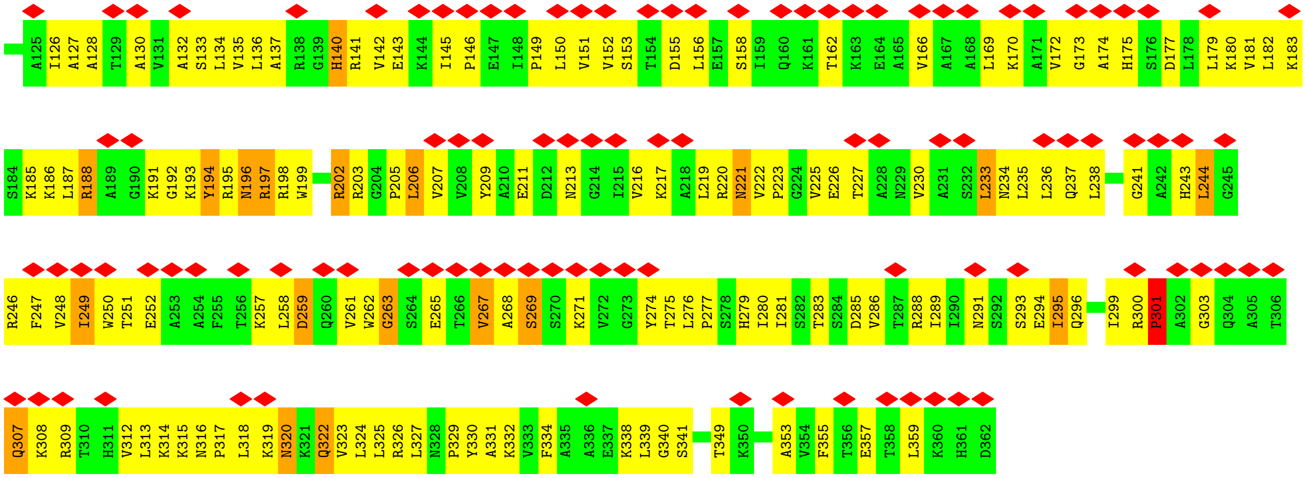

- Molecule 9: uL18 (yeast L5)

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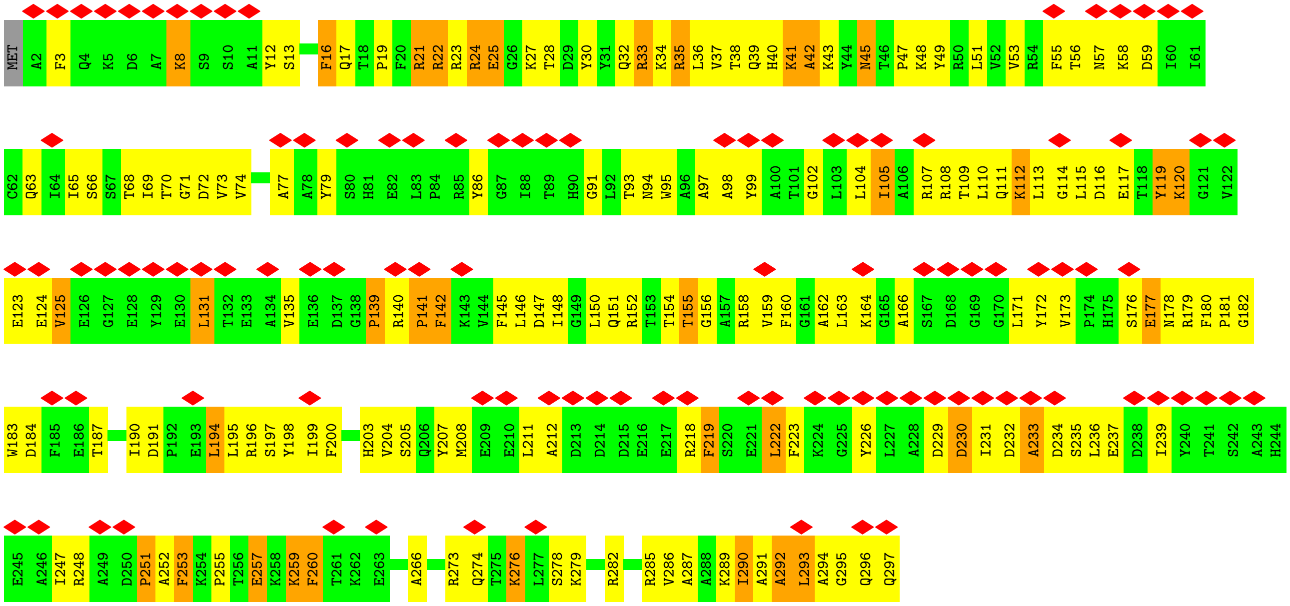

- Molecule 10: eL6 (yeast L6)

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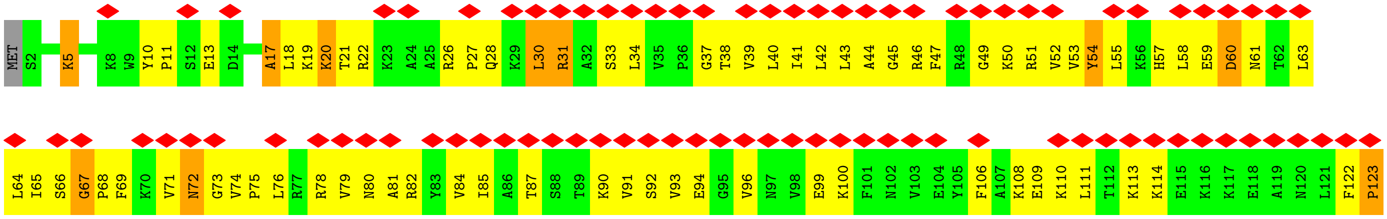
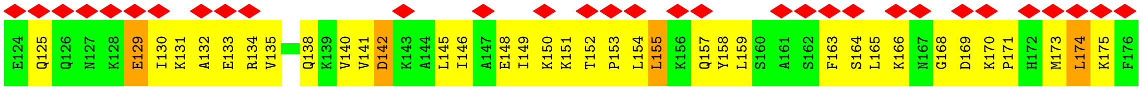
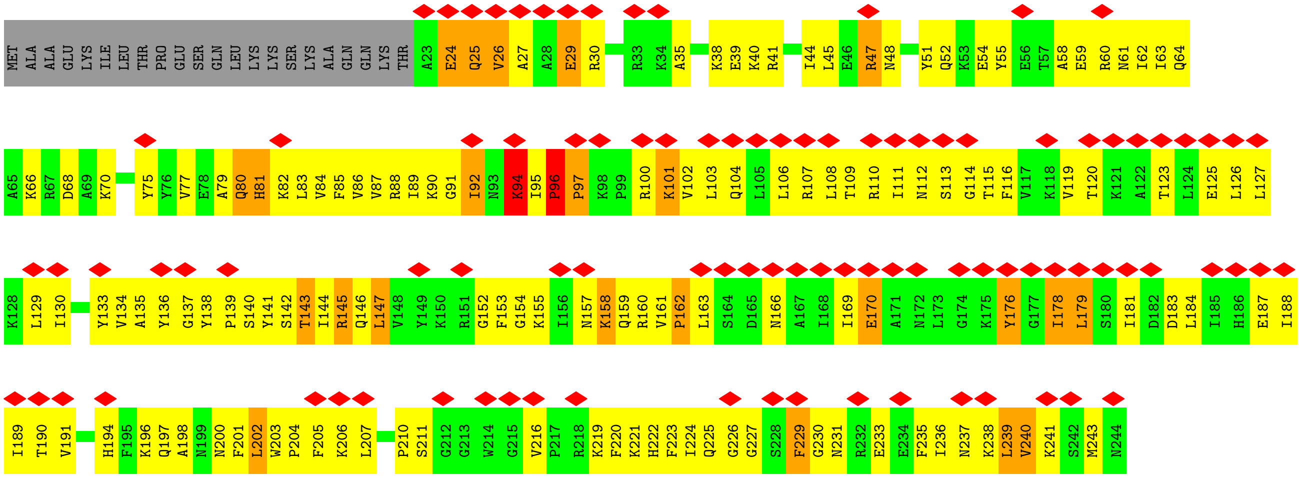




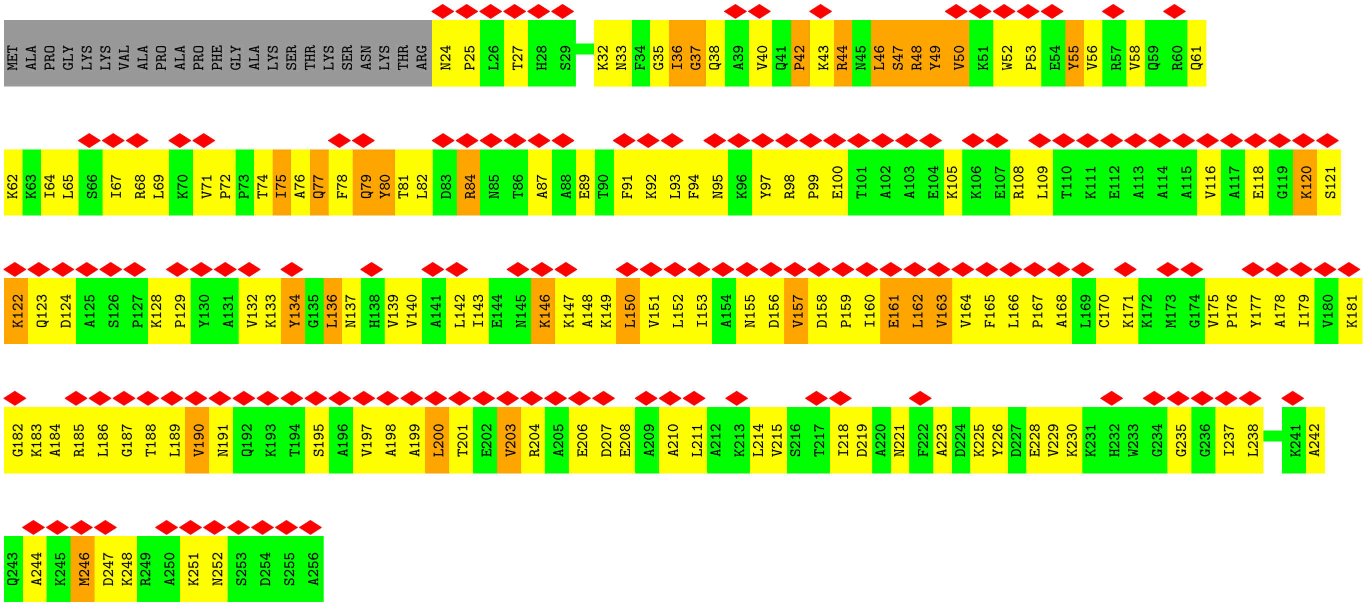
- Molecule 11: uL30 (yeast L7)

Chain K:



- Molecule 12: eL8 (yeast L8)

Chain L:

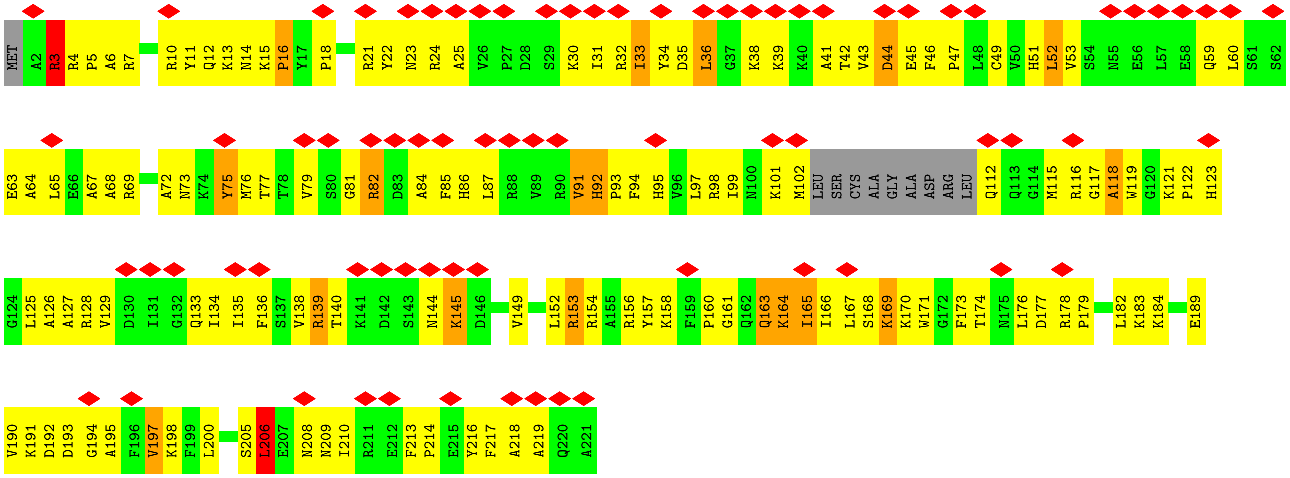


- Molecule 13: uL6 (yeast L9)

Chain M:

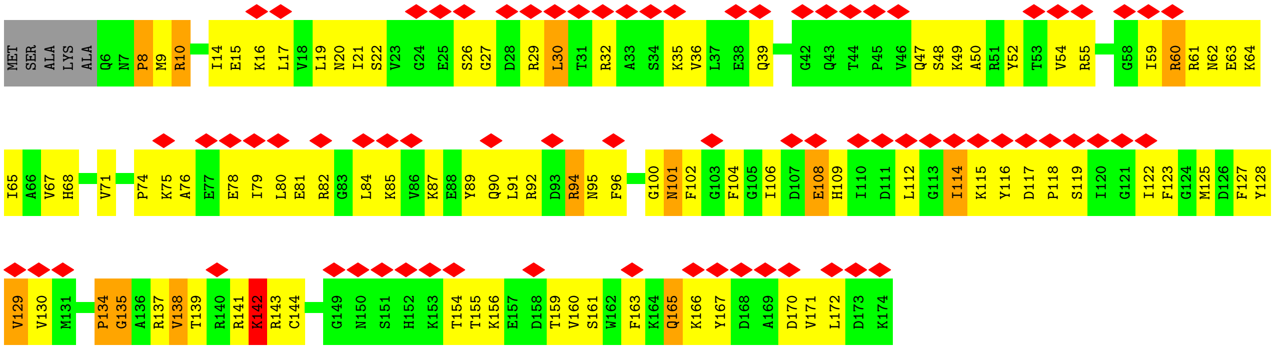
- Molecule 14: uL16 (yeast L10)

Chain N:



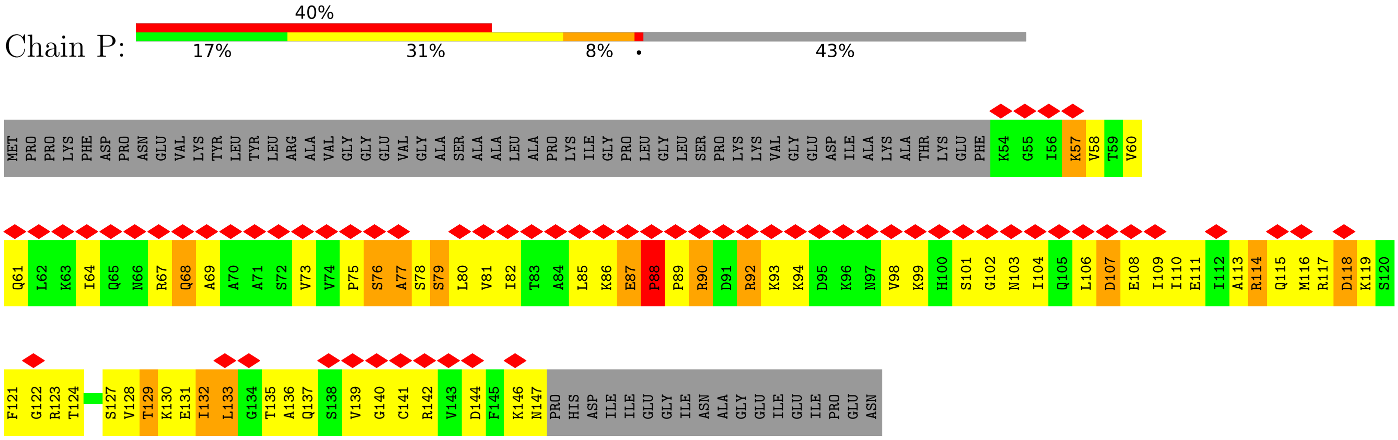
- Molecule 15: uL5 (yeast L11)

Chain O:



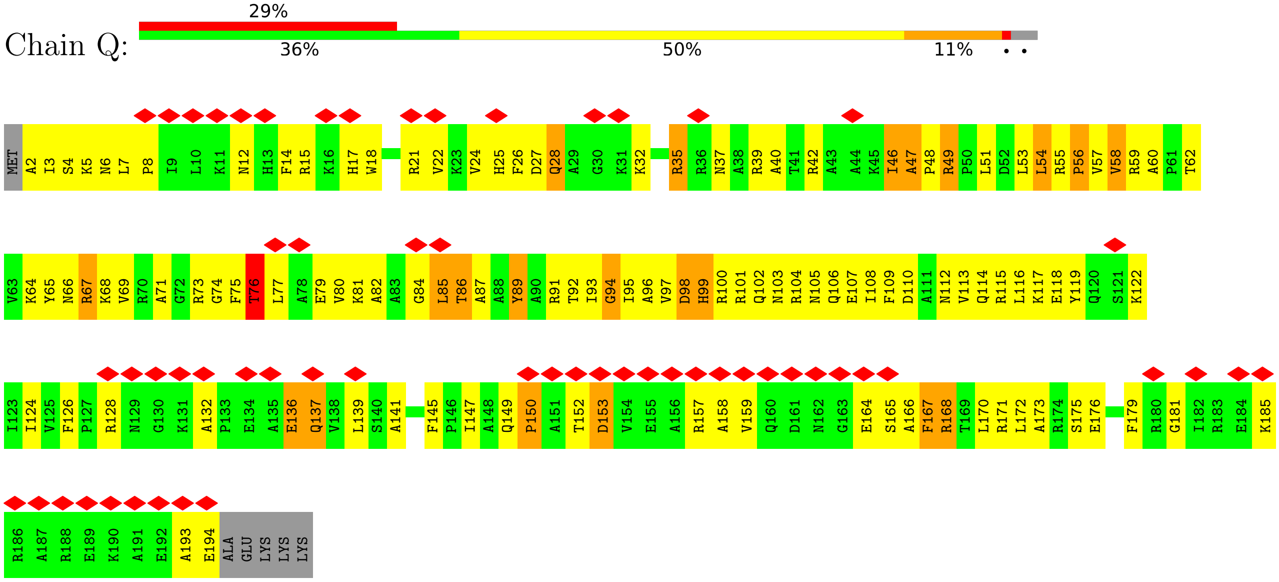
- Molecule 16: uL11 (yeast L12)

Chain P:



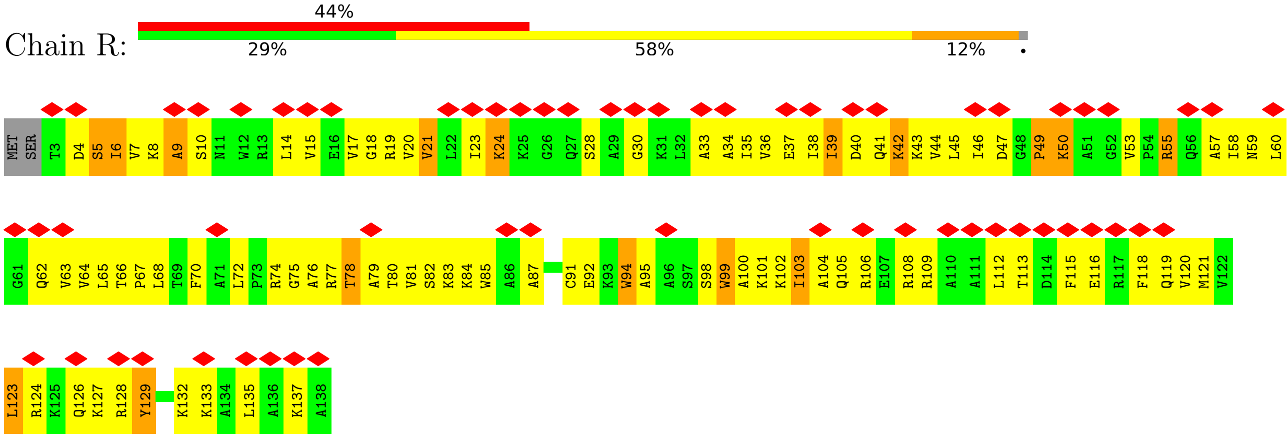
- Molecule 17: eL13 (yeast L13)

Chain Q:



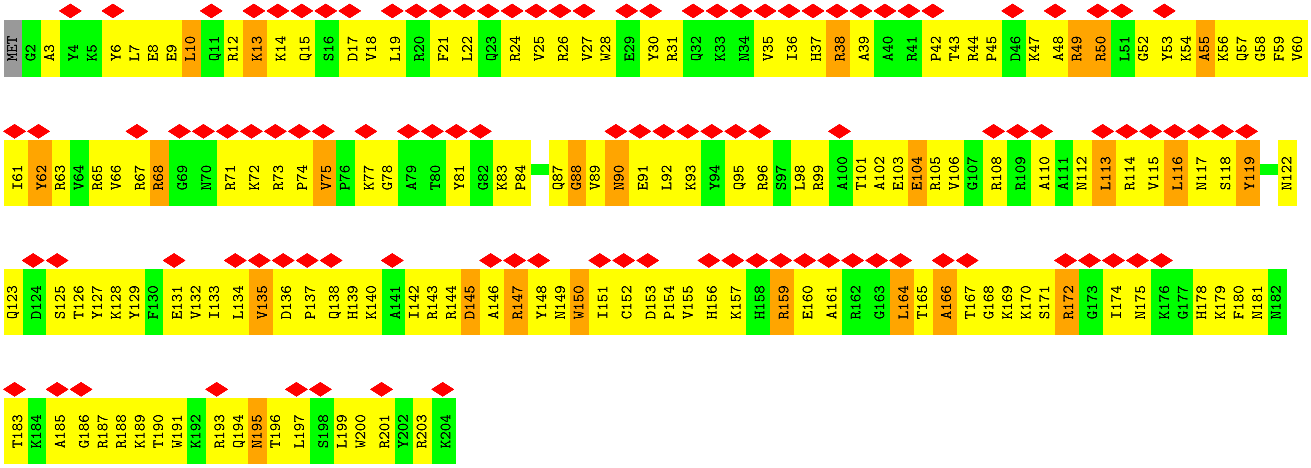
- Molecule 18: eL14 (yeast L14)

Chain R:



- Molecule 19: eL15 (yeast L15)

Chain S:

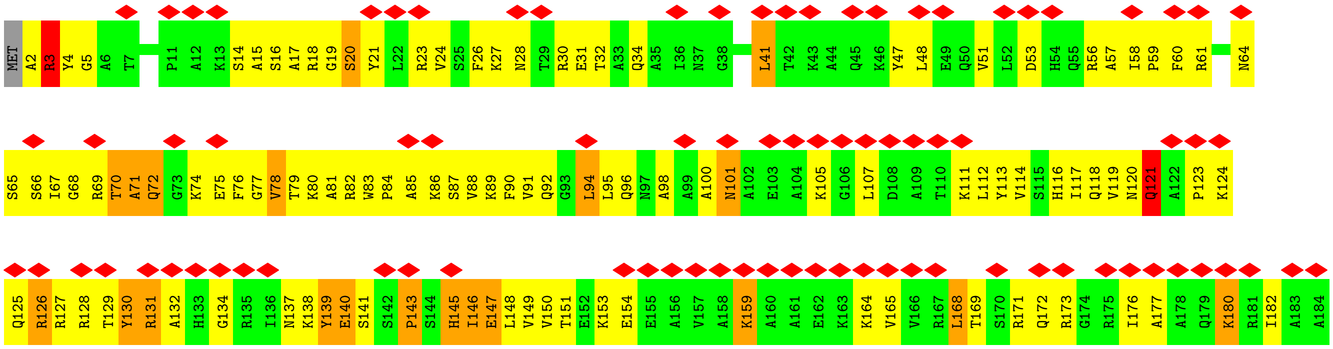


- Molecule 20: uL13 (yeast L16)

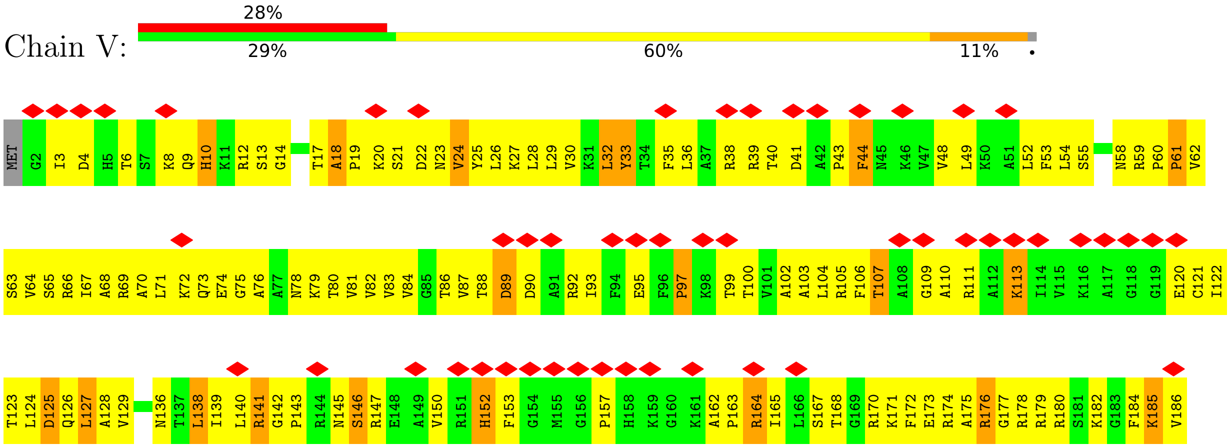
Chain T:

- Molecule 21: uL22 (yeast L17)

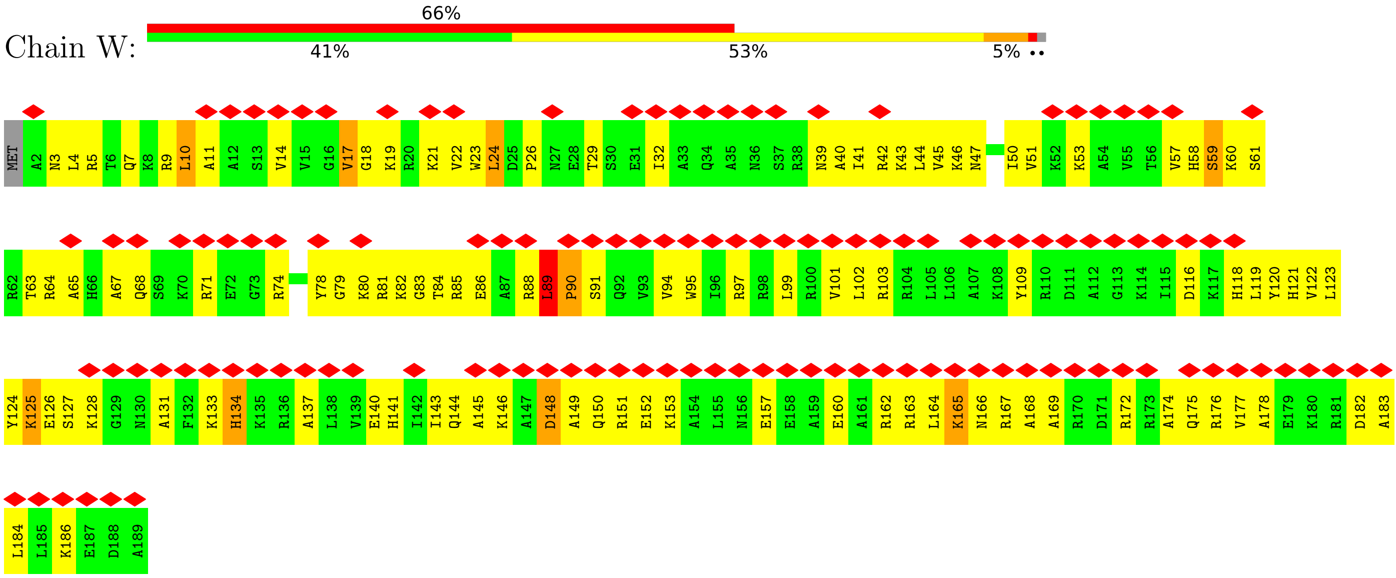
Chain U:



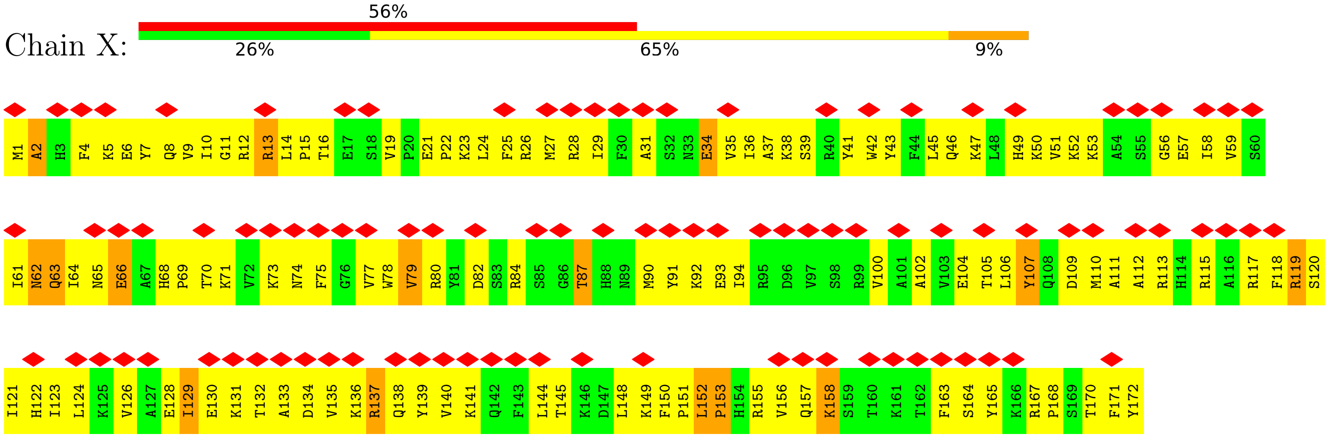
- Molecule 22: eL18 (yeast L18)



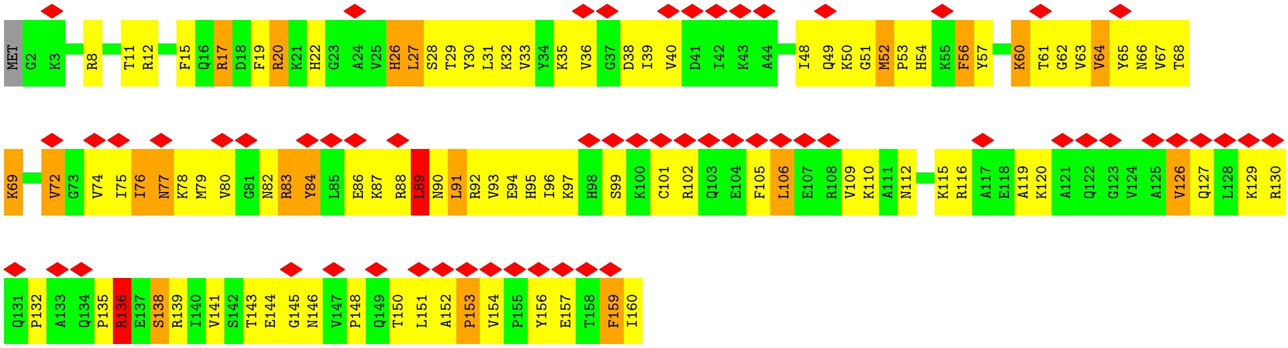
- Molecule 23: eL19 (yeast L19)



- Molecule 24: eL20 (yeast L20)

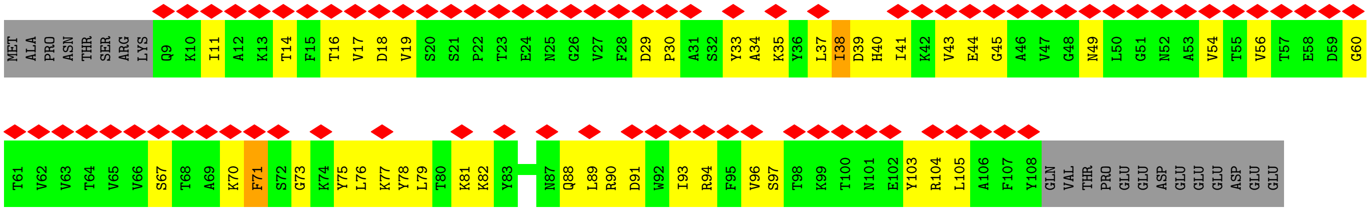


- Molecule 25: eL21 (yeast L21)



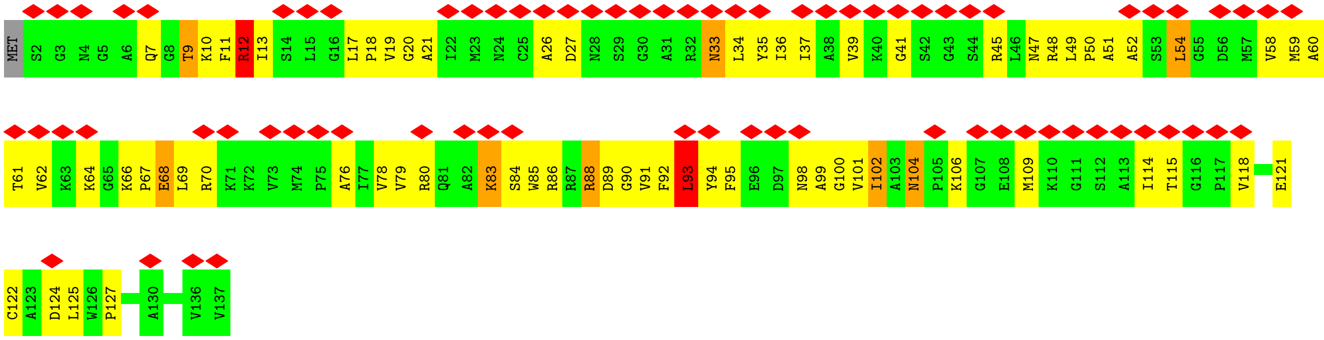
- Molecule 26: eL22 (yeast L22)

Chain Z:



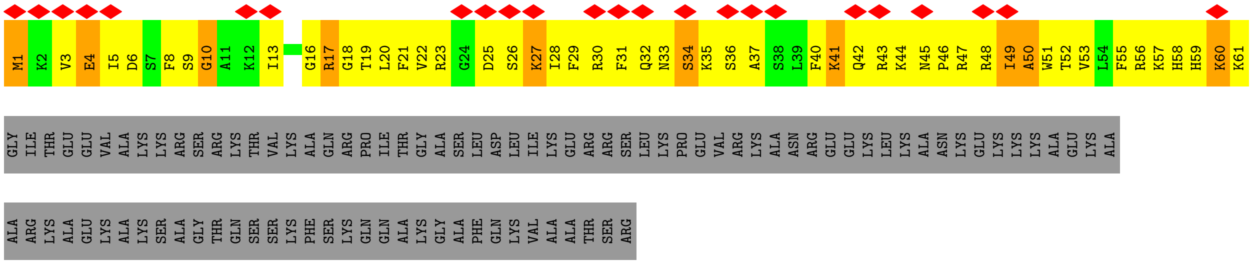
- Molecule 27: uL14 (yeast L23)

Chain AA:



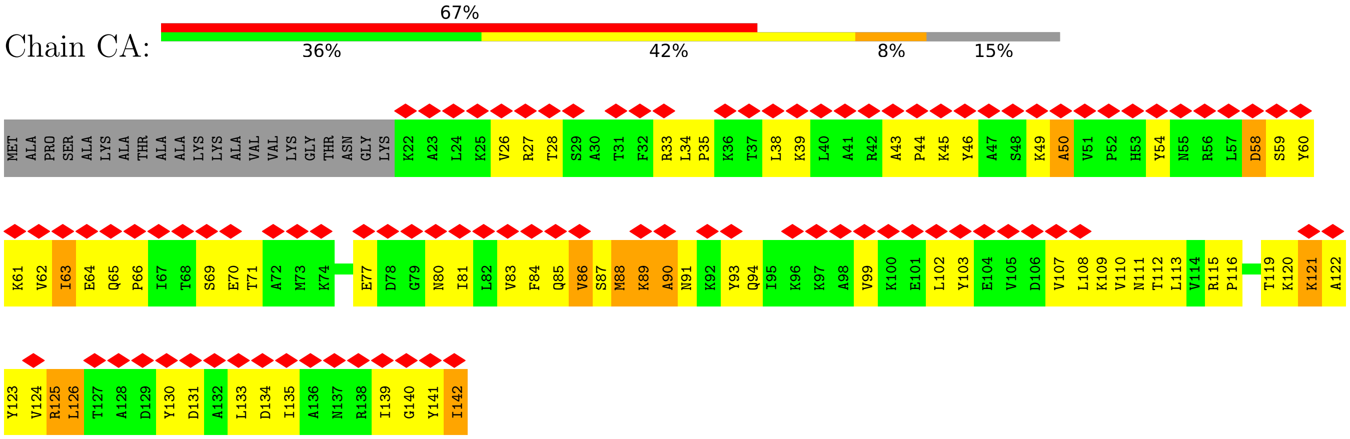
- Molecule 28: eL24 (yeast L24)

Chain BA:



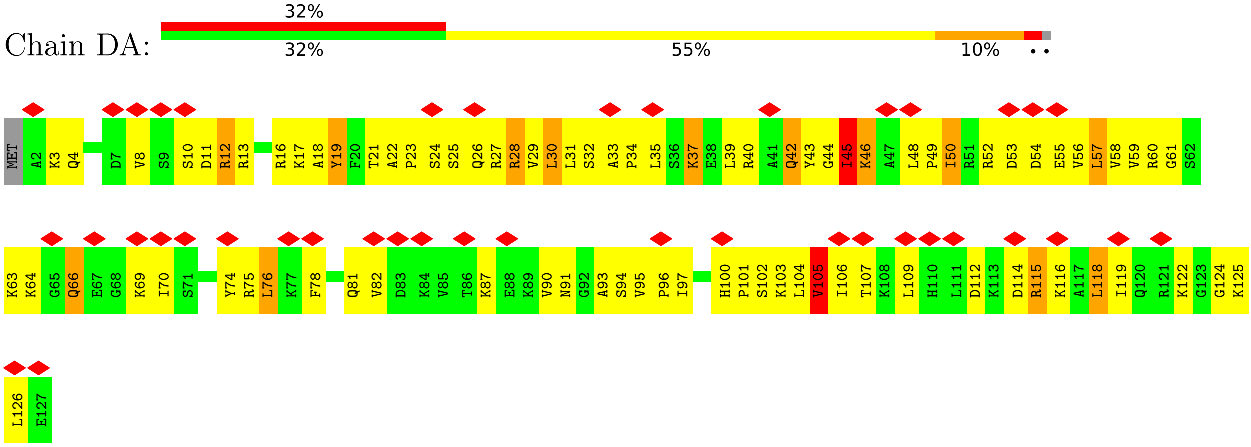
- Molecule 29: uL23 (yeast L25)

Chain CA:



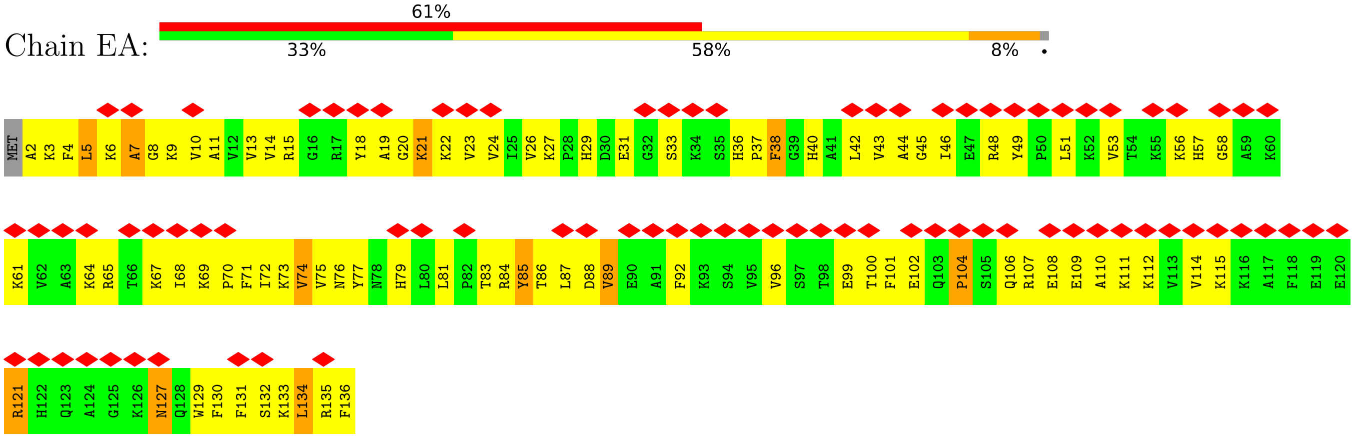
• Molecule 30: uL24 (yeast L26)

Chain DA:



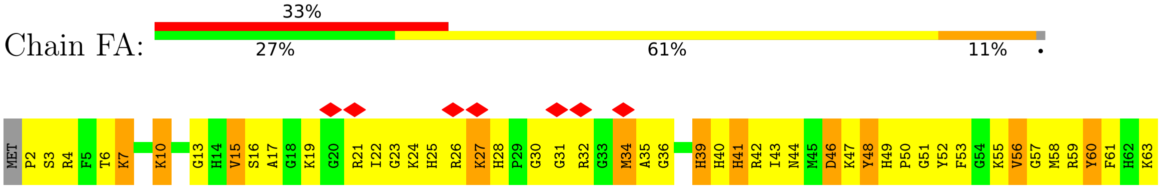
• Molecule 31: eL27 (yeast L27)

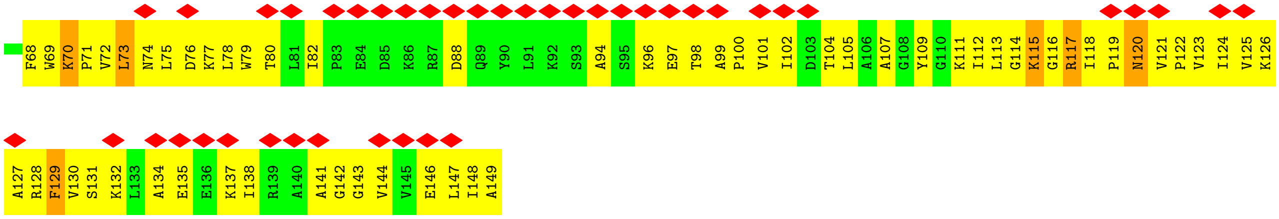
Chain EA:



• Molecule 32: uL15 (yeast L28)

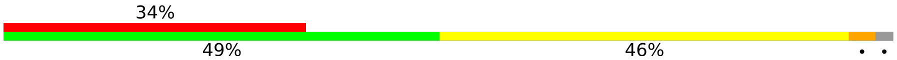
Chain FA:

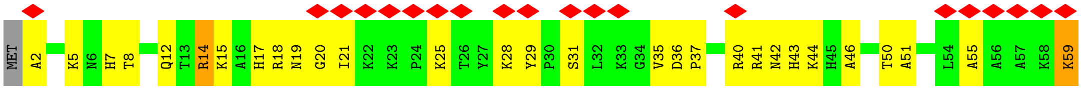




- Molecule 33: eL29 (yeast L29)

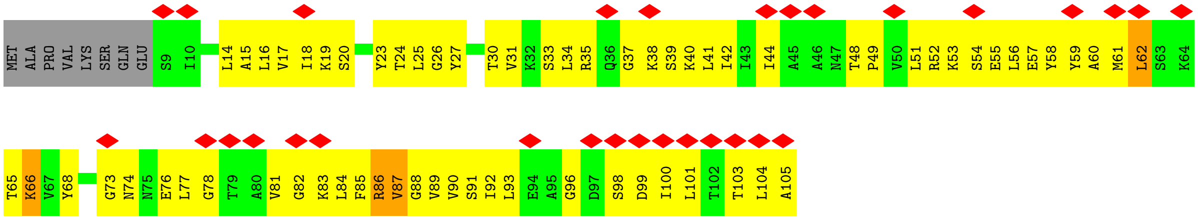
Chain GA:





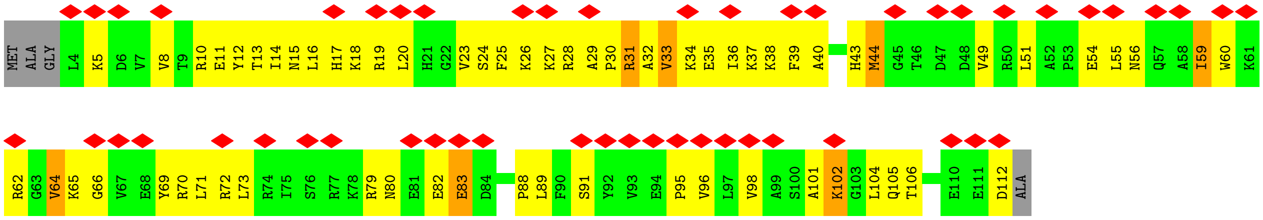
- Molecule 34: eL30 (yeast L30)

Chain HA:



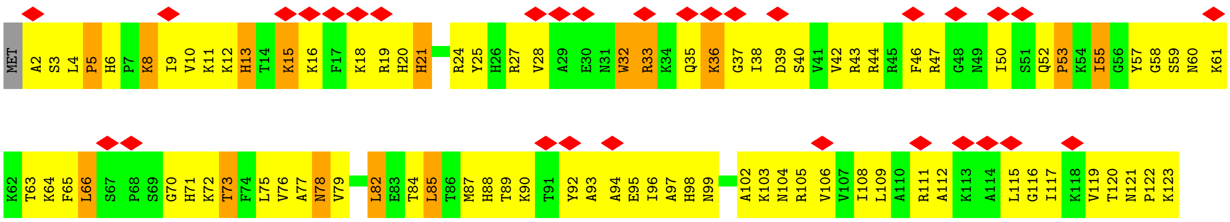
- Molecule 35: eL31 (yeast L31)

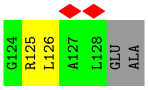
Chain IA:



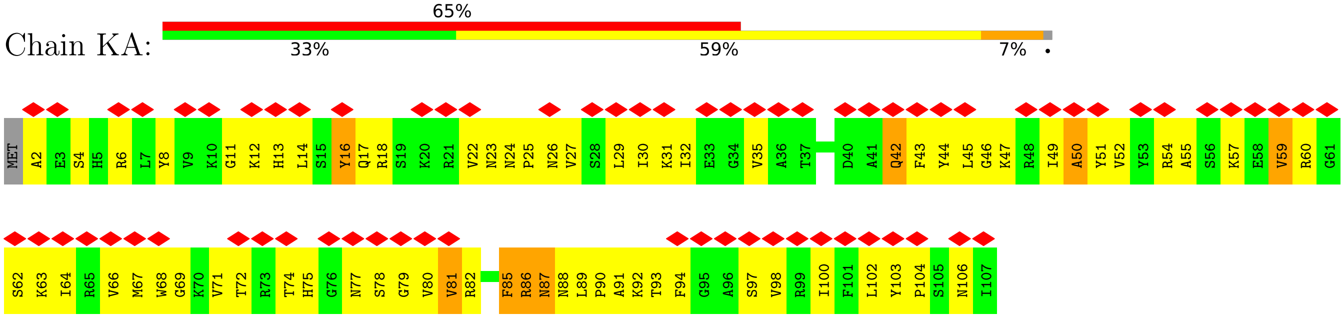
- Molecule 36: eL32 (yeast L32)

Chain JA:

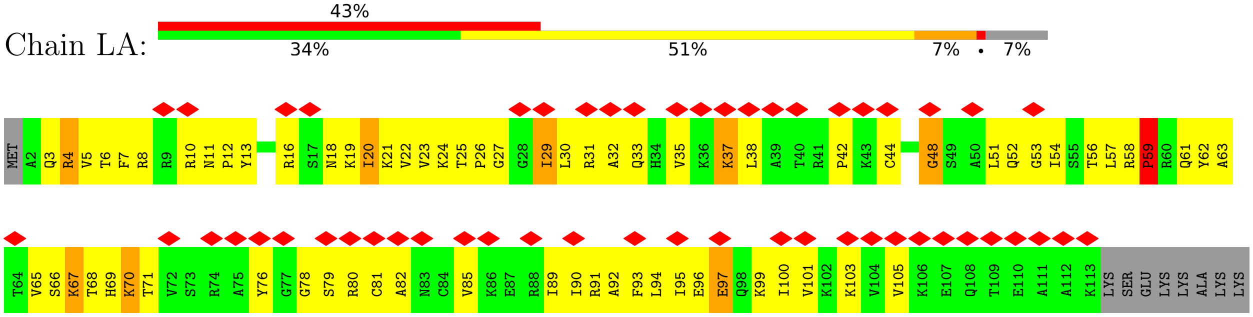




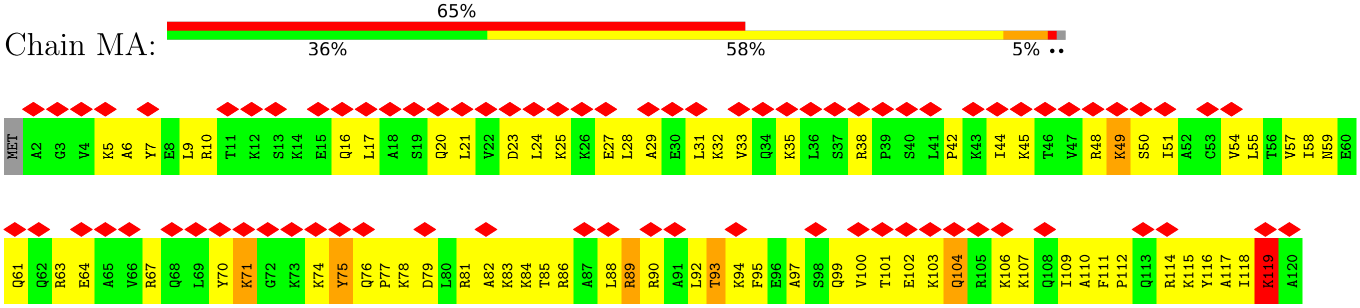
- Molecule 37: eL33 (yeast L33)



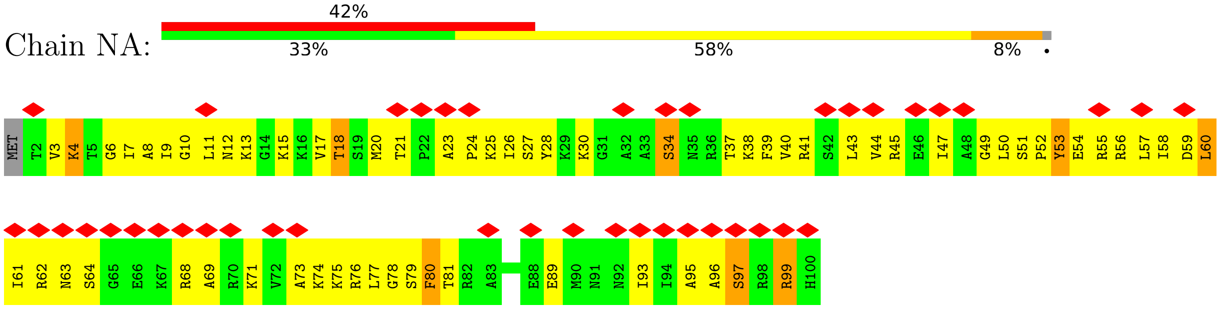
- Molecule 38: eL34 (yeast L34)



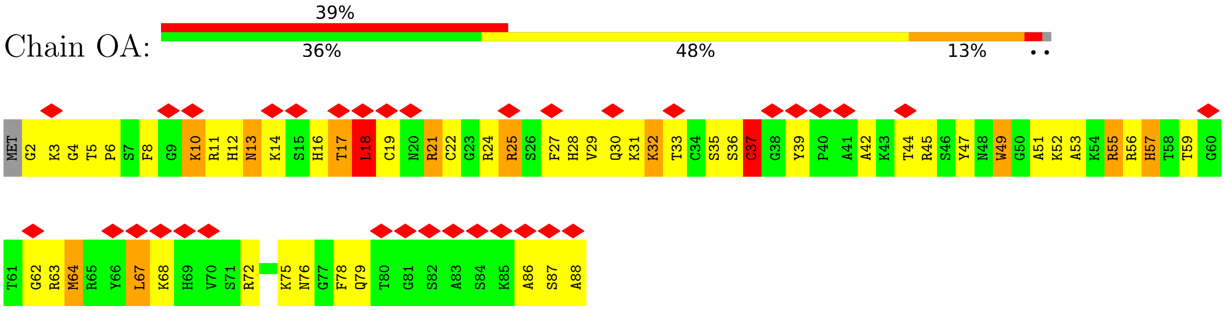
- Molecule 39: uL29 (yeast L35)



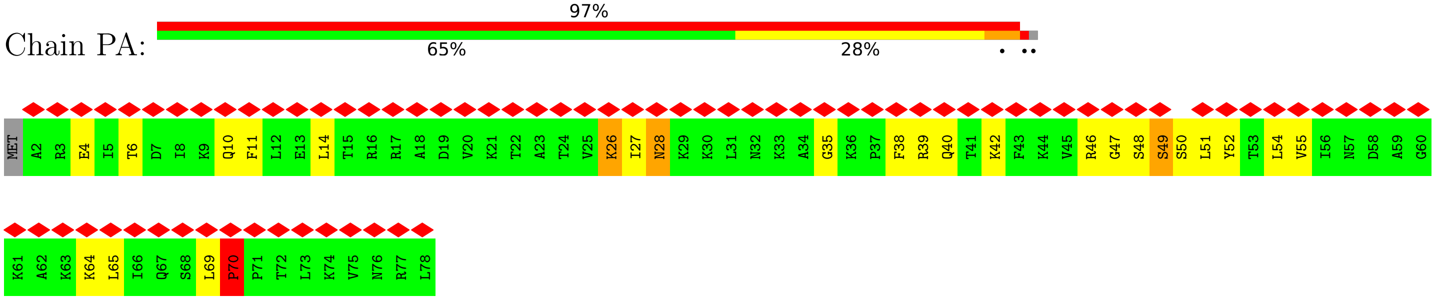
- Molecule 40: eL36 (yeast L36)



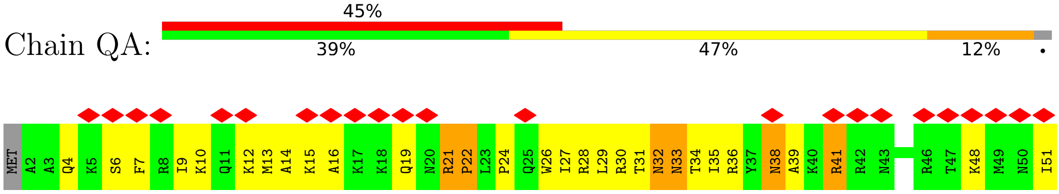
- Molecule 41: eL37 (yeast L37)



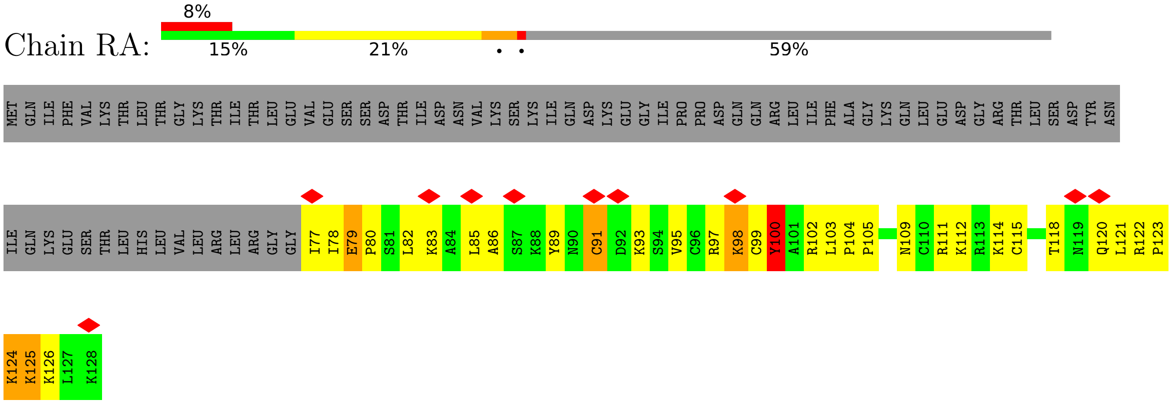
- Molecule 42: eL38 (yeast L38)



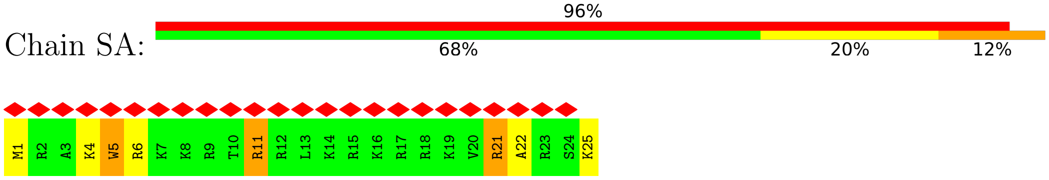
- Molecule 43: eL39 (yeast L39)



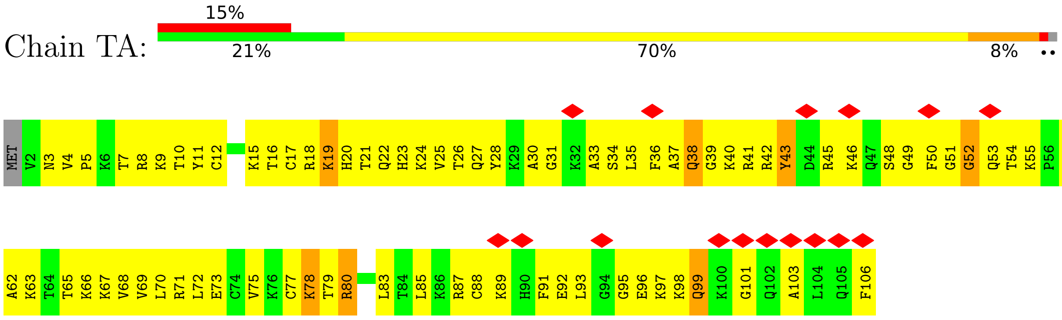
- Molecule 44: eL40 (yeast L40)



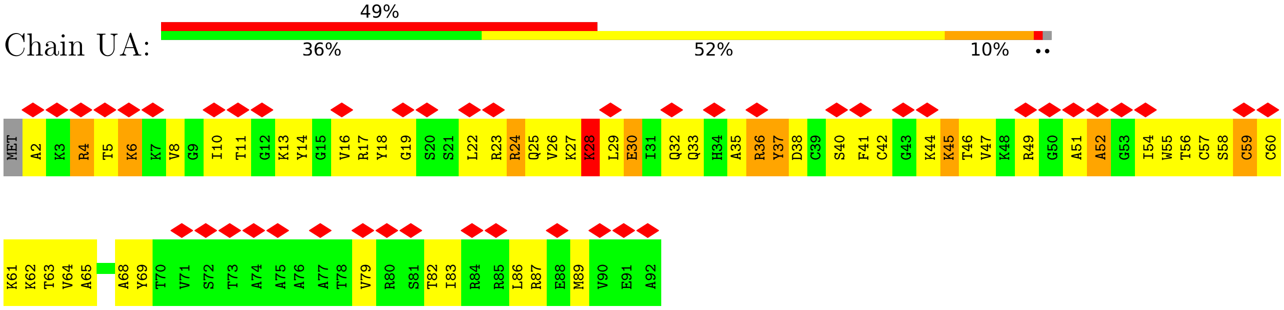
- Molecule 45: eL41 (yeast L41)



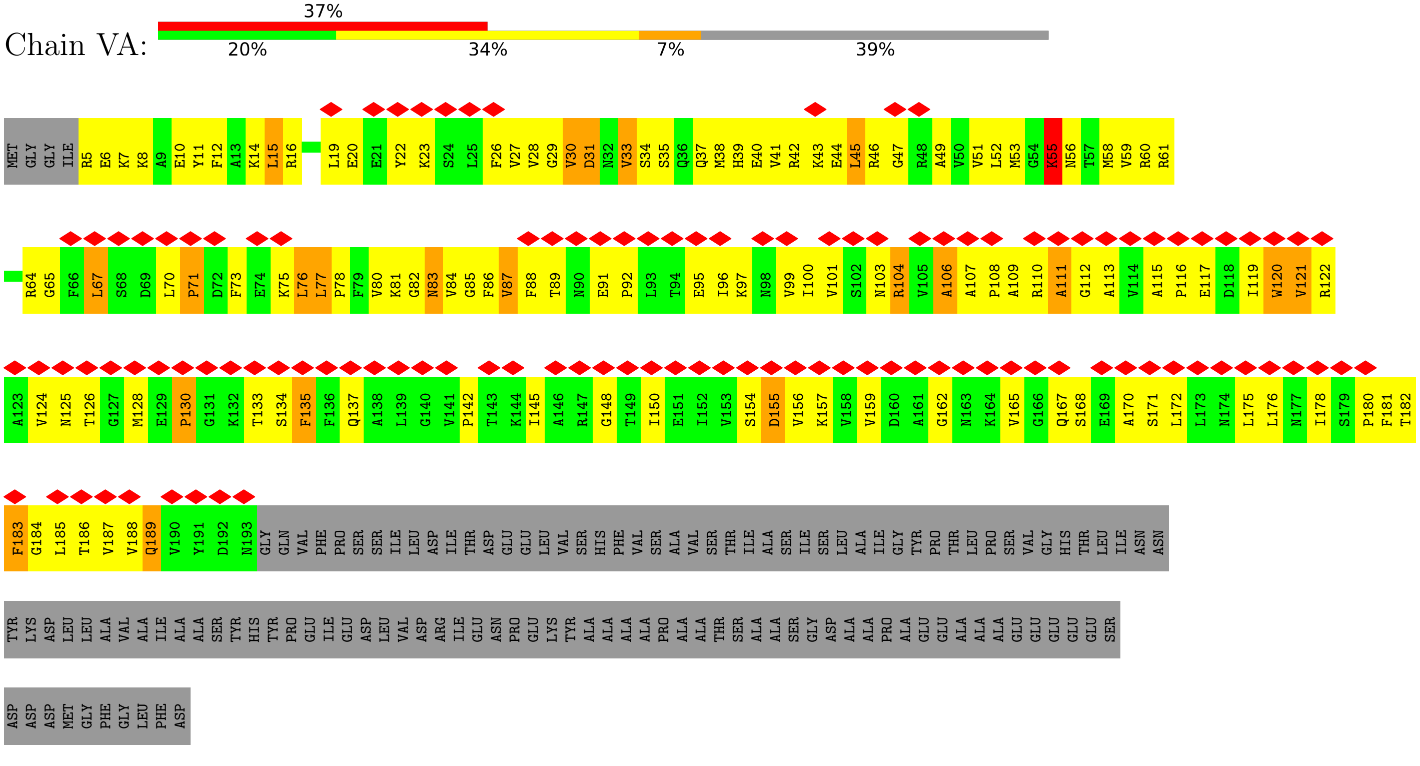
- Molecule 46: eL42 (yeast L42)



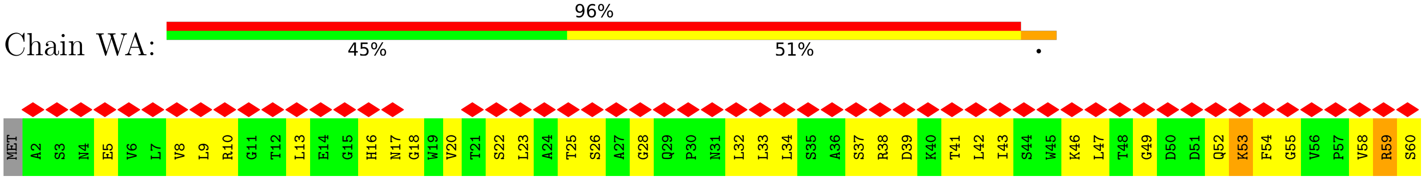
- Molecule 47: eL43 (yeast L43)

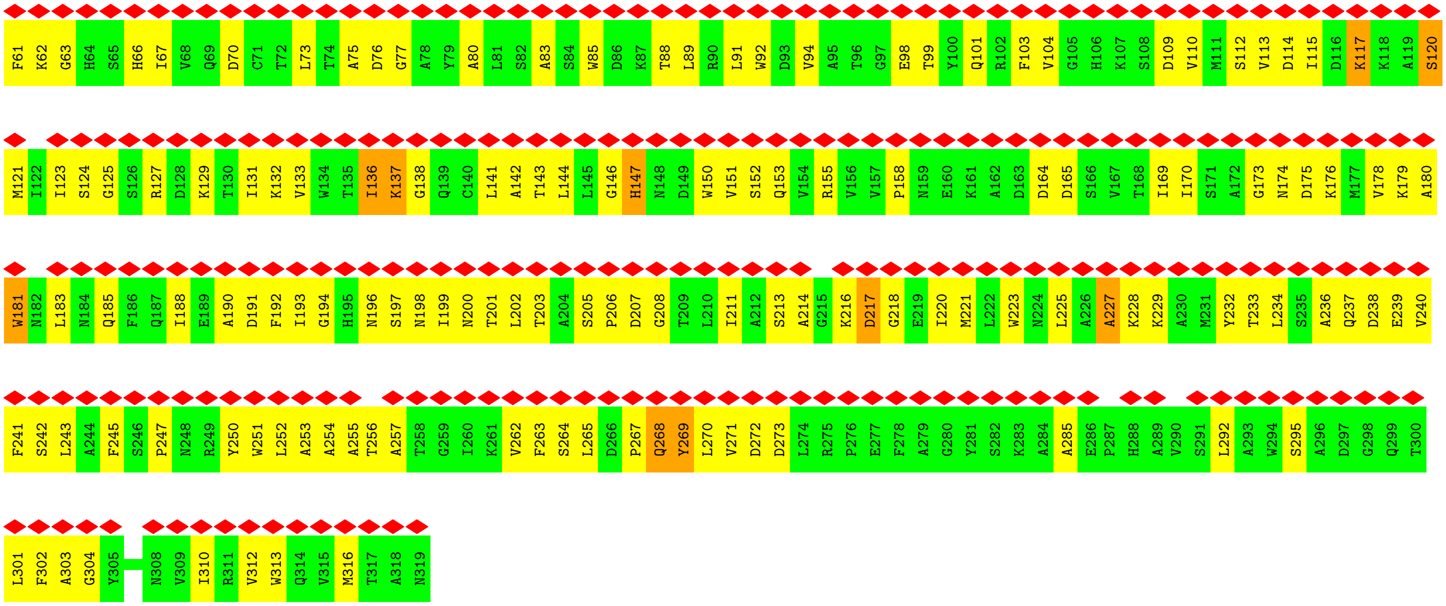


- Molecule 48: uL10 (yeast P0)



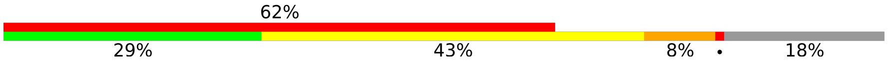
- Molecule 49: RACK1 (yeast Asc1)

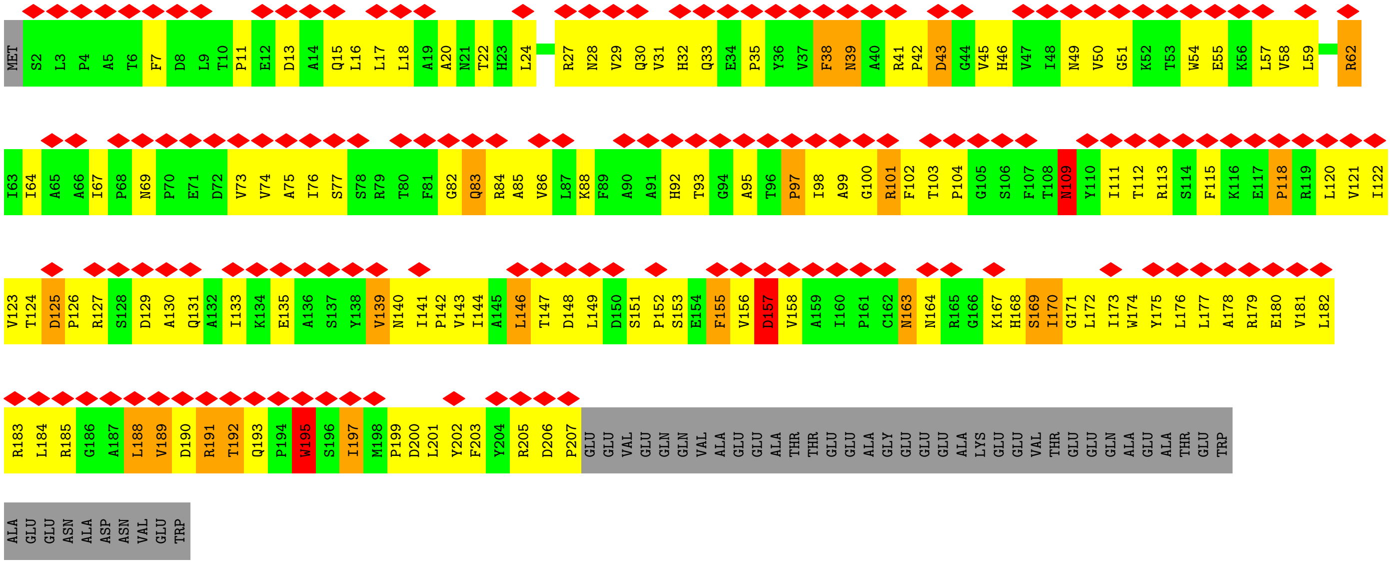




- Molecule 50: uS2 (yeast S0)

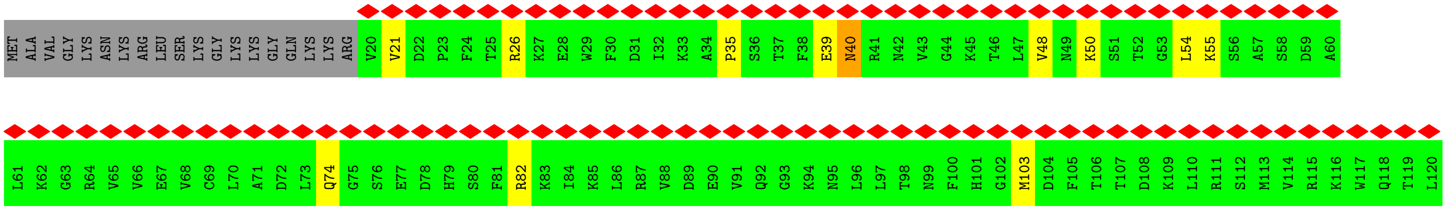
Chain XA:

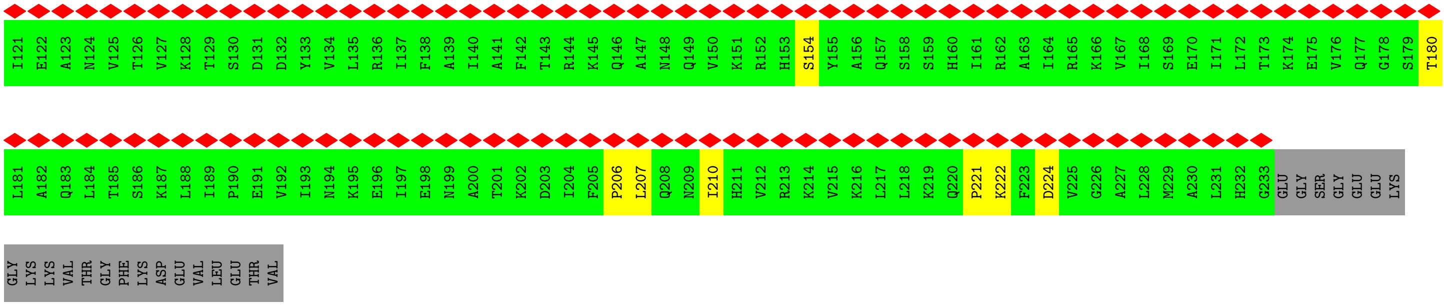




- Molecule 51: eS1 (yeast S1)

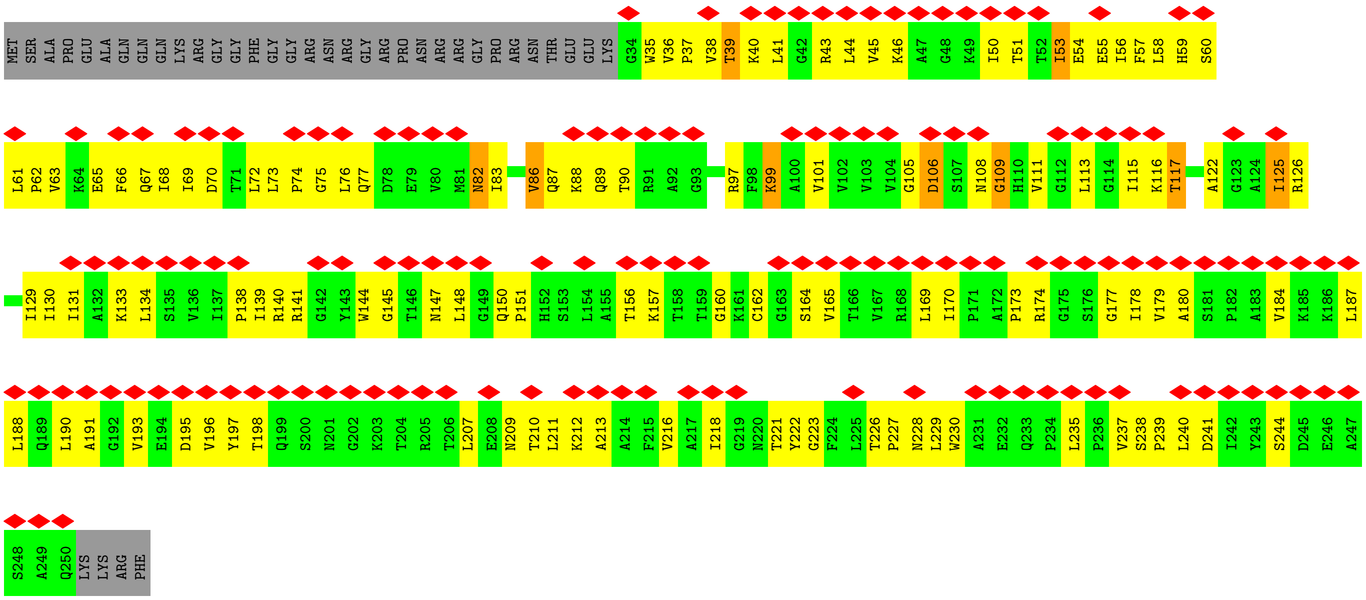
Chain YA:





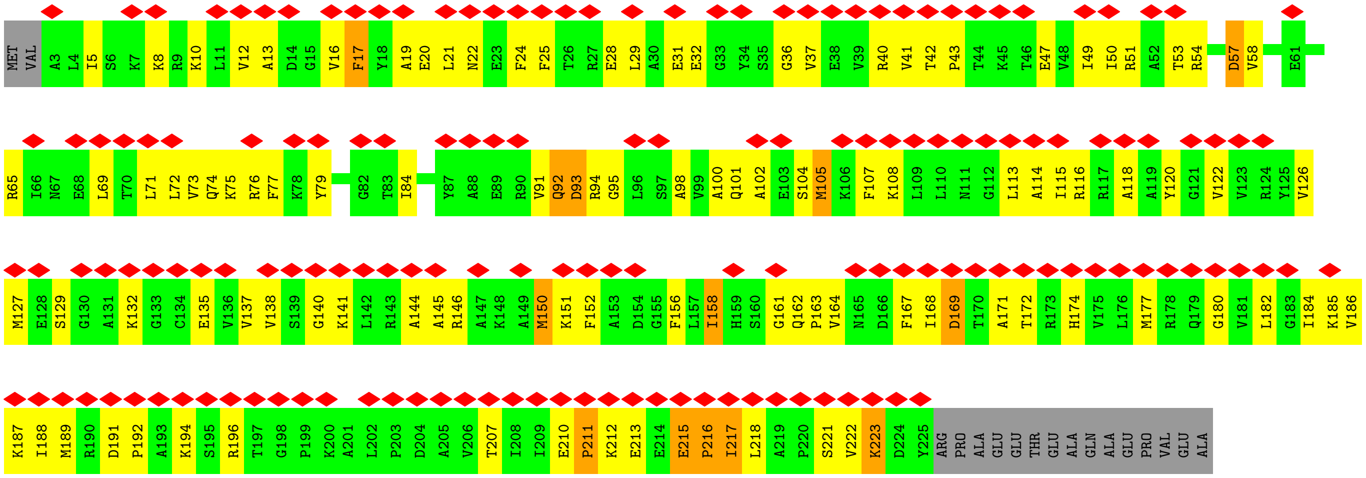
- Molecule 52: uS5 (yeast S2)

Chain ZA:

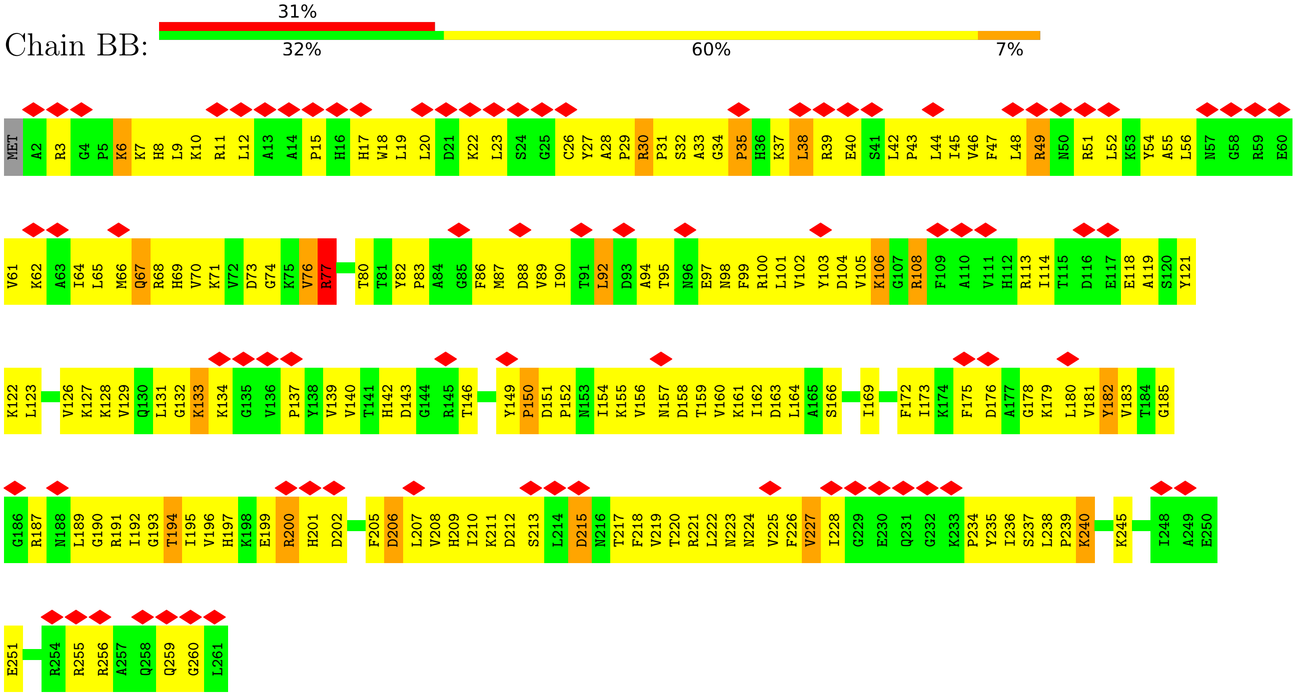


- Molecule 53: uS3 (yeast S3)

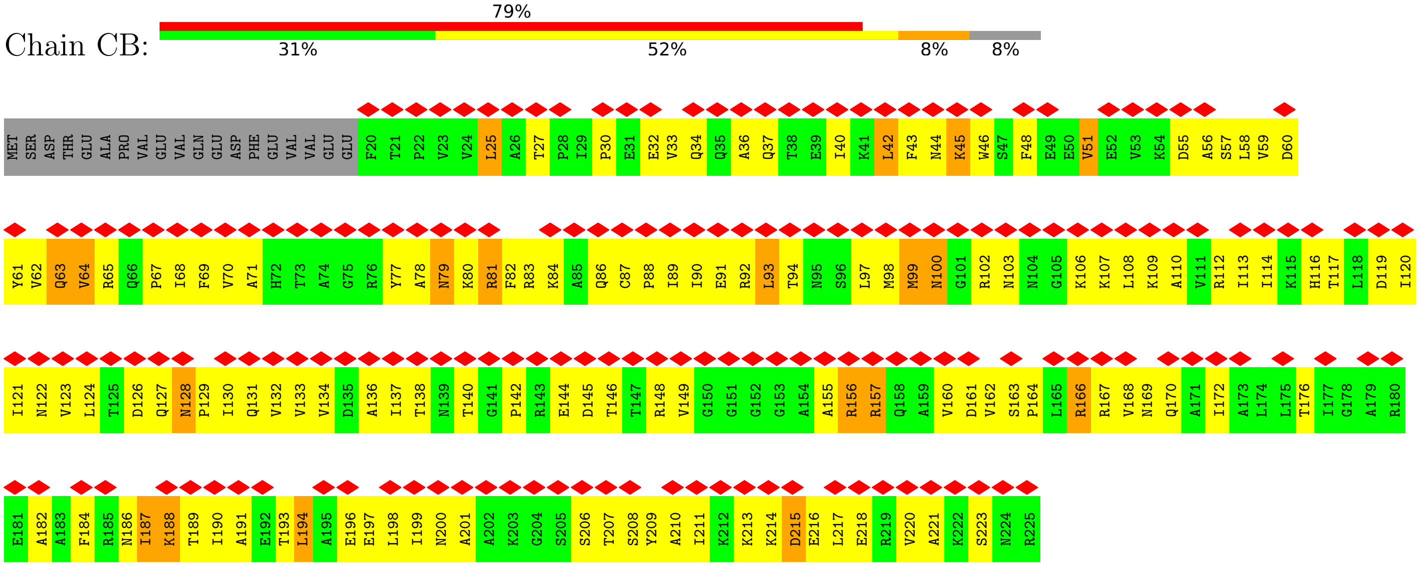
Chain AB:



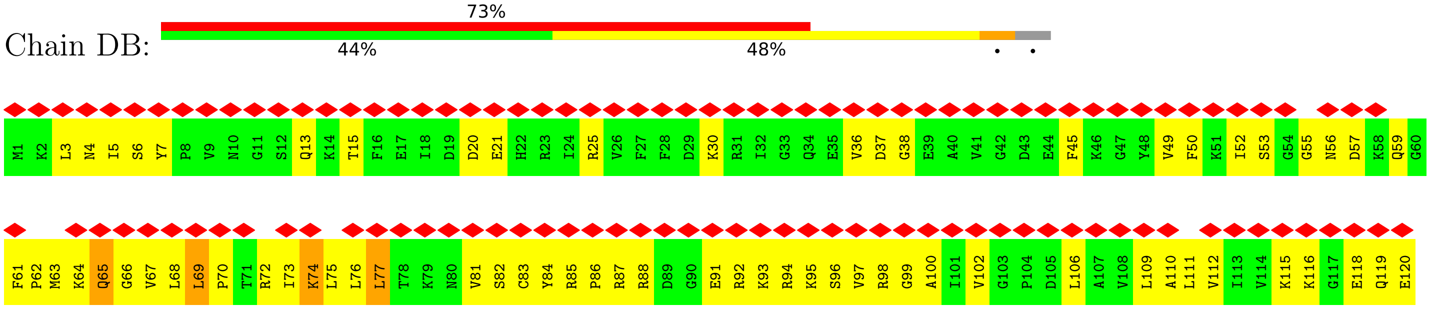
- Molecule 54: eS4 (yeast S4)

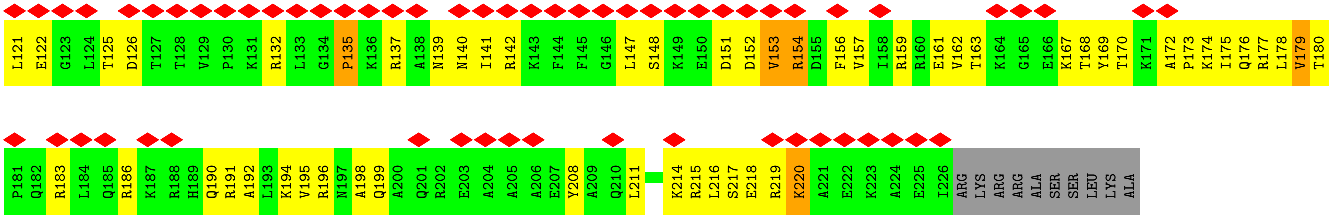


- Molecule 55: uS7 (yeast S5)



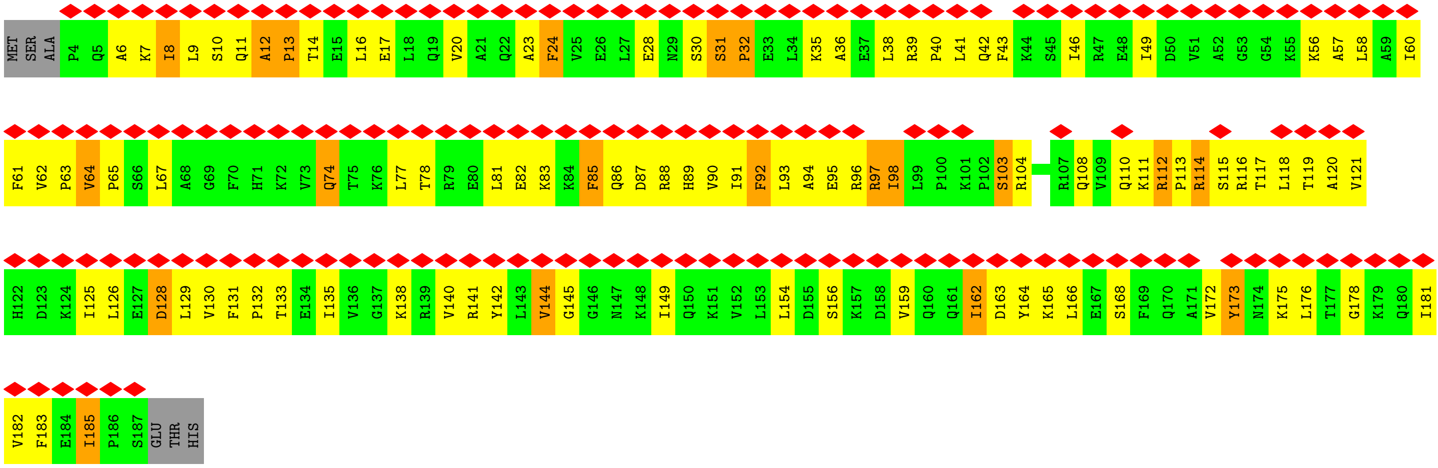
- Molecule 56: eS6 (yeast S6)





- Molecule 57: eS7 (yeast S7)

Chain EB:



- Molecule 58: eS8 (yeast S8)

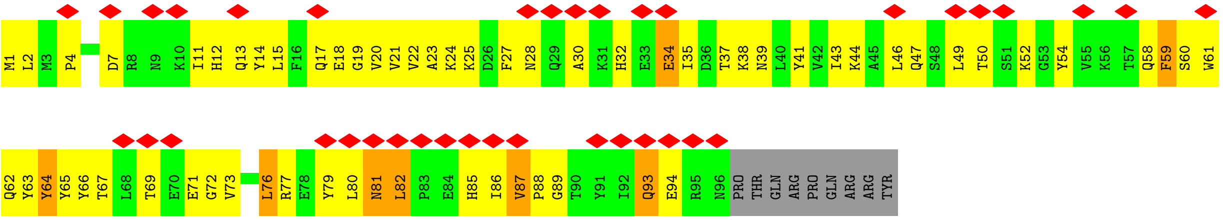
Chain FB:

- Molecule 59: uS4 (yeast S9)

Chain GB:

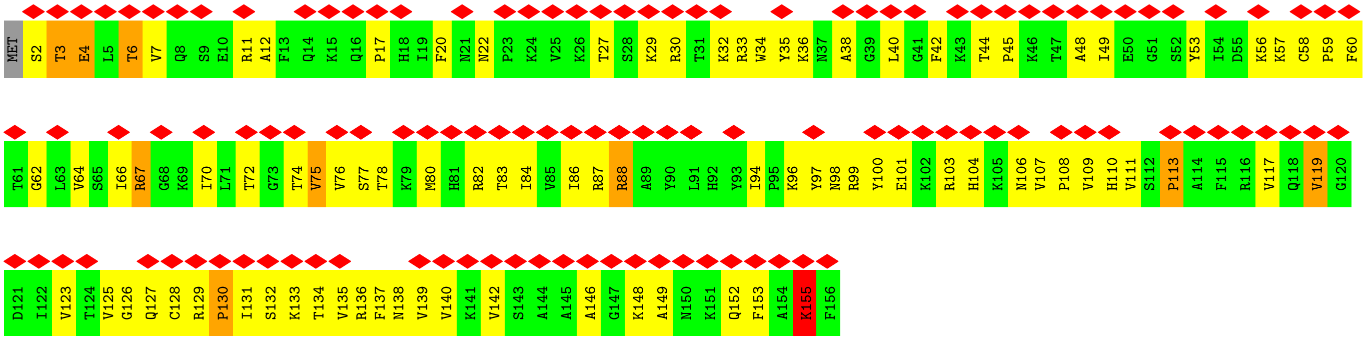
- Molecule 60: eS10 (yeast S10)

Chain HB:

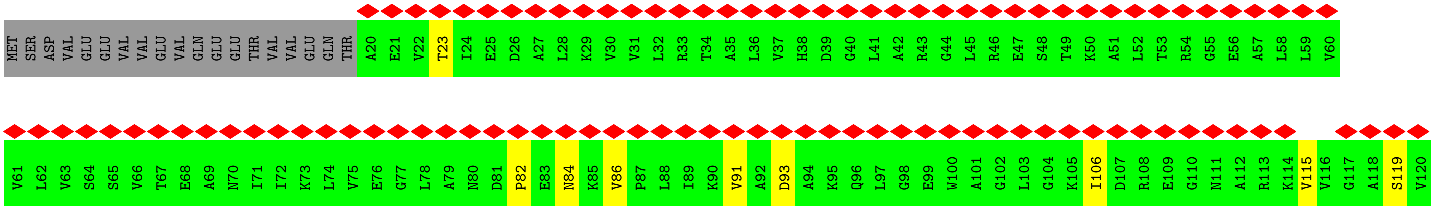
- Molecule 61: uS17 (yeast S11)

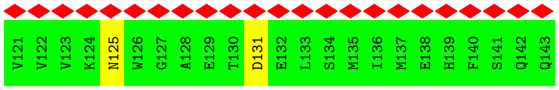
Chain IB:

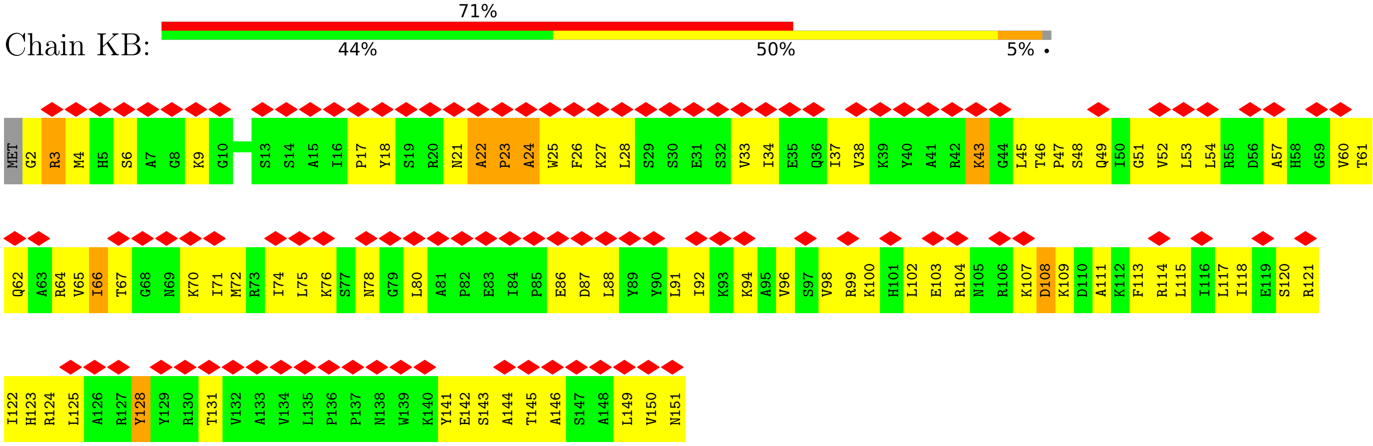
- Molecule 62: eS12 (yeast S12)

Chain JB:

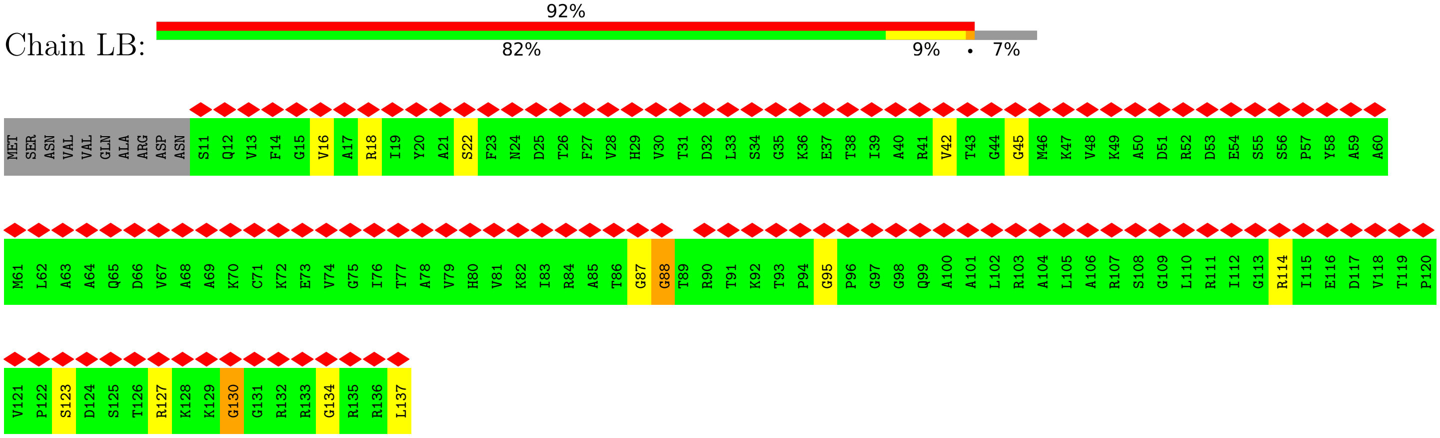





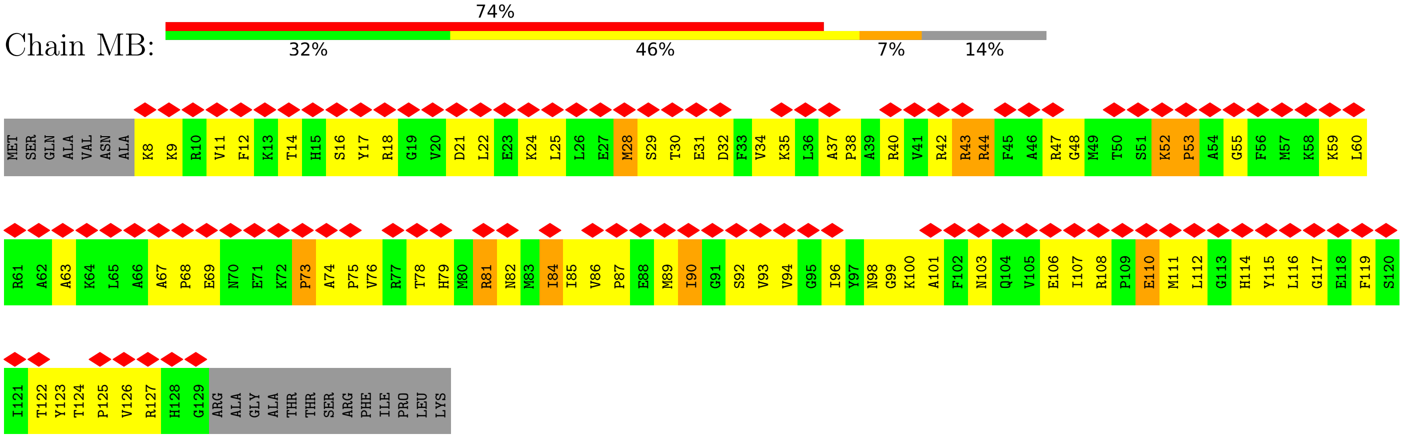
- Molecule 63: uS15 (yeast S13)



- Molecule 64: uS11 (yeast S14)

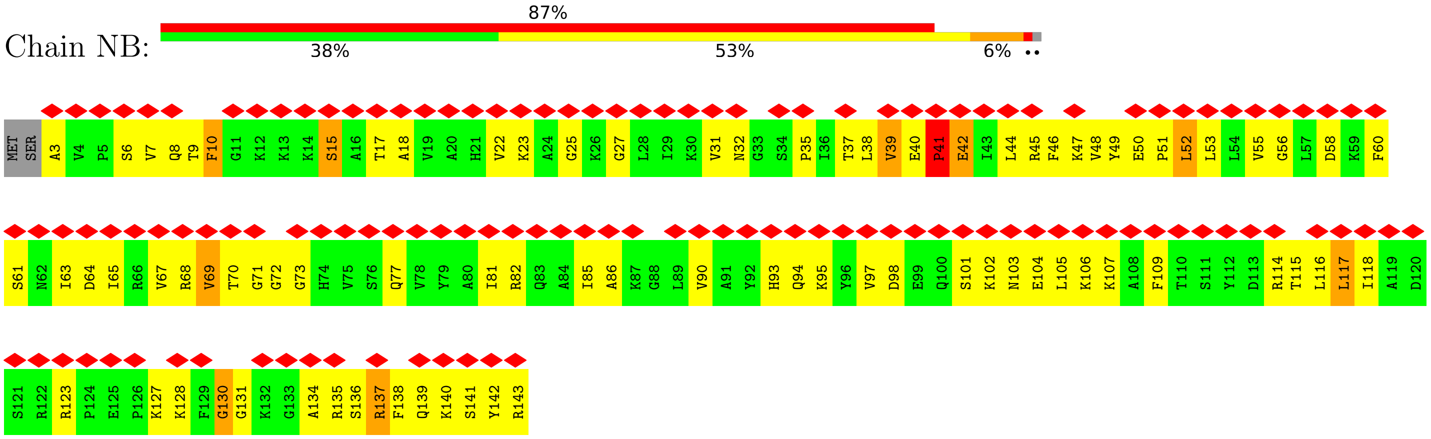


- Molecule 65: uS19 (yeast S15)



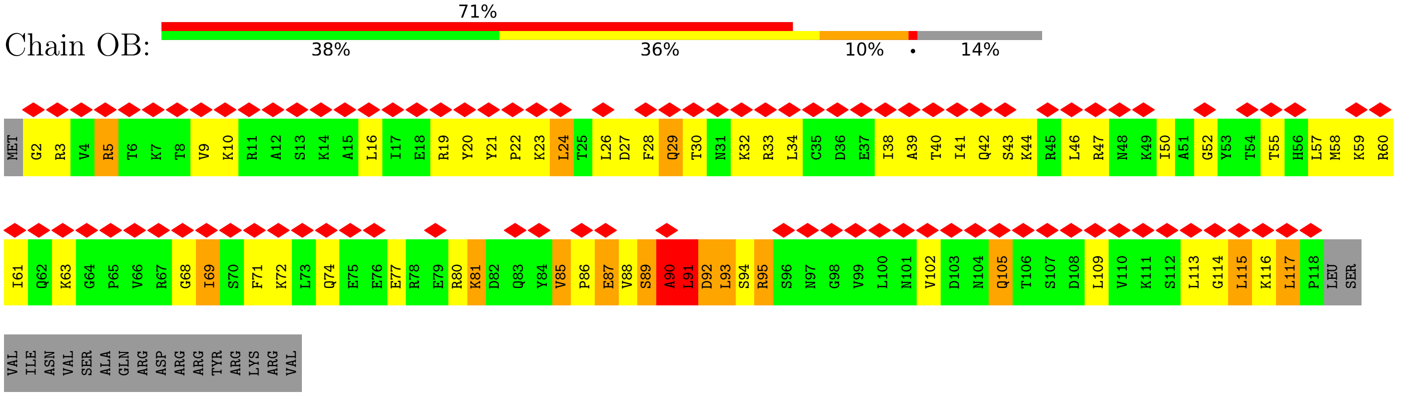
- Molecule 66: uS9 (yeast S16)

Chain NB:



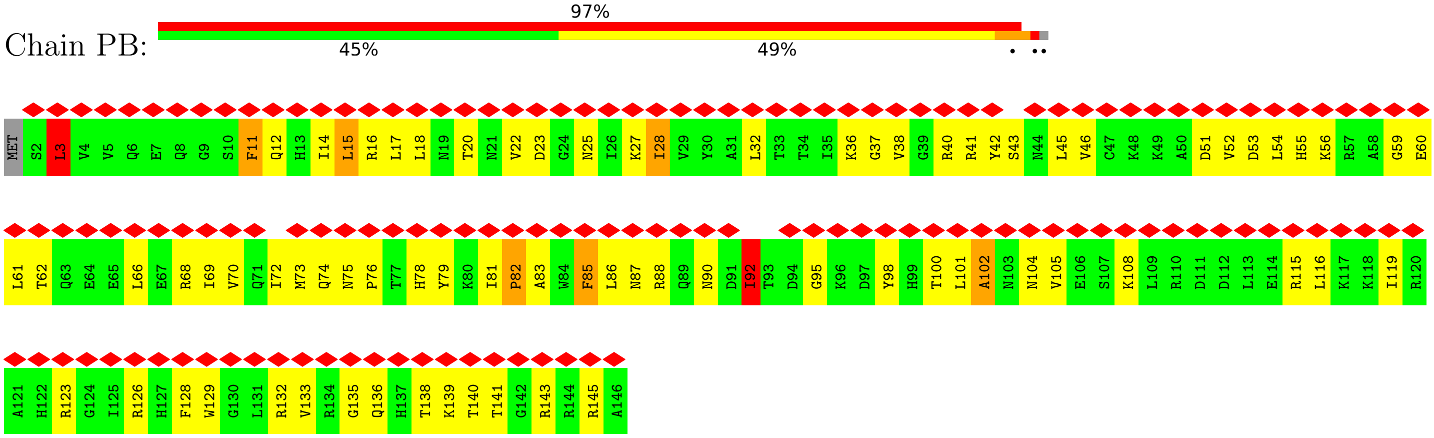
- Molecule 67: eS17 (yeast S17)

Chain OB:



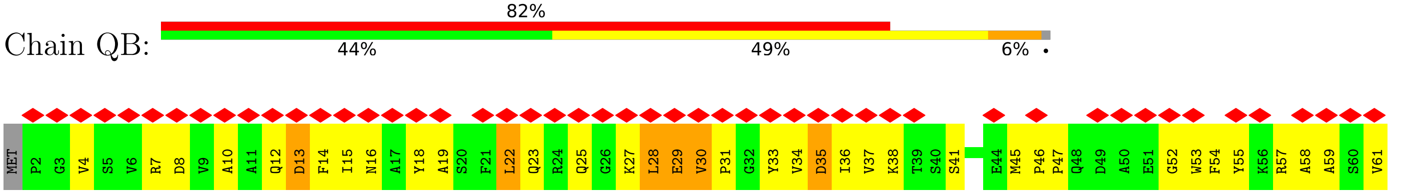
- Molecule 68: uS13 (yeast S18)

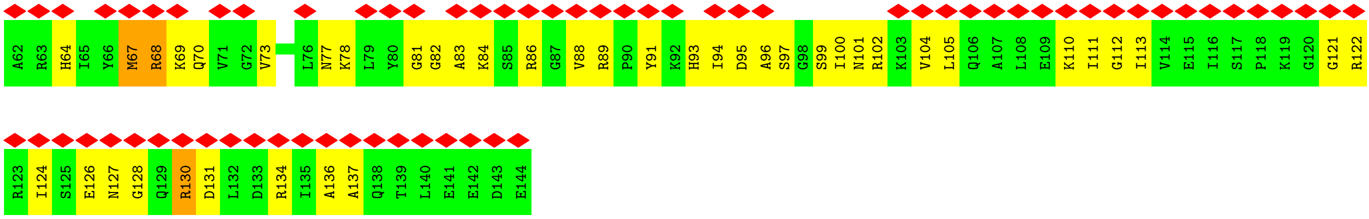
Chain PB:



- Molecule 69: eS19 (yeast S19)

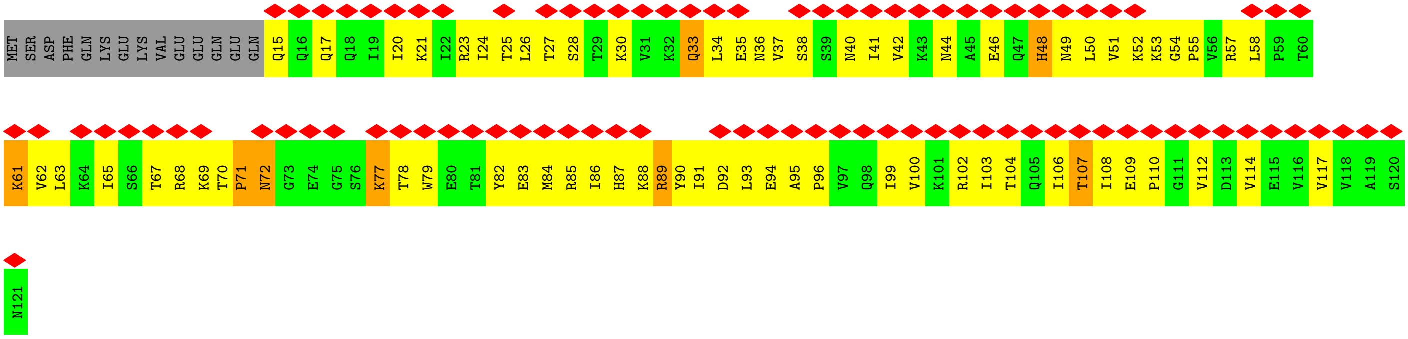
Chain QB:





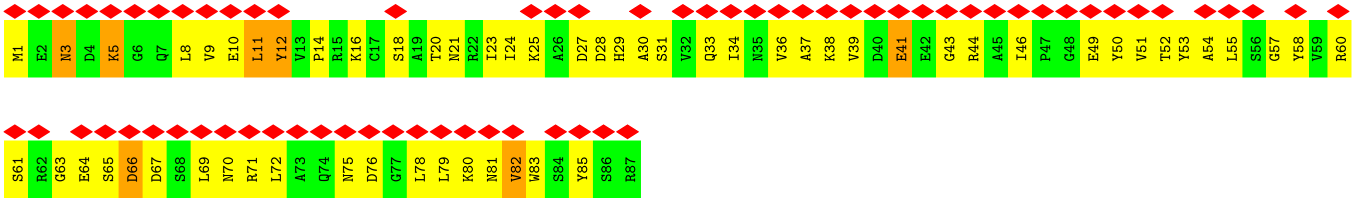
- Molecule 70: uS10 (yeast S20)

Chain RB:



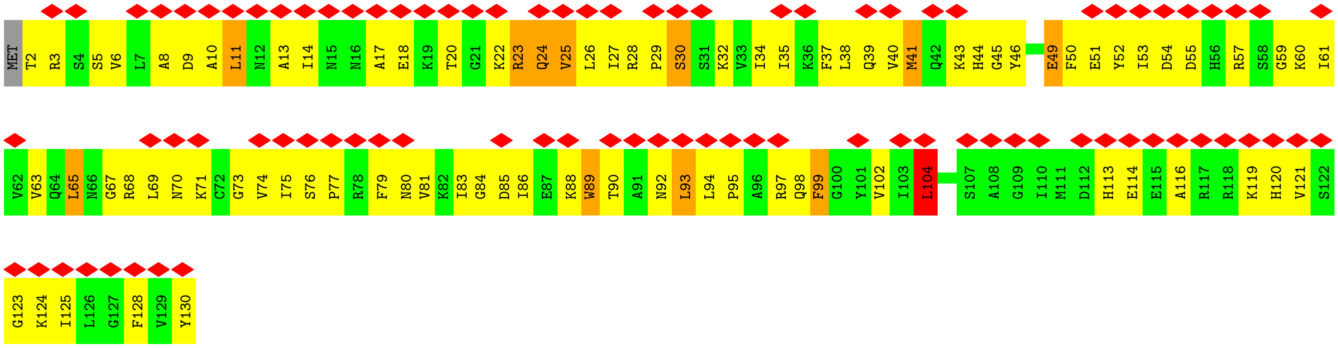
- Molecule 71: eS21 (yeast S21)

Chain SB:



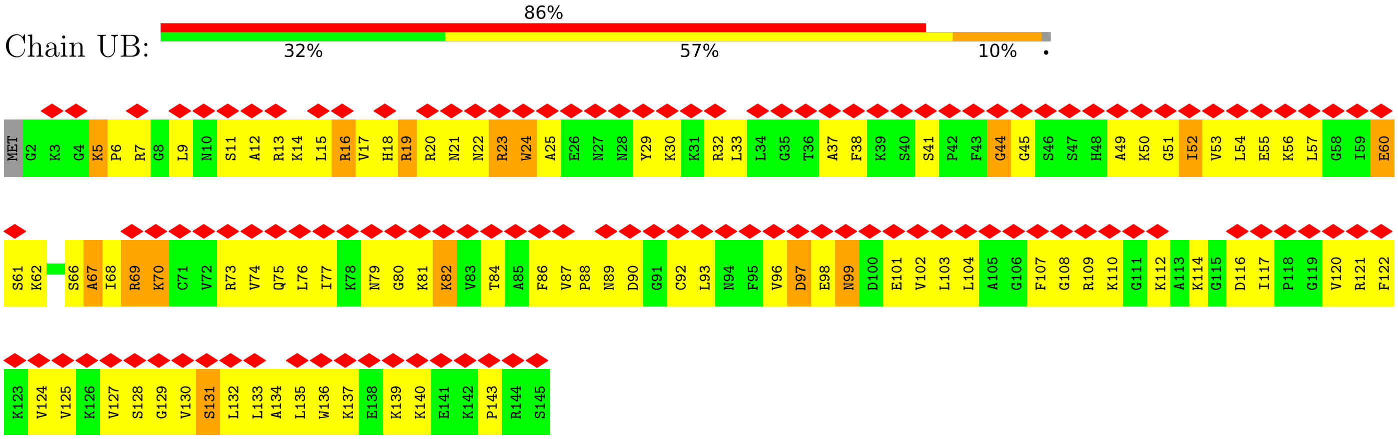
- Molecule 72: uS8 (yeast S22)

Chain TB:



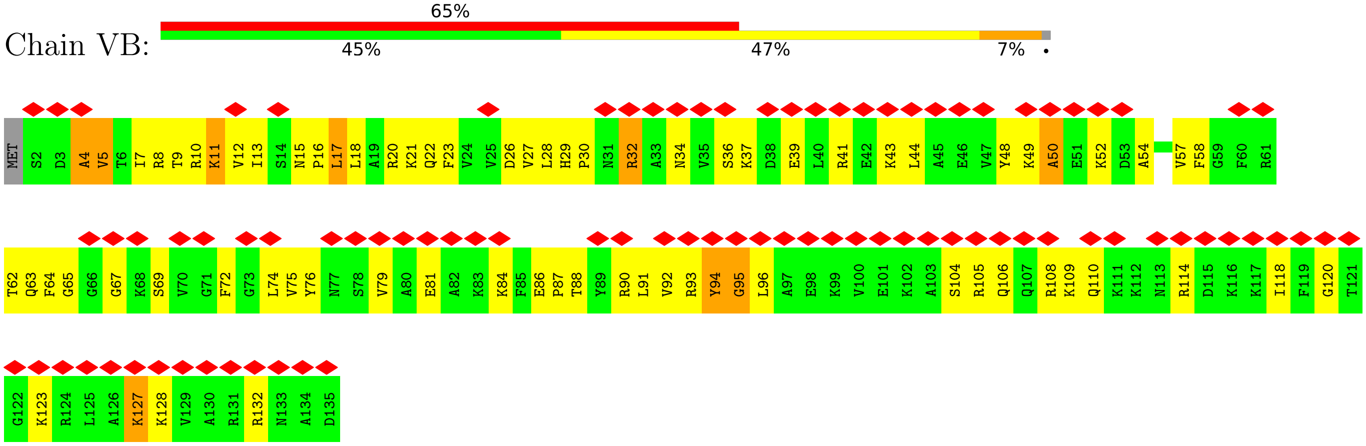
- Molecule 73: uS12 (yeast S23)

Chain UB:



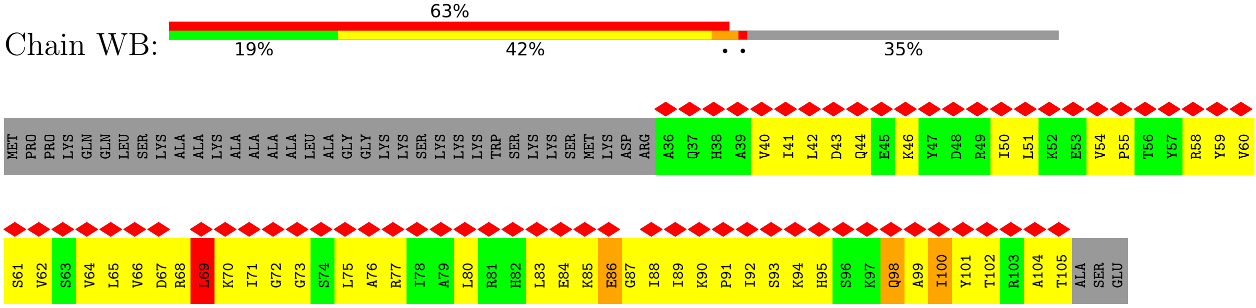
- Molecule 74: eS24 (yeast S24)

Chain VB:



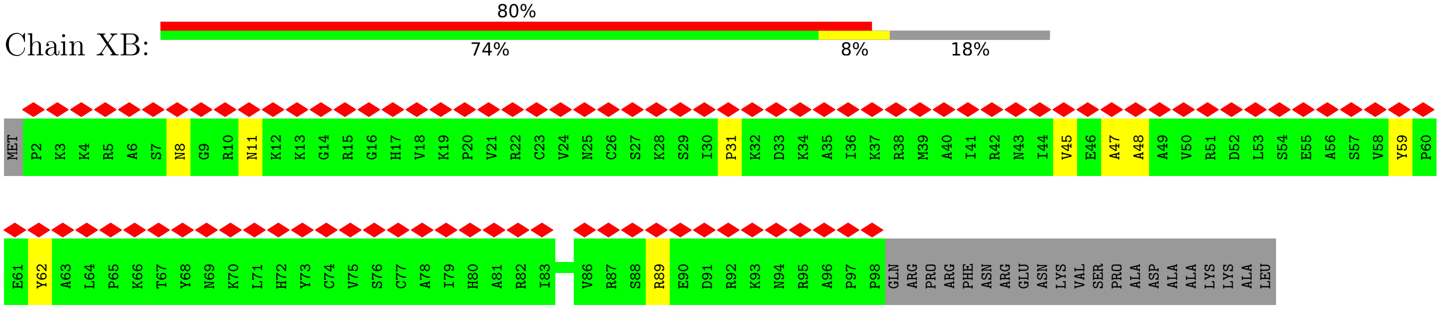
- Molecule 75: eS25 (yeast S25)

Chain WB:



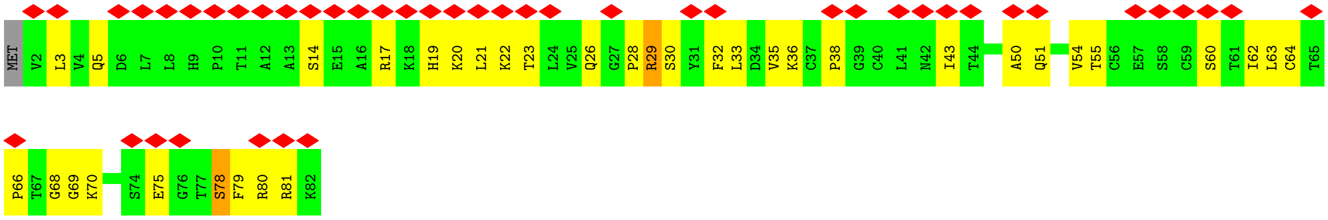
- Molecule 76: eS26 (yeast S26)

Chain XB:



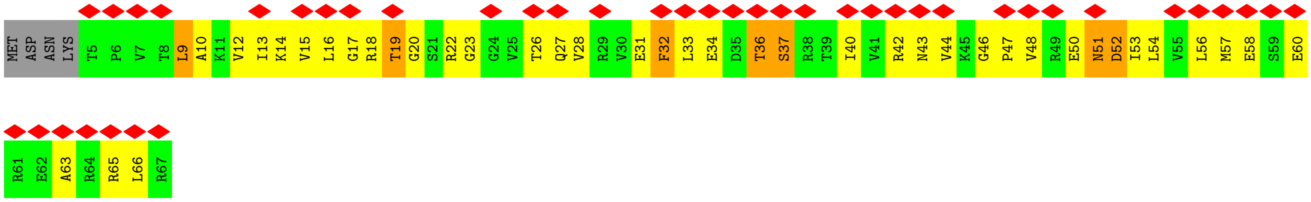
- Molecule 77: eS27 (yeast S27)

Chain YB:



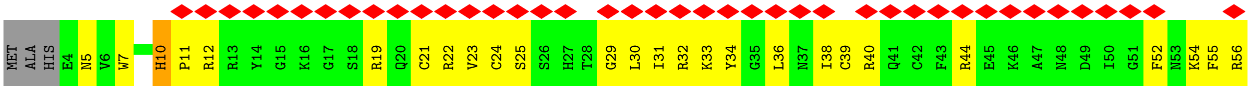
- Molecule 78: eS28 (yeast S28)

Chain ZB:



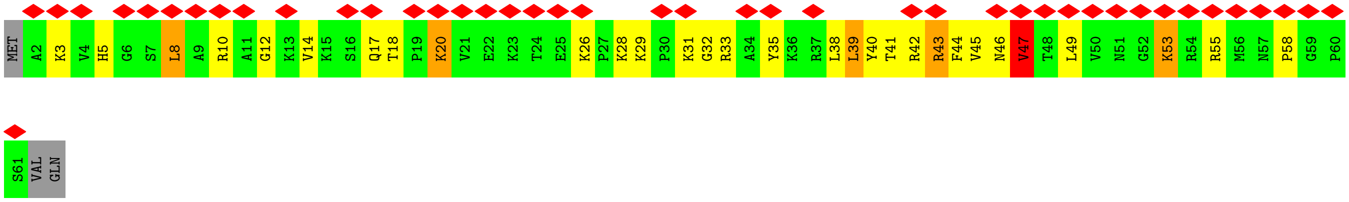
- Molecule 79: uS14 (yeast S29)

Chain AC:



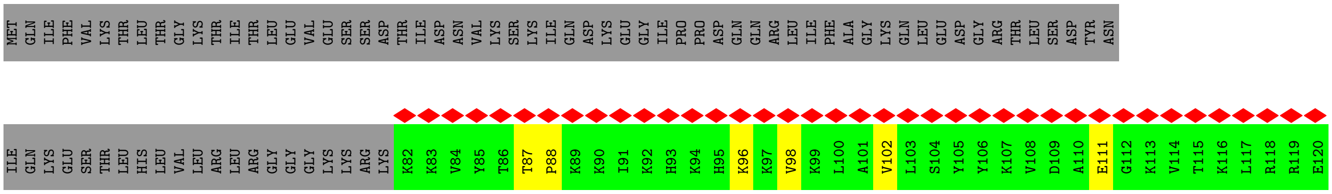
- Molecule 80: eS30 (yeast S30)

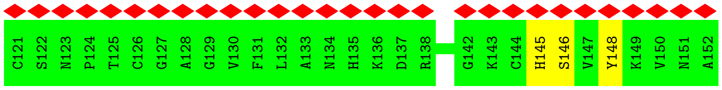
Chain BC:



- Molecule 81: eS31 (yeast S31)

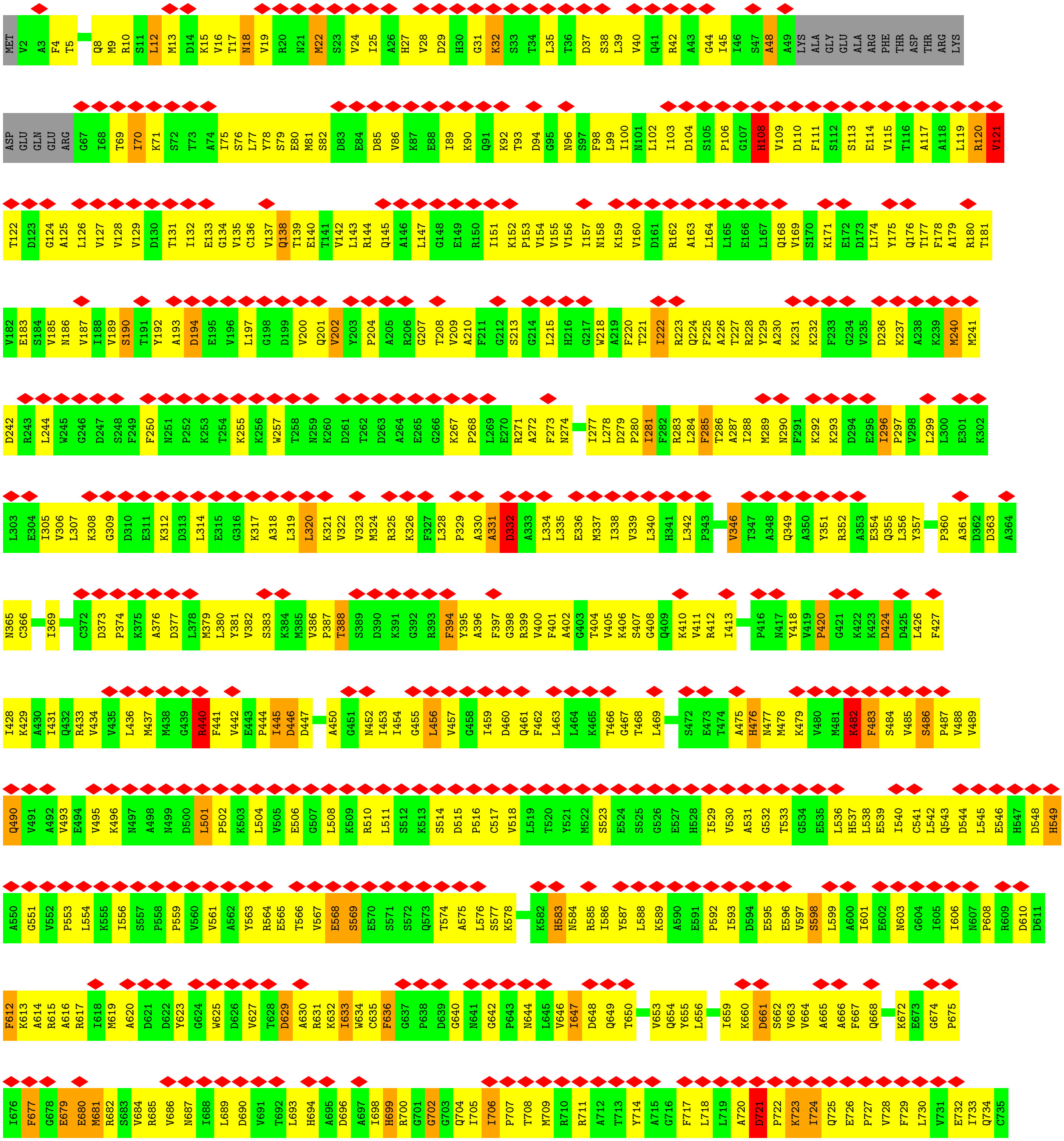
Chain CC:

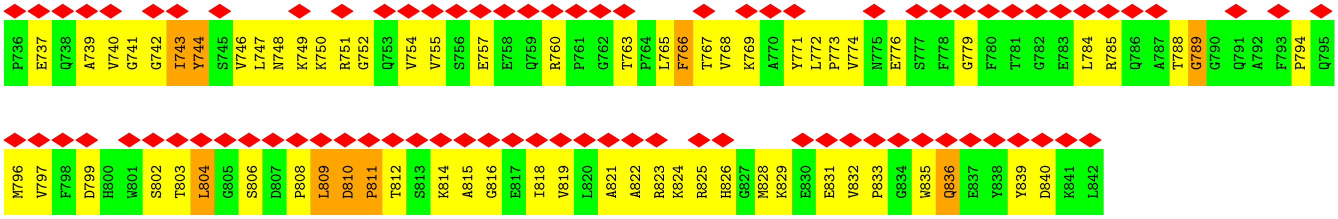




- Molecule 82: yeast eEF2

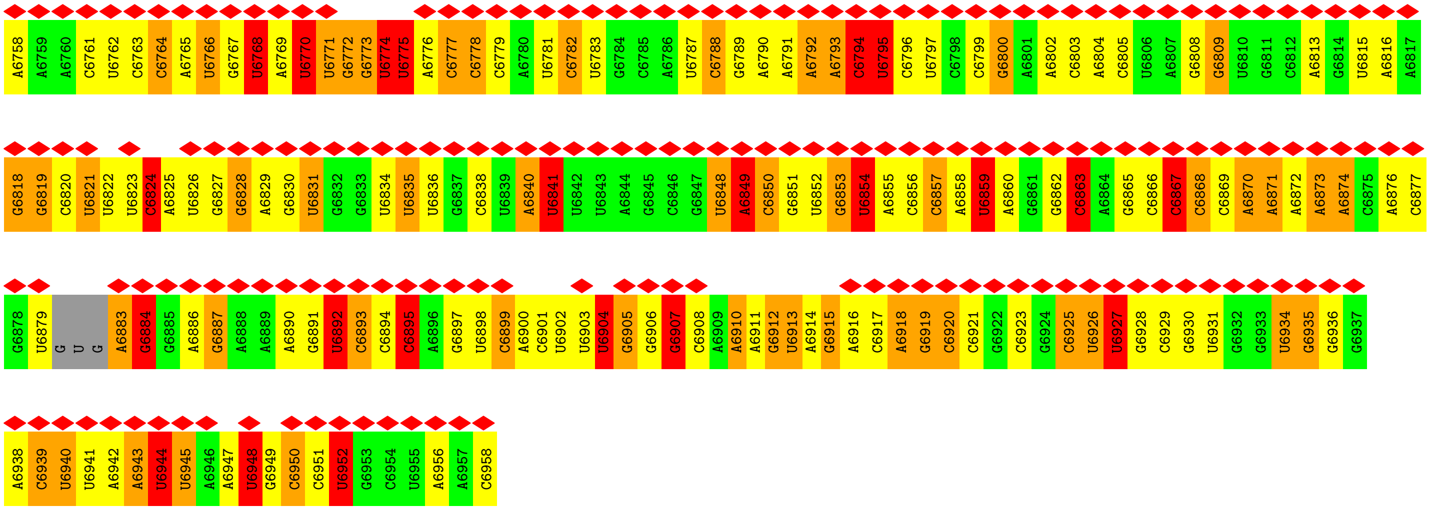
Chain DC:





- Molecule 83: IRES

Chain EC:



4 Experimental information ⓘ

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38054	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 ($e^-/\text{Å}^2$)	1.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.055	Depositor
Minimum map value	-0.025	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	419.84, 419.84, 419.84	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, GDP, SO1, 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	$\#|Z| >5$	RMSZ	$\#|Z| >5$
1	A	1.15	8/41014 (0.0%)	0.77	15/63809 (0.0%)
2	B	1.62	229/78631 (0.3%)	0.82	50/122552 (0.0%)
3	C	1.60	10/3747 (0.3%)	0.79	0/5832
4	D	1.44	6/2884 (0.2%)	0.77	2/4491 (0.0%)
5	E	1.93	0/1377	0.71	0/1844
6	F	1.35	0/1952	0.67	2/2622 (0.1%)
7	G	1.35	0/3153	0.65	0/4239
8	H	1.45	0/2802	0.70	0/3792
9	I	1.15	0/2426	0.60	0/3271
10	J	1.34	0/1425	0.66	0/1912
11	K	1.49	1/1822 (0.1%)	0.68	0/2451
12	L	1.15	0/1850	0.65	0/2495
13	M	1.27	0/1540	0.65	0/2073
14	N	1.32	0/1754	0.65	1/2350 (0.0%)
15	O	1.03	0/1375	0.57	0/1842
16	P	1.82	0/728	0.73	0/975
17	Q	1.32	0/1568	0.68	0/2106
18	R	1.40	1/1069 (0.1%)	0.67	0/1438
19	S	1.43	0/1758	0.70	0/2354
20	T	1.45	0/1586	0.67	0/2128
21	U	1.46	0/1466	0.70	1/1968 (0.1%)
22	V	1.43	0/1466	0.70	0/1965
23	W	1.13	0/1539	0.65	0/2050
24	X	1.54	0/1482	0.67	0/1990
25	Y	1.47	0/1301	0.64	1/1743 (0.1%)
26	Z	0.99	0/812	0.54	0/1099
27	AA	1.37	0/1019	0.66	1/1369 (0.1%)
28	BA	1.50	0/521	0.66	0/691
29	CA	1.33	0/984	0.65	0/1325
30	DA	1.34	0/1005	0.73	3/1341 (0.2%)
31	EA	1.06	0/1119	0.54	0/1497
32	FA	1.41	0/1205	0.67	0/1612

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	GA	1.28	0/474	0.68	0/629
34	HA	1.02	0/751	0.60	0/1008
35	IA	1.23	0/904	0.63	0/1213
36	JA	1.47	0/1041	0.67	1/1394 (0.1%)
37	KA	1.56	0/869	0.70	0/1168
38	LA	1.22	0/891	0.65	0/1191
39	MA	1.22	0/979	0.64	0/1301
40	NA	1.17	0/779	0.63	0/1034
41	OA	1.53	0/697	0.70	1/923 (0.1%)
42	PA	1.06	0/619	0.61	0/826
43	QA	1.38	0/444	0.77	0/588
44	RA	1.31	0/424	0.66	0/562
45	SA	1.57	0/235	0.71	0/300
46	TA	1.30	0/861	0.70	0/1136
47	UA	1.30	0/702	0.65	0/934
48	VA	1.78	0/1498	0.83	3/2025 (0.1%)
49	WA	0.92	0/2498	0.56	0/3398
50	XA	0.78	0/1653	0.58	0/2261
51	YA	1.13	0/855	0.51	0/1067
52	ZA	0.91	0/1665	0.59	0/2263
53	AB	0.97	0/1759	0.56	0/2368
54	BB	0.89	0/2110	0.59	0/2839
55	CB	0.85	0/1630	0.56	0/2202
56	DB	0.89	0/1844	0.57	0/2464
57	EB	0.92	0/1506	0.58	0/2028
58	FB	1.07	0/1515	0.61	0/2021
59	GB	0.84	0/1519	0.59	0/2035
60	HB	1.03	0/837	0.57	0/1131
61	IB	1.16	0/1273	0.62	0/1712
62	JB	1.06	0/495	0.56	0/617
63	KB	1.01	0/1216	0.59	0/1638
64	LB	1.02	0/507	0.53	0/632
65	MB	1.03	0/996	0.60	0/1335
66	NB	0.94	0/1126	0.55	0/1510
67	OB	1.04	2/844 (0.2%)	0.90	4/1120 (0.4%)
68	PB	0.93	0/1212	0.59	2/1628 (0.1%)
69	QB	0.89	0/1131	0.58	0/1517
70	RB	0.97	0/866	0.56	0/1169
71	SB	0.85	0/694	0.55	0/935
72	TB	0.95	0/1039	0.62	2/1395 (0.1%)
73	UB	1.12	0/1140	0.62	0/1518
74	VB	0.89	0/1088	0.54	0/1449
75	WB	0.87	0/571	0.57	0/768

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	XB	1.09	0/387	0.62	0/482
77	YB	0.87	0/621	0.55	0/838
78	ZB	0.85	0/500	0.56	0/670
79	AC	1.09	0/454	0.57	0/602
80	BC	0.96	0/483	0.59	0/643
81	CC	0.97	0/283	0.59	0/352
82	DC	1.63	0/6521	0.69	1/8830 (0.0%)
83	EC	2.33	88/4608 (1.9%)	0.94	11/7166 (0.2%)
All	All	1.41	345/227994 (0.2%)	0.75	101/334061 (0.0%)

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

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

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

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

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

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

There are no chirality outliers.

5 of 100 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	313	U	Sidechain
1	A	324	U	Sidechain
1	A	447	U	Sidechain
1	A	53	G	Sidechain
1	A	568	G	Sidechain

5.2 Too-close contacts ⓘ

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

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

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

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

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

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

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

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

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%)	129 (78%)	26 (16%)	10 (6%)	1	20
6	F	250/254 (98%)	177 (71%)	56 (22%)	17 (7%)	1	18
7	G	384/387 (99%)	293 (76%)	70 (18%)	21 (6%)	2	22
8	H	359/362 (99%)	259 (72%)	77 (21%)	23 (6%)	1	19
9	I	294/297 (99%)	226 (77%)	49 (17%)	19 (6%)	1	19
10	J	173/176 (98%)	125 (72%)	33 (19%)	15 (9%)	1	13
11	K	220/244 (90%)	165 (75%)	39 (18%)	16 (7%)	1	16
12	L	231/256 (90%)	180 (78%)	38 (16%)	13 (6%)	2	21
13	M	189/191 (99%)	150 (79%)	36 (19%)	3 (2%)	9	45
14	N	207/221 (94%)	169 (82%)	28 (14%)	10 (5%)	2	24
15	O	167/174 (96%)	128 (77%)	31 (19%)	8 (5%)	2	24
16	P	92/165 (56%)	62 (67%)	20 (22%)	10 (11%)	0	8
17	Q	191/199 (96%)	144 (75%)	35 (18%)	12 (6%)	1	19
18	R	134/138 (97%)	103 (77%)	23 (17%)	8 (6%)	1	20
19	S	201/204 (98%)	144 (72%)	46 (23%)	11 (6%)	2	22
20	T	195/199 (98%)	160 (82%)	27 (14%)	8 (4%)	3	26
21	U	181/184 (98%)	133 (74%)	35 (19%)	13 (7%)	1	17
22	V	183/186 (98%)	131 (72%)	39 (21%)	13 (7%)	1	17
23	W	186/189 (98%)	162 (87%)	19 (10%)	5 (3%)	5	34
24	X	170/172 (99%)	130 (76%)	31 (18%)	9 (5%)	2	22
25	Y	157/160 (98%)	124 (79%)	25 (16%)	8 (5%)	2	22
26	Z	98/121 (81%)	69 (70%)	23 (24%)	6 (6%)	1	20
27	AA	134/137 (98%)	107 (80%)	24 (18%)	3 (2%)	6	38
28	BA	59/155 (38%)	43 (73%)	11 (19%)	5 (8%)	1	13
29	CA	119/142 (84%)	84 (71%)	29 (24%)	6 (5%)	2	23
30	DA	124/127 (98%)	89 (72%)	28 (23%)	7 (6%)	2	21
31	EA	133/136 (98%)	108 (81%)	19 (14%)	6 (4%)	2	25
32	FA	146/149 (98%)	106 (73%)	31 (21%)	9 (6%)	1	20
33	GA	56/59 (95%)	48 (86%)	8 (14%)	0	100	100
34	HA	95/105 (90%)	80 (84%)	13 (14%)	2 (2%)	7	39

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	NB	139/143 (97%)	108 (78%)	24 (17%)	7 (5%)	2	23
67	OB	115/136 (85%)	79 (69%)	24 (21%)	12 (10%)	0	9
68	PB	143/146 (98%)	111 (78%)	24 (17%)	8 (6%)	2	21
69	QB	141/144 (98%)	122 (86%)	16 (11%)	3 (2%)	7	39
70	RB	105/121 (87%)	85 (81%)	15 (14%)	5 (5%)	2	24
71	SB	85/87 (98%)	63 (74%)	17 (20%)	5 (6%)	1	20
72	TB	127/130 (98%)	99 (78%)	24 (19%)	4 (3%)	4	31
73	UB	142/145 (98%)	108 (76%)	22 (16%)	12 (8%)	1	13
74	VB	132/135 (98%)	105 (80%)	20 (15%)	7 (5%)	2	22
75	WB	68/108 (63%)	47 (69%)	17 (25%)	4 (6%)	1	20
76	XB	95/119 (80%)	54 (57%)	32 (34%)	9 (10%)	0	12
77	YB	79/82 (96%)	59 (75%)	17 (22%)	3 (4%)	3	27
78	ZB	61/67 (91%)	43 (70%)	15 (25%)	3 (5%)	2	23
79	AC	51/56 (91%)	39 (76%)	11 (22%)	1 (2%)	7	40
80	BC	58/63 (92%)	38 (66%)	16 (28%)	4 (7%)	1	17
81	CC	69/152 (45%)	42 (61%)	18 (26%)	9 (13%)	0	5
82	DC	819/842 (97%)	646 (79%)	137 (17%)	36 (4%)	2	25
All	All	12207/13416 (91%)	9316 (76%)	2192 (18%)	699 (6%)	3	21

5 of 699 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	157/198 (79%)	136 (87%)	21 (13%)	4	20
6	F	194/196 (99%)	172 (89%)	22 (11%)	6	25
7	G	322/323 (100%)	295 (92%)	27 (8%)	11	37
8	H	288/289 (100%)	249 (86%)	39 (14%)	4	20
9	I	244/245 (100%)	220 (90%)	24 (10%)	8	29
10	J	152/153 (99%)	141 (93%)	11 (7%)	14	41
11	K	186/205 (91%)	165 (89%)	21 (11%)	6	25
12	L	191/208 (92%)	169 (88%)	22 (12%)	5	24
13	M	171/171 (100%)	154 (90%)	17 (10%)	8	29
14	N	180/187 (96%)	161 (89%)	19 (11%)	6	27
15	O	147/150 (98%)	134 (91%)	13 (9%)	10	34
16	P	81/136 (60%)	70 (86%)	11 (14%)	3	20
17	Q	154/159 (97%)	136 (88%)	18 (12%)	5	23
18	R	107/109 (98%)	96 (90%)	11 (10%)	7	28
19	S	175/176 (99%)	150 (86%)	25 (14%)	3	18
20	T	160/162 (99%)	141 (88%)	19 (12%)	5	23
21	U	145/146 (99%)	122 (84%)	23 (16%)	2	16
22	V	150/151 (99%)	134 (89%)	16 (11%)	6	27
23	W	153/154 (99%)	138 (90%)	15 (10%)	8	29
24	X	156/156 (100%)	141 (90%)	15 (10%)	8	30
25	Y	136/137 (99%)	114 (84%)	22 (16%)	2	15
26	Z	87/107 (81%)	85 (98%)	2 (2%)	50	70
27	AA	104/105 (99%)	93 (89%)	11 (11%)	6	27
28	BA	54/129 (42%)	45 (83%)	9 (17%)	2	14
29	CA	105/118 (89%)	97 (92%)	8 (8%)	13	40
30	DA	109/110 (99%)	94 (86%)	15 (14%)	3	20
31	EA	115/116 (99%)	105 (91%)	10 (9%)	10	34
32	FA	118/119 (99%)	105 (89%)	13 (11%)	6	26
33	GA	46/47 (98%)	42 (91%)	4 (9%)	10	34
34	HA	81/88 (92%)	75 (93%)	6 (7%)	13	40
35	IA	96/97 (99%)	89 (93%)	7 (7%)	14	41
36	JA	109/111 (98%)	100 (92%)	9 (8%)	11	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	KA	90/91 (99%)	80 (89%)	10 (11%)	6	25
38	LA	95/103 (92%)	90 (95%)	5 (5%)	22	50
39	MA	104/105 (99%)	96 (92%)	8 (8%)	13	39
40	NA	81/82 (99%)	75 (93%)	6 (7%)	13	40
41	OA	70/71 (99%)	60 (86%)	10 (14%)	3	18
42	PA	68/69 (99%)	63 (93%)	5 (7%)	13	40
43	QA	45/46 (98%)	39 (87%)	6 (13%)	4	21
44	RA	47/116 (40%)	44 (94%)	3 (6%)	17	45
45	SA	23/23 (100%)	20 (87%)	3 (13%)	4	21
46	TA	90/91 (99%)	80 (89%)	10 (11%)	6	25
47	UA	71/72 (99%)	65 (92%)	6 (8%)	10	36
48	VA	160/254 (63%)	147 (92%)	13 (8%)	11	38
49	WA	261/262 (100%)	246 (94%)	15 (6%)	20	48
50	XA	173/210 (82%)	155 (90%)	18 (10%)	7	27
52	ZA	176/205 (86%)	170 (97%)	6 (3%)	37	61
53	AB	182/195 (93%)	167 (92%)	15 (8%)	11	37
54	BB	221/222 (100%)	202 (91%)	19 (9%)	10	36
55	CB	173/191 (91%)	162 (94%)	11 (6%)	17	45
56	DB	193/201 (96%)	187 (97%)	6 (3%)	40	62
57	EB	165/170 (97%)	157 (95%)	8 (5%)	25	52
58	FB	150/161 (93%)	141 (94%)	9 (6%)	19	47
59	GB	158/166 (95%)	143 (90%)	15 (10%)	8	30
60	HB	89/98 (91%)	83 (93%)	6 (7%)	16	43
61	IB	136/137 (99%)	127 (93%)	9 (7%)	16	44
63	KB	127/128 (99%)	119 (94%)	8 (6%)	18	45
65	MB	103/118 (87%)	98 (95%)	5 (5%)	25	52
66	NB	117/119 (98%)	108 (92%)	9 (8%)	13	39
67	OB	82/124 (66%)	77 (94%)	5 (6%)	18	46
68	PB	128/129 (99%)	116 (91%)	12 (9%)	8	30
69	QB	115/116 (99%)	105 (91%)	10 (9%)	10	34
70	RB	100/114 (88%)	90 (90%)	10 (10%)	7	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	SB	74/74 (100%)	66 (89%)	8 (11%)	6	26
72	TB	110/111 (99%)	99 (90%)	11 (10%)	7	28
73	UB	119/120 (99%)	110 (92%)	9 (8%)	13	40
74	VB	112/113 (99%)	103 (92%)	9 (8%)	12	38
75	WB	61/89 (68%)	56 (92%)	5 (8%)	11	37
77	YB	70/71 (99%)	69 (99%)	1 (1%)	67	80
78	ZB	56/60 (93%)	49 (88%)	7 (12%)	4	22
79	AC	47/49 (96%)	44 (94%)	3 (6%)	17	45
80	BC	51/54 (94%)	45 (88%)	6 (12%)	5	23
82	DC	699/714 (98%)	641 (92%)	58 (8%)	11	37
All	All	9865/10602 (93%)	8962 (91%)	903 (9%)	13	31

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

Mol	Chain	Res	Type
31	EA	121	ARG
82	DC	654	GLN
47	UA	28	LYS
82	DC	568	GLU
72	TB	41	MET

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

Mol	Chain	Res	Type
65	MB	98	ASN
67	OB	29	GLN
72	TB	80	ASN
24	X	3	HIS
23	W	34	GLN

5.3.3 RNA ⓘ

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

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

5 of 1062 RNA backbone outliers are listed below:

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

5 of 40 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	2513	U
2	B	3269	U
2	B	2525	G
2	B	3218	A
2	B	3375	A

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	14,20,21	2.11	6 (42%)	14,28,30	1.90	6 (42%)

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	-	1/20/21/23	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	DC	699	DDE	CBW-CBI	4.59	1.60	1.53
82	DC	699	DDE	CAT-CE1	3.52	1.55	1.50
82	DC	699	DDE	CB-CG	2.46	1.59	1.51
82	DC	699	DDE	OAG-CBI	2.24	1.28	1.23
82	DC	699	DDE	CB-CA	2.13	1.58	1.53

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
82	DC	699	DDE	OAG-CBI-CBW	-3.77	115.72	120.49
82	DC	699	DDE	CAU-CBW-CBI	-2.80	105.65	111.20
82	DC	699	DDE	CG-ND1-CE1	2.53	110.53	103.05
82	DC	699	DDE	CB-CA-C	2.23	115.65	111.47
82	DC	699	DDE	OAG-CBI-NAD	2.19	126.80	123.00

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
82	DC	699	DDE	CA-CB-CG-ND1

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 ⓘ

There are no monosaccharides 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	24,30,30	1.93	5 (20%)	30,47,47	1.74	6 (20%)
86	SO1	DC	903	-	35,39,39	2.82	20 (57%)	39,64,64	2.03	8 (20%)

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	-	3/12/32/32	0/3/3/3
86	SO1	DC	903	-	-	4/21/104/104	0/7/5/5

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	DC	901	GDP	O4'-C1'	5.55	1.48	1.41
86	DC	903	SO1	O17-C52	5.13	1.49	1.40
86	DC	903	SO1	C12-C6	4.56	1.64	1.53
86	DC	903	SO1	C1-C5	4.35	1.60	1.50
86	DC	903	SO1	C8-C2	4.30	1.61	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
86	DC	903	SO1	C12-C6-C10	-6.91	102.42	107.91
84	DC	901	GDP	PA-O3A-PB	-5.95	112.41	132.83
86	DC	903	SO1	C25-C22-C24	4.93	129.42	113.56
86	DC	903	SO1	C10-C6-C2	3.71	108.62	104.16
84	DC	901	GDP	C8-N7-C5	3.44	109.54	102.99

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
84	DC	901	GDP	O4'-C4'-C5'-O5'
84	DC	901	GDP	C3'-C4'-C5'-O5'
86	DC	903	SO1	C2-C1-C5-O14
86	DC	903	SO1	C2-C1-C5-O15
86	DC	903	SO1	C3-C1-C5-O15

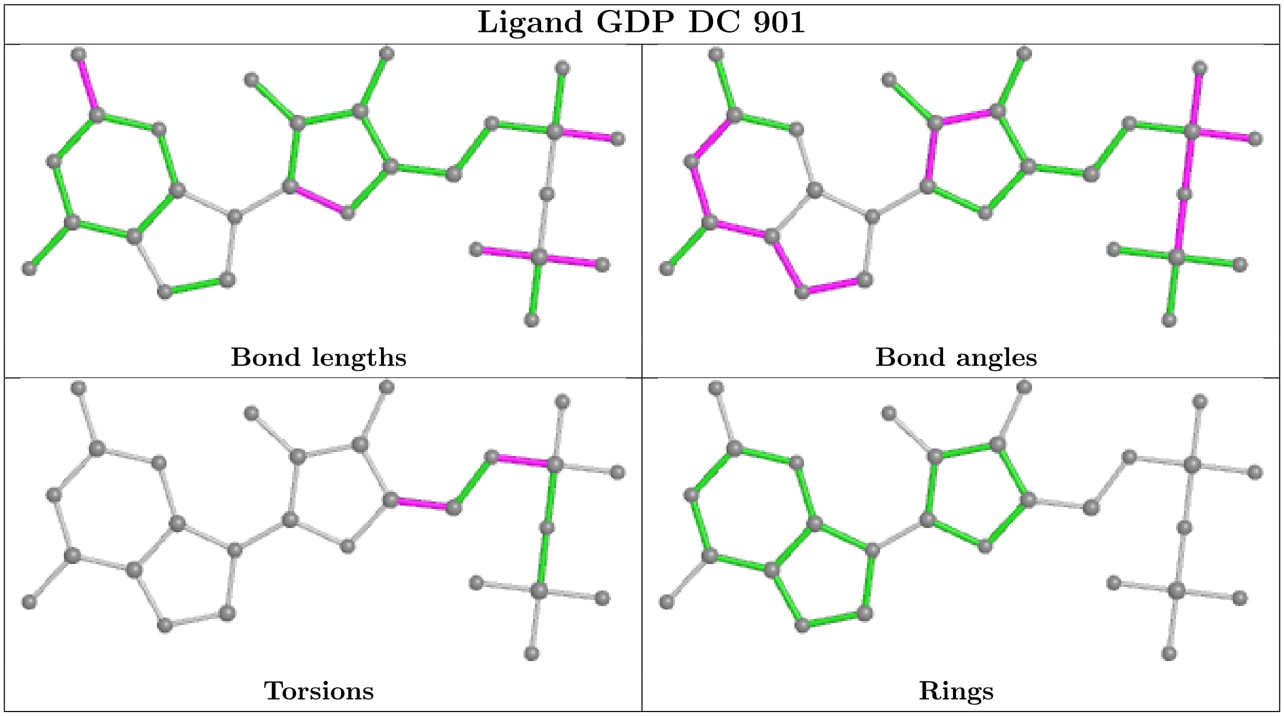
There are no ring outliers.

2 monomers are involved in 4 short contacts:

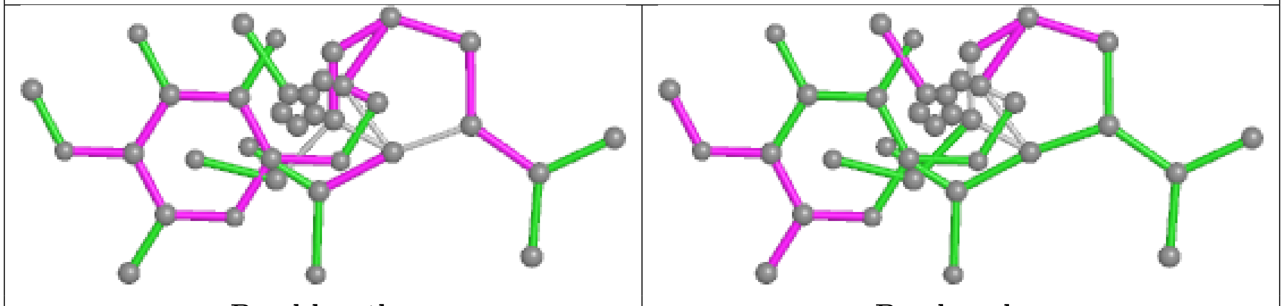
Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	DC	901	GDP	2	0
86	DC	903	SO1	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GDP DC 901

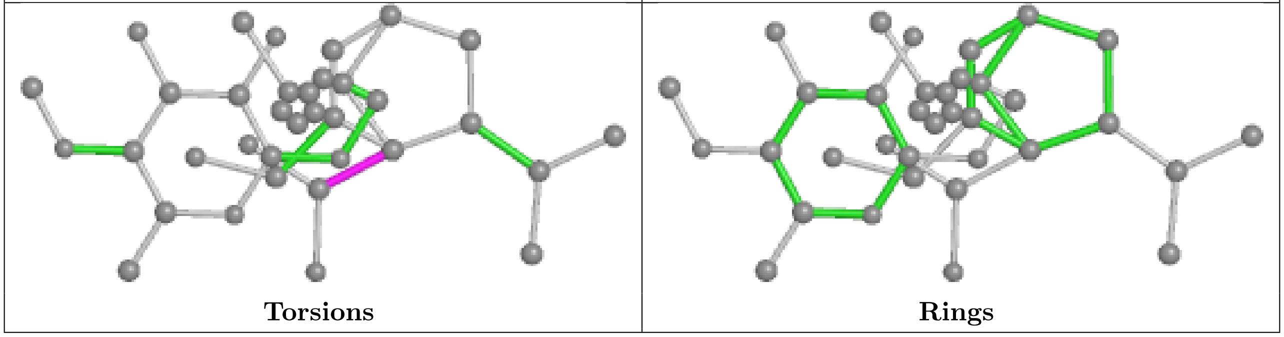


Ligand SO1 DC 903



Bond lengths

Bond angles



Torsions

Rings

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.

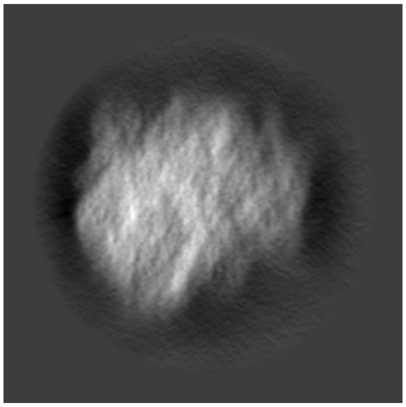
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-6645. These allow visual inspection of the internal detail of the map and identification of artifacts.

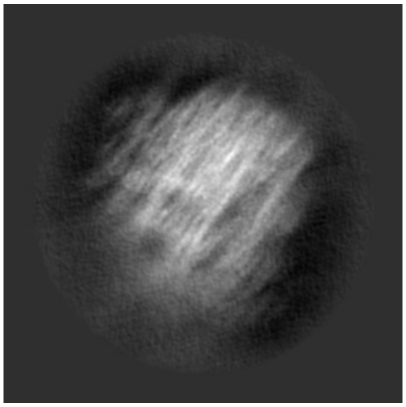
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

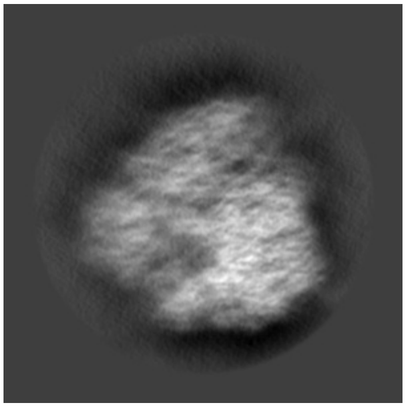
6.1.1 Primary map



X



Y

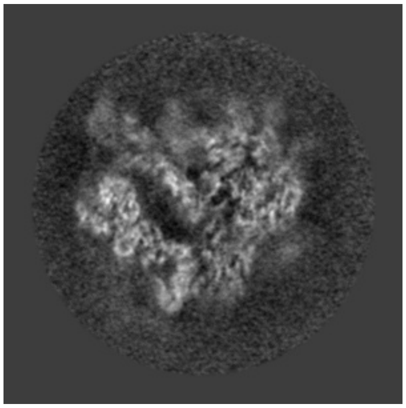


Z

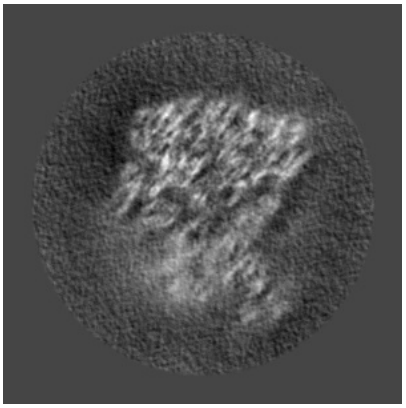
The images above show the map projected in three orthogonal directions.

6.2 Central slices

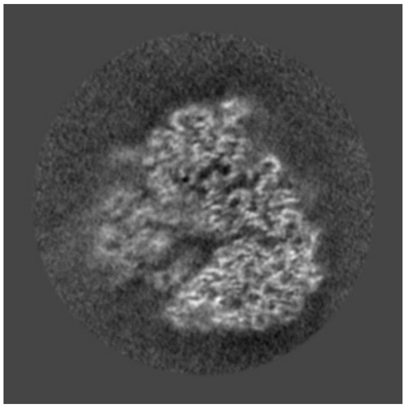
6.2.1 Primary map



X Index: 256



Y Index: 256

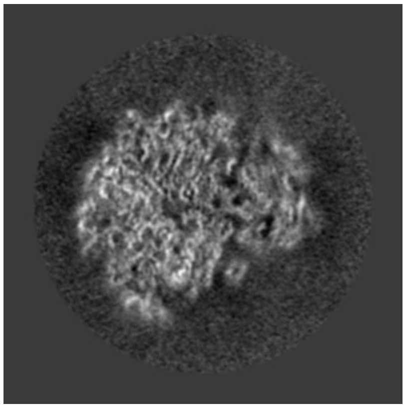


Z Index: 256

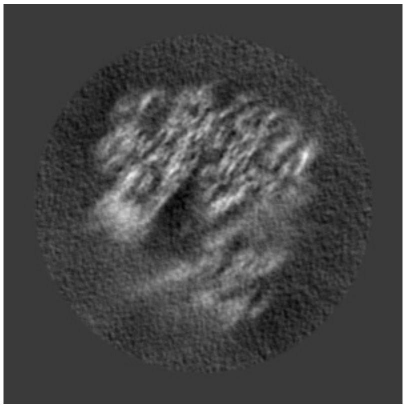
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices ⓘ

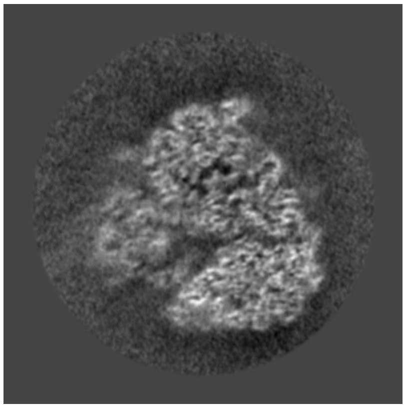
6.3.1 Primary map



X Index: 287



Y Index: 221

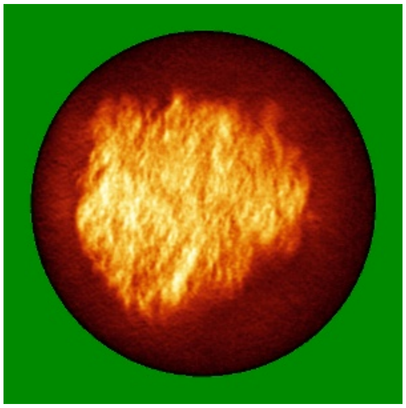


Z Index: 258

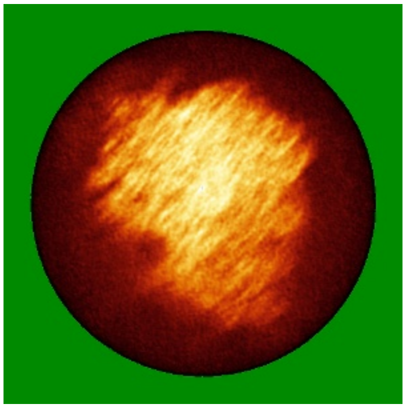
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

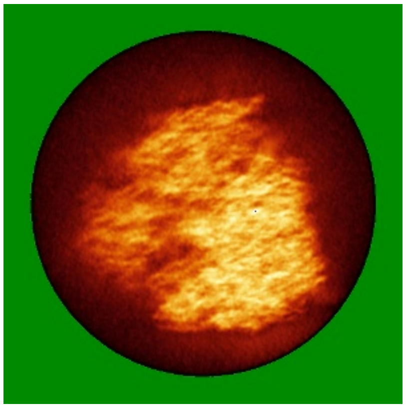
6.4.1 Primary map



X



Y

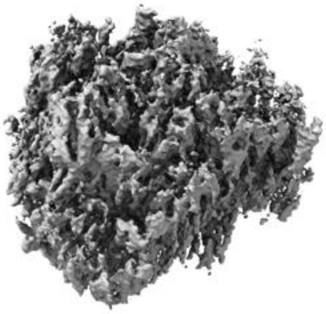


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

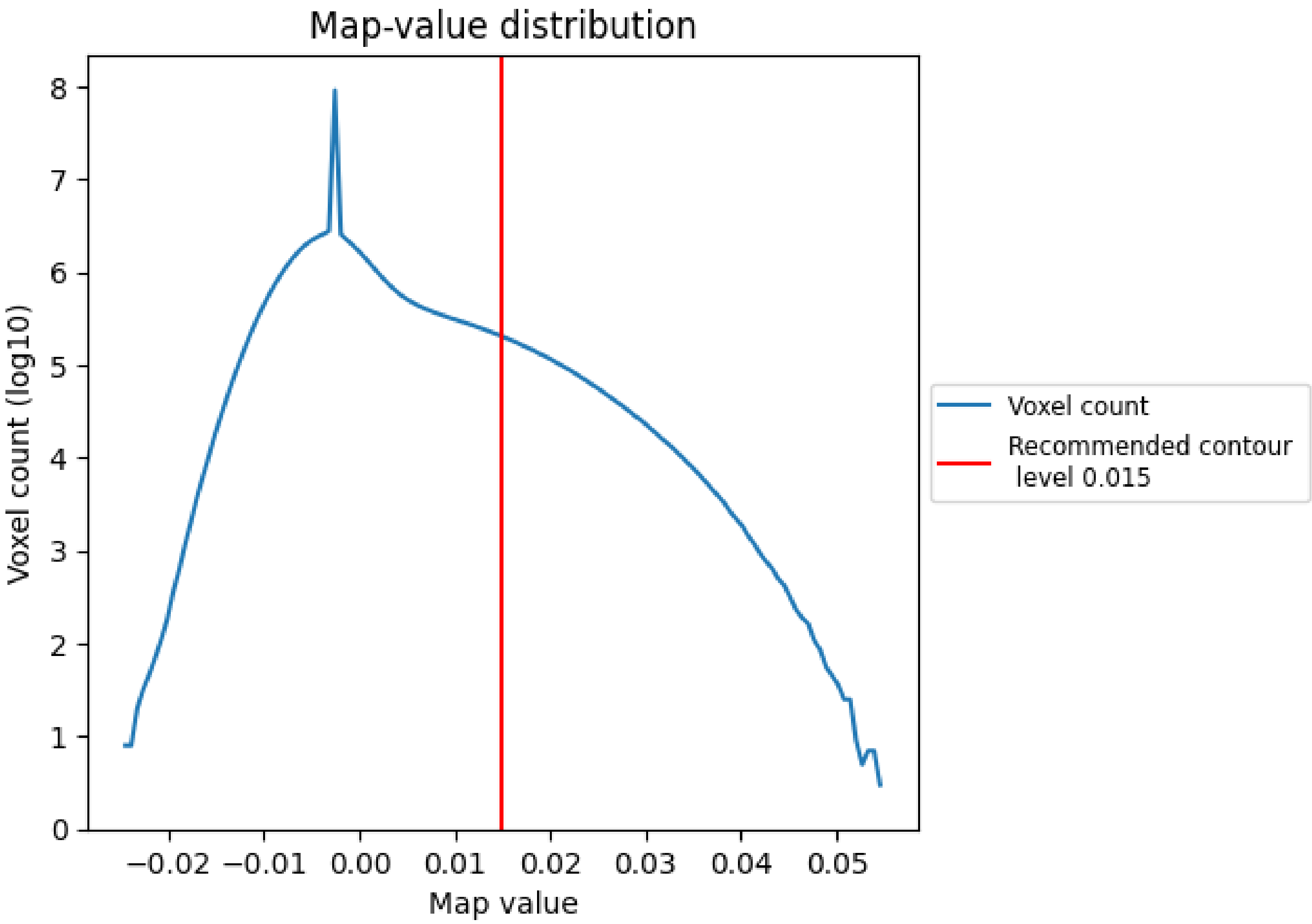
6.6 Mask visualisation (i)

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

7 Map analysis ⓘ

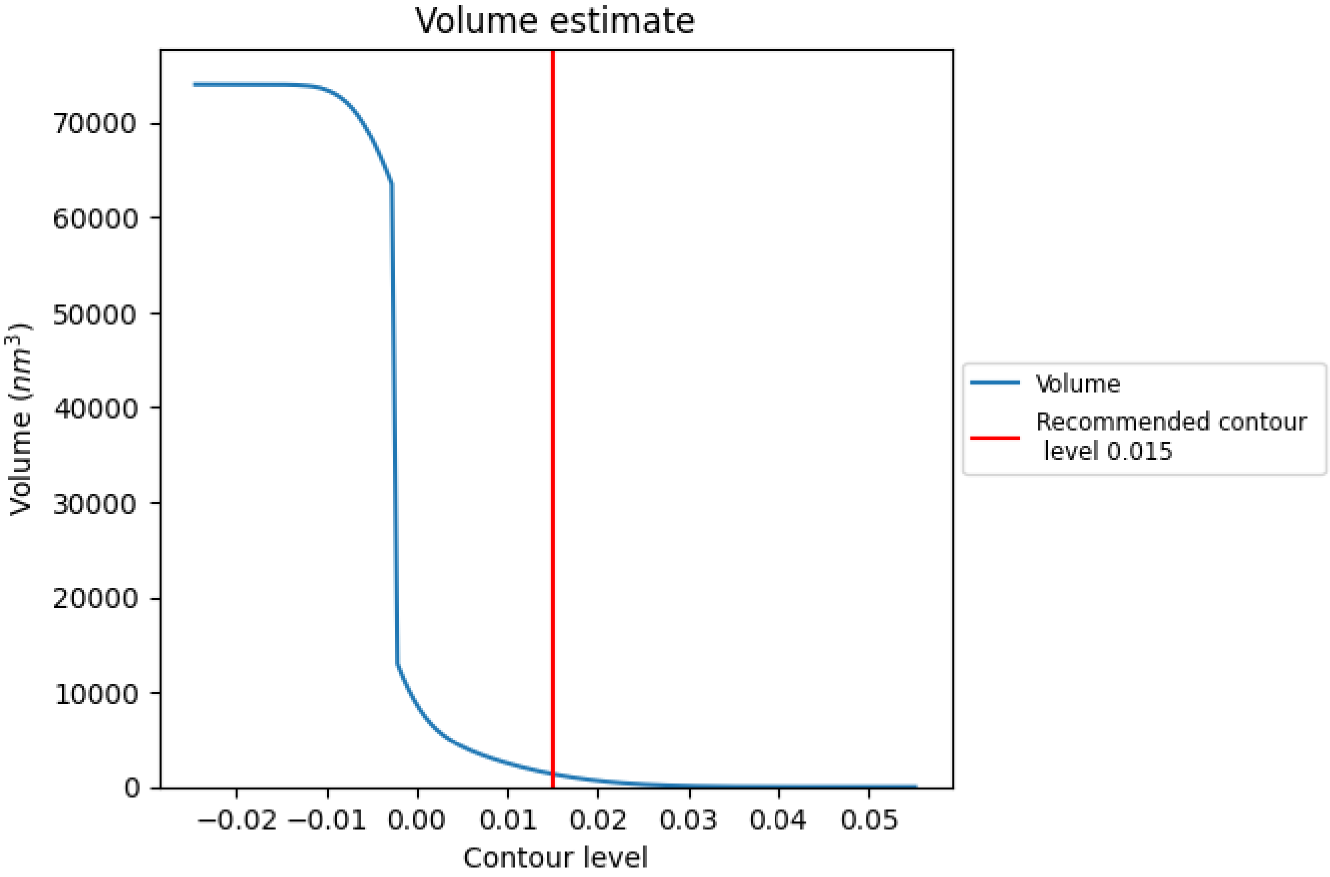
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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

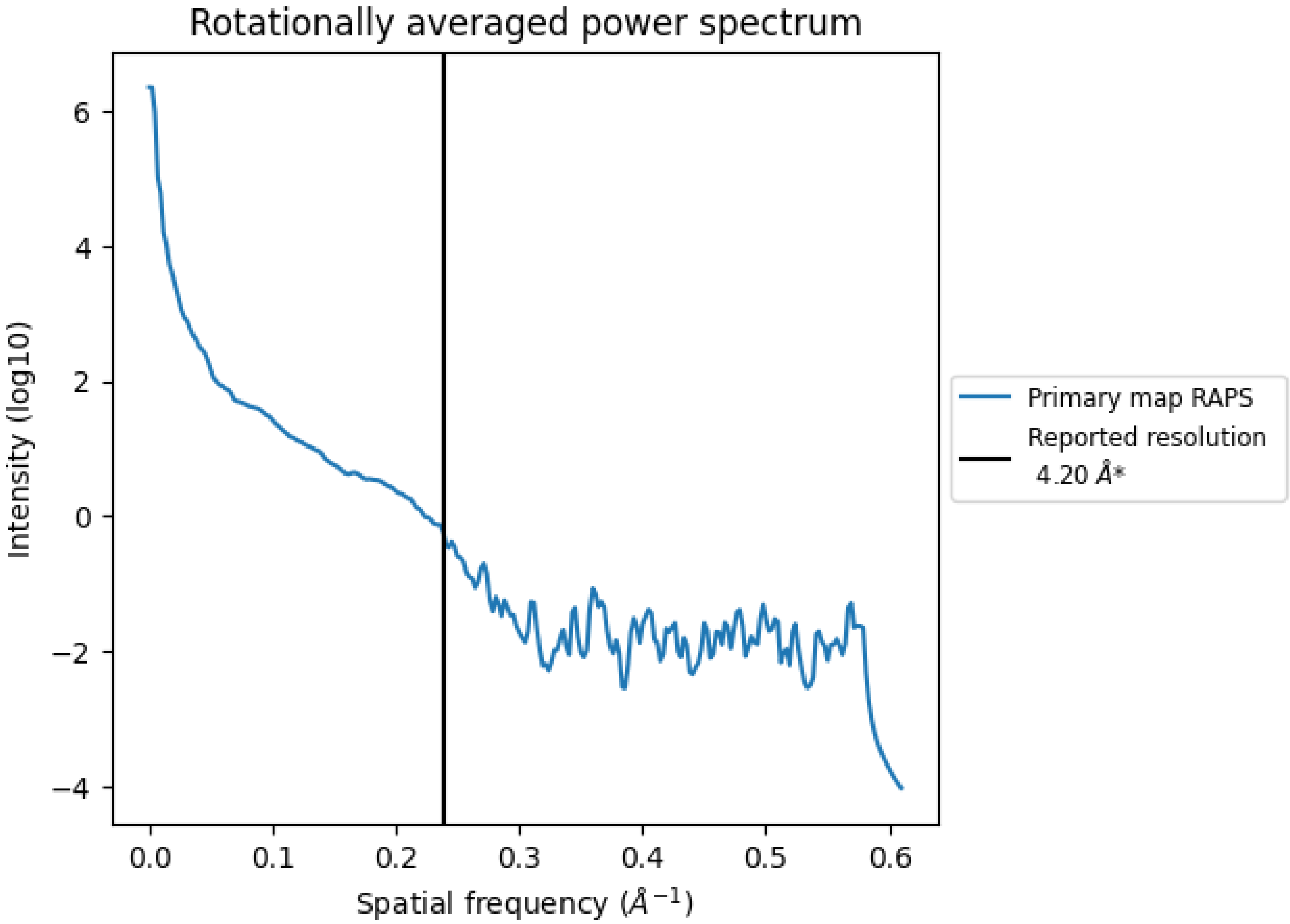
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 1368 nm^3; this corresponds to an approximate mass of 1236 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.238 $Å^{-1}$

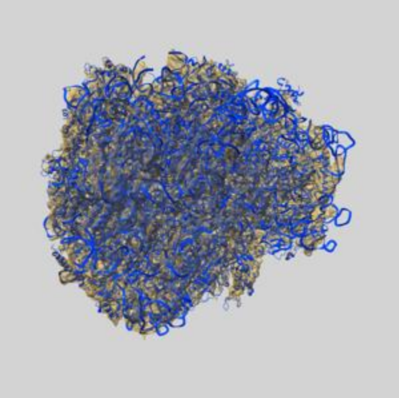
8 Fourier-Shell correlation ⓘ

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

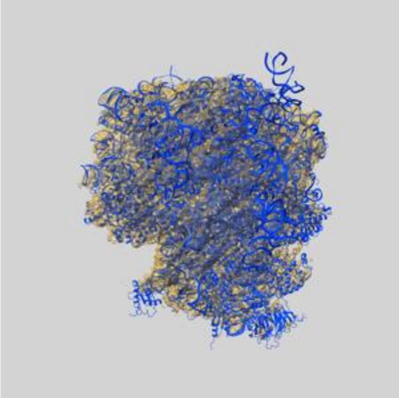
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-6645 and PDB model 5JUS. Per-residue inclusion information can be found in section 3 on page 21.

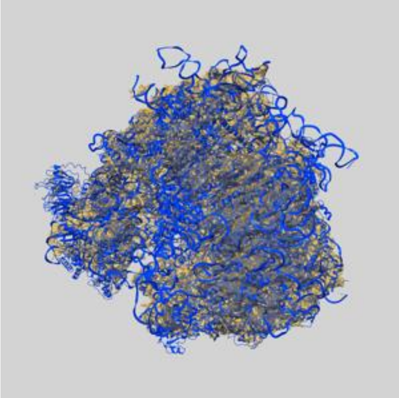
9.1 Map-model overlay



X



Y



Z

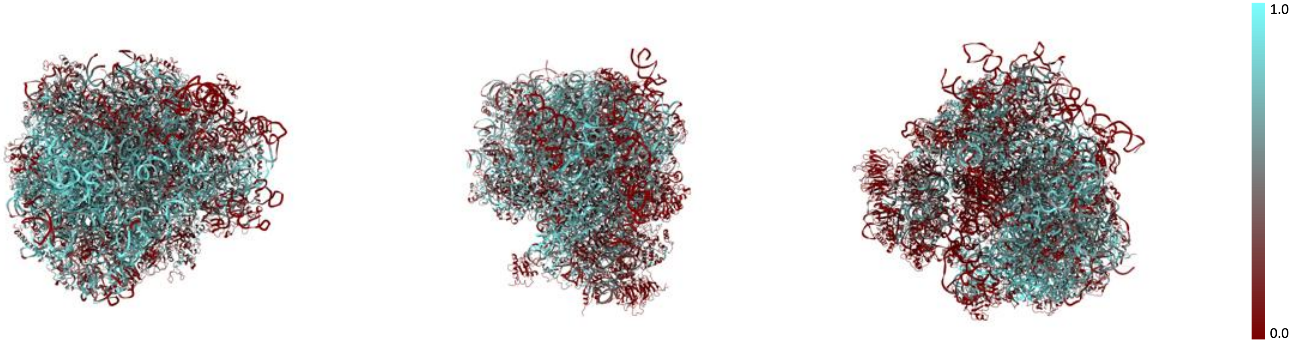
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model ⓘ

X Y Z

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

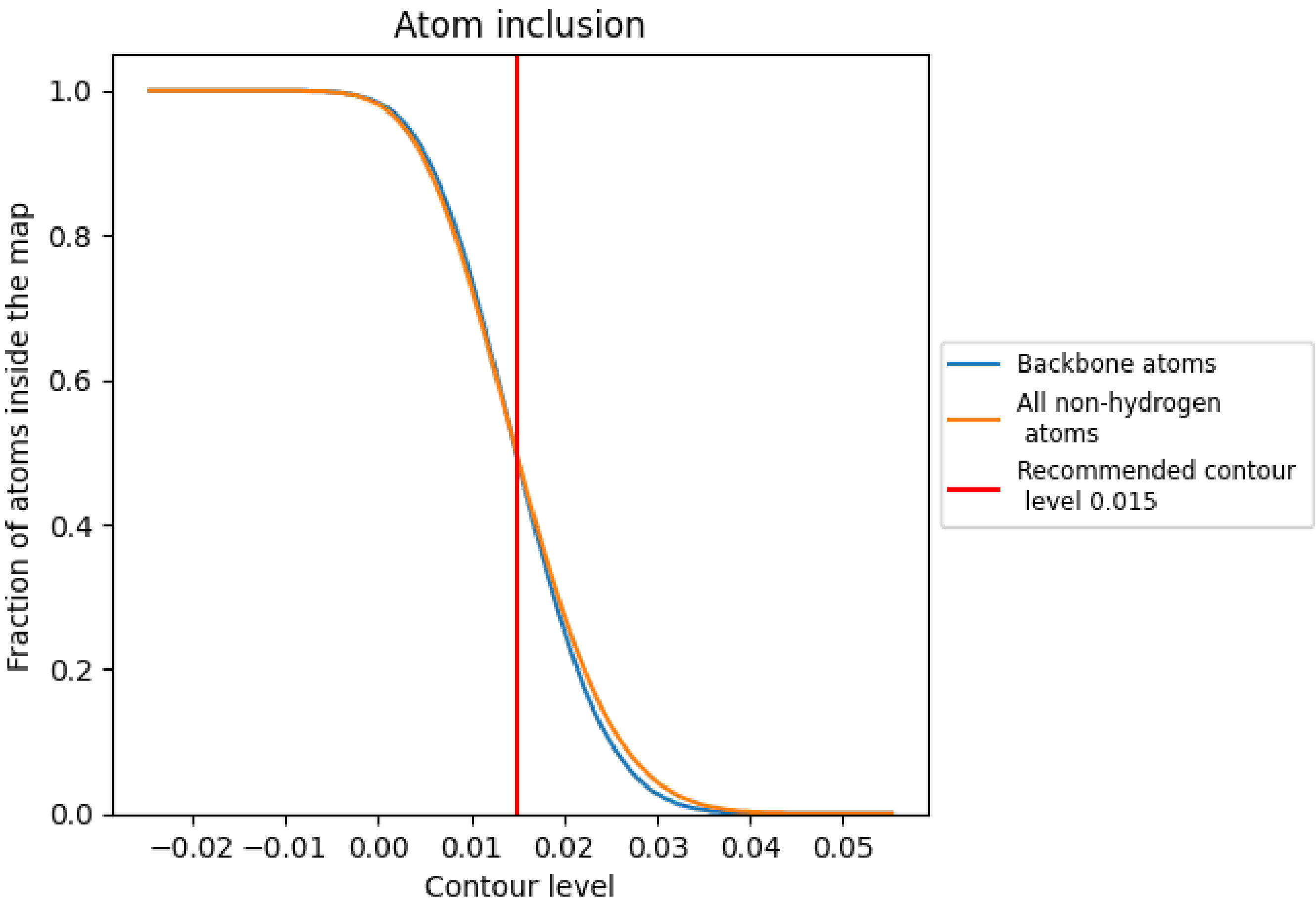
9.3 Atom inclusion mapped to coordinate model ⓘ



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).

9.4 Atom inclusion ⓘ



At the recommended contour level, 49% of all backbone atoms, 49% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4940	0.2100
A	0.4890	0.1870
AA	0.3890	0.2650
AB	0.2650	0.1660
AC	0.2640	0.1450
B	0.6930	0.2430
BA	0.5090	0.2440
BB	0.5820	0.2120
BC	0.2550	0.1610
C	0.6220	0.2320
CA	0.2000	0.2000
CB	0.1550	0.1440
CC	0.0320	0.0500
D	0.8630	0.2350
DA	0.5640	0.2180
DB	0.2030	0.1920
DC	0.3240	0.1850
E	0.0290	0.1090
EA	0.3060	0.1650
EB	0.0790	0.1560
EC	0.1000	0.0830
F	0.4860	0.2290
FA	0.5790	0.2680
FB	0.3700	0.1920
G	0.4470	0.2570
GA	0.5720	0.2360
GB	0.5620	0.1960
H	0.5190	0.2580
HA	0.6100	0.2070
HB	0.4860	0.1050
I	0.5650	0.1950
IA	0.4440	0.2540
IB	0.2370	0.1940
J	0.2930	0.2270
JA	0.6190	0.2830

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Chain	Atom inclusion	Q-score
JB	0.0180	0.0670
K	0.4350	0.2330
KA	0.2970	0.2550
KB	0.2790	0.1800
L	0.2930	0.1840
LA	0.4540	0.2080
LB	0.0080	0.0460
M	0.3220	0.2300
MA	0.2900	0.2020
MB	0.1540	0.1380
N	0.5280	0.2150
NA	0.5190	0.2510
NB	0.1230	0.1430
O	0.4570	0.1960
OA	0.4970	0.2240
OB	0.1350	0.1630
P	0.2850	0.1070
PA	0.0170	0.1330
PB	0.0530	0.1280
Q	0.6110	0.2470
QA	0.4640	0.2600
QB	0.1440	0.1430
R	0.4980	0.2340
RA	0.6660	0.2650
RB	0.1520	0.1520
S	0.4270	0.2240
SA	0.0240	0.0800
SB	0.2130	0.2110
T	0.4000	0.2400
TA	0.7620	0.2350
TB	0.2740	0.2240
U	0.4690	0.2450
UA	0.4280	0.2330
UB	0.1640	0.2150
V	0.5590	0.2570
VA	0.3580	0.1540
VB	0.2890	0.1760
W	0.3160	0.2080
WA	0.0400	0.1300
WB	0.0460	0.1330
X	0.3870	0.2450
XA	0.2230	0.2070

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Chain	Atom inclusion	Q-score
XB	🟥 0.0210	🟥 0.0390
Y	⬜ 0.5290	🟫 0.2540
YA	🟥 0.0040	🟥 0.0120
YB	🟫 0.3650	🟫 0.2160
Z	🟫 0.2290	🟫 0.1930
ZA	🟫 0.3090	🟫 0.2340
ZB	🟫 0.2930	🟫 0.2090