



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:38 AM UTC

PDB ID : 5JUO / pdb_00005juo
EMDB ID : EMD-6643
Title : Saccharomyces cerevisiae 80S ribosome bound with elongation factor eEF2-GDP-sordarin and Taura Syndrome Virus IRES, Structure I (fully rotated 40S subunit)
Authors : Abeyrathne, P.; Koh, C.S.; Grant, T.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2016-05-10
Resolution : 4.00 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

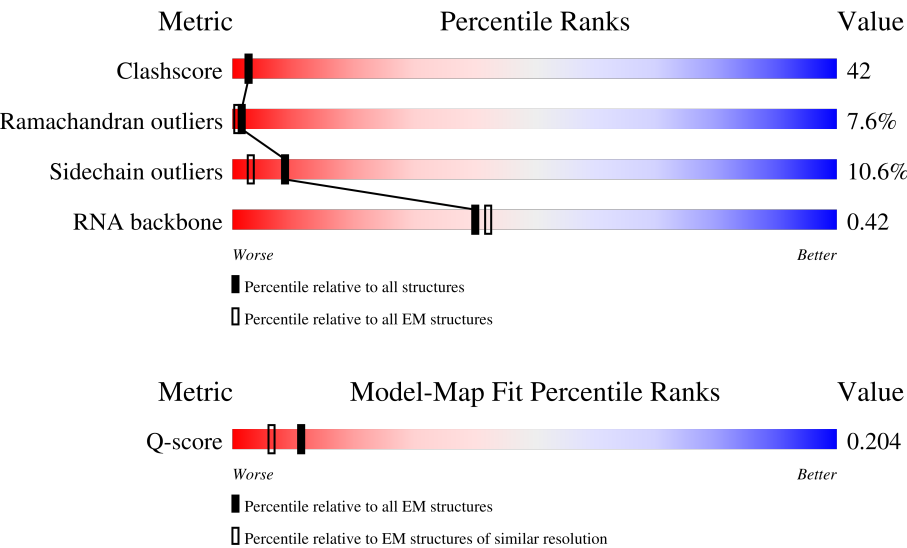
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.00 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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 $\leq 5\%$. 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	38% 25% 59% 15% ..
2	B	3396	19% 20% 59% 17% ..
3	C	158	20% 19% 61% 18% .

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Mol	Chain	Length	Quality of chain
4	D	121	
5	E	217	
6	F	254	
7	G	387	
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	

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Mol	Chain	Length	Quality of chain
29	CA	142	
30	DA	127	
31	EA	136	
32	FA	149	
33	GA	59	
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	

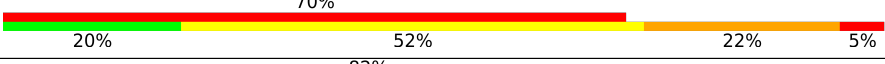
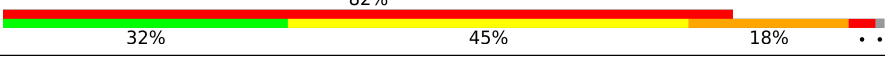
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Mol	Chain	Length	Quality of chain
54	BB	261	
55	CB	225	
56	DB	236	
57	EB	190	
58	FB	200	
59	GB	197	
60	HB	105	
61	IB	156	
62	JB	143	
63	KB	151	
64	LB	137	
65	MB	142	
66	NB	143	
67	OB	136	
68	PB	146	
69	QB	144	
70	RB	121	
71	SB	87	
72	TB	130	
73	UB	145	
74	VB	135	
75	WB	108	
76	XB	119	
77	YB	82	
78	ZB	67	

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Mol	Chain	Length	Quality of chain
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 215363 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	3309	Total	C	N	O	P	0	0
			70288	31354	12595	23030	3309		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	193	Total	C	N	O	S	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
			1611	1033	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		0	0
			1481	951	265	265			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

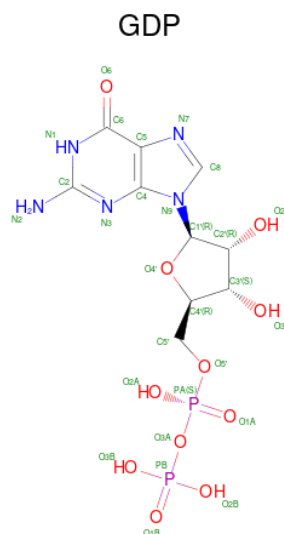
- Molecule 82 is a protein called yeast eEF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	DC	841	Total	C	N	O	S	0	0
			6561	4168	1125	1238	30		

- Molecule 83 is a RNA chain called IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	EC	198	Total	C	N	O	P	0	0
			4105	1826	718	1363	198		

- Molecule 84 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

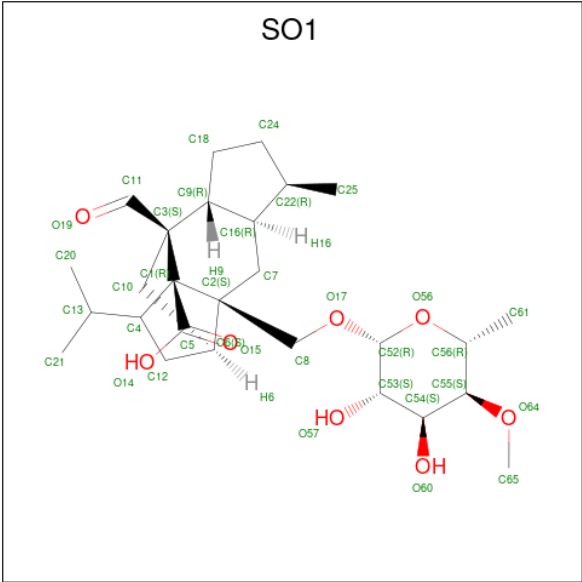


Mol	Chain	Residues	Atoms					AltConf
84	DC	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

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



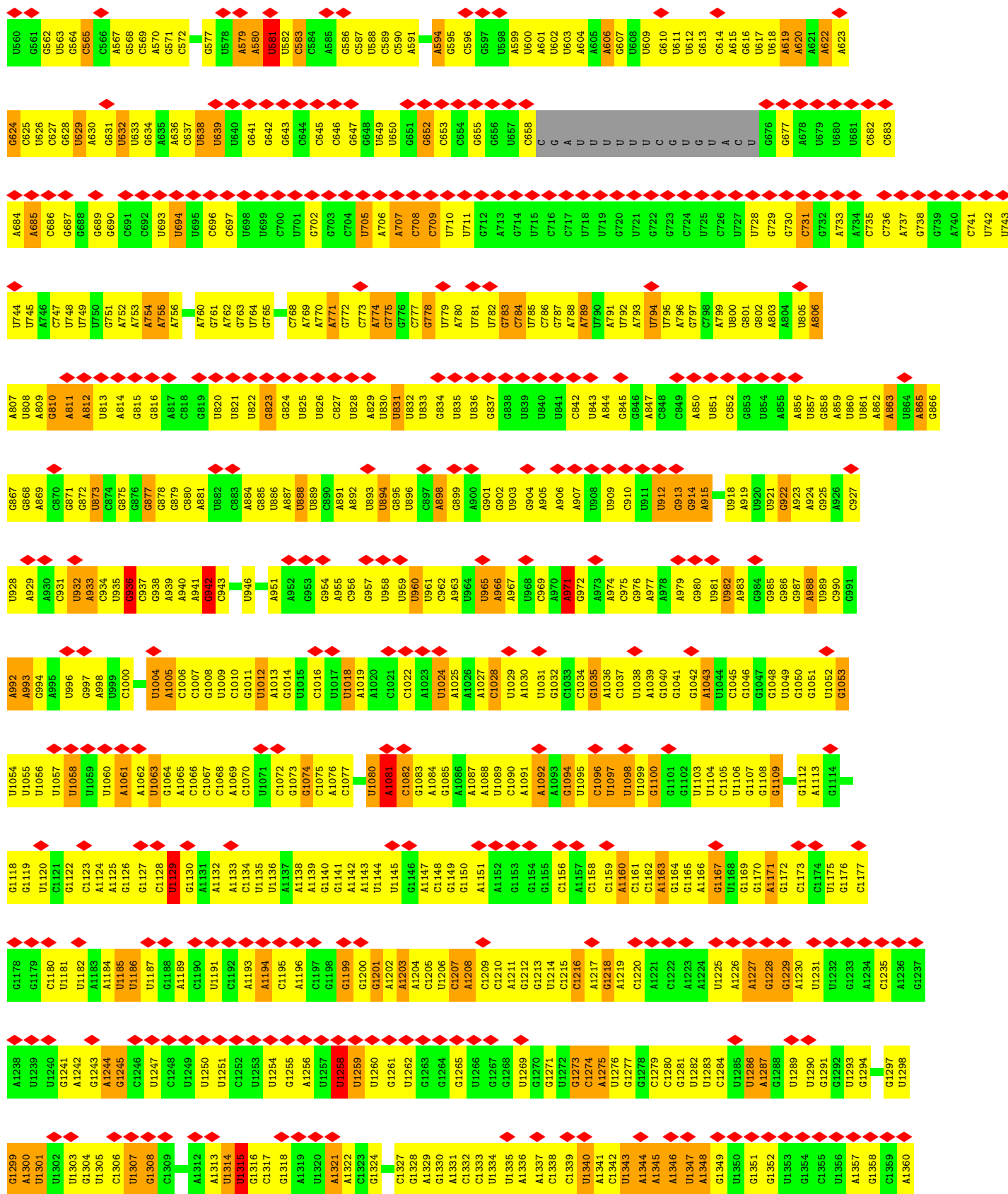
Mol	Chain	Residues	Atoms			AltConf
86	DC	1	Total	C	O	0
			35	27	8	

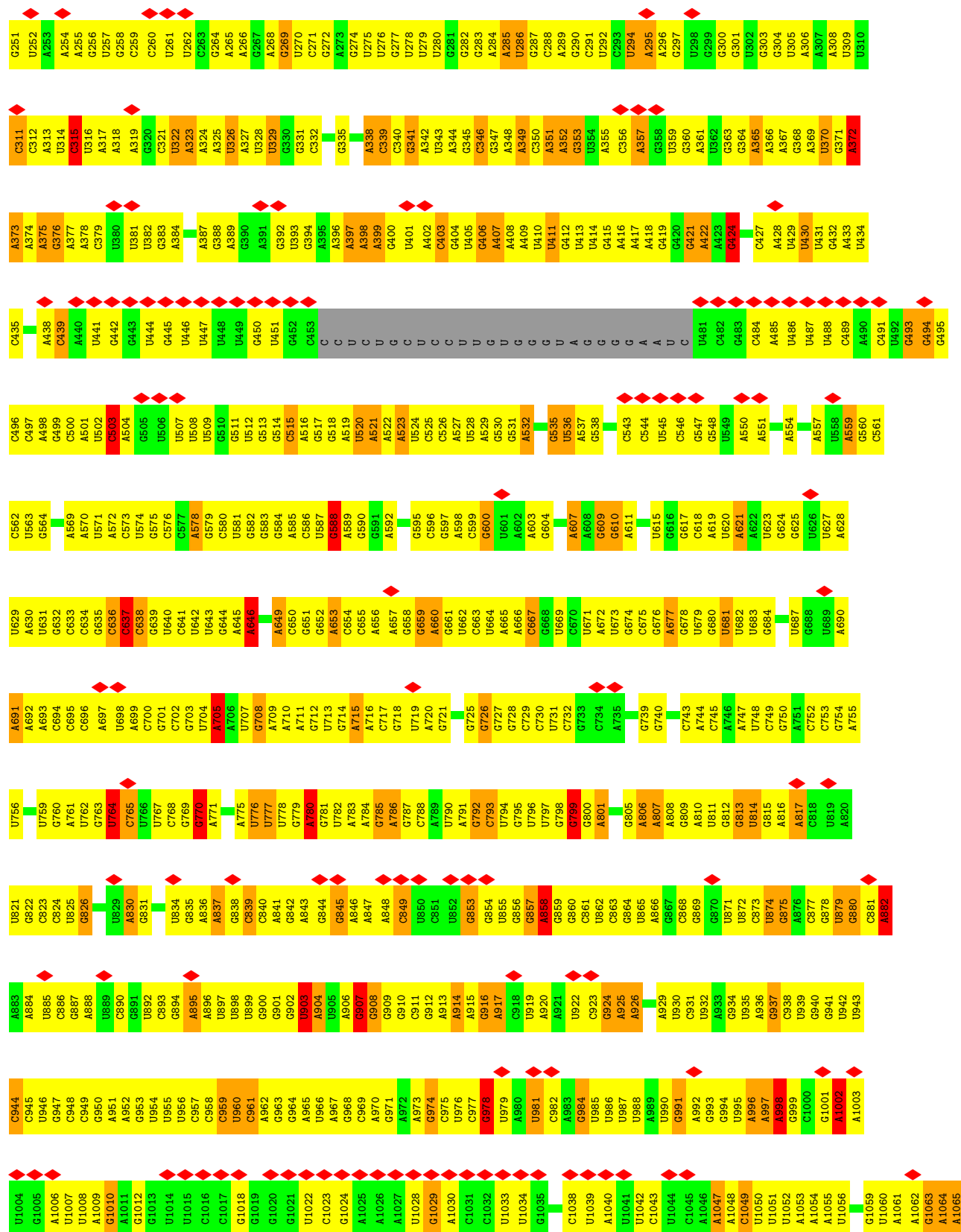
3 Residue-property plots

These plots are drawn for all protein, RNA, 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

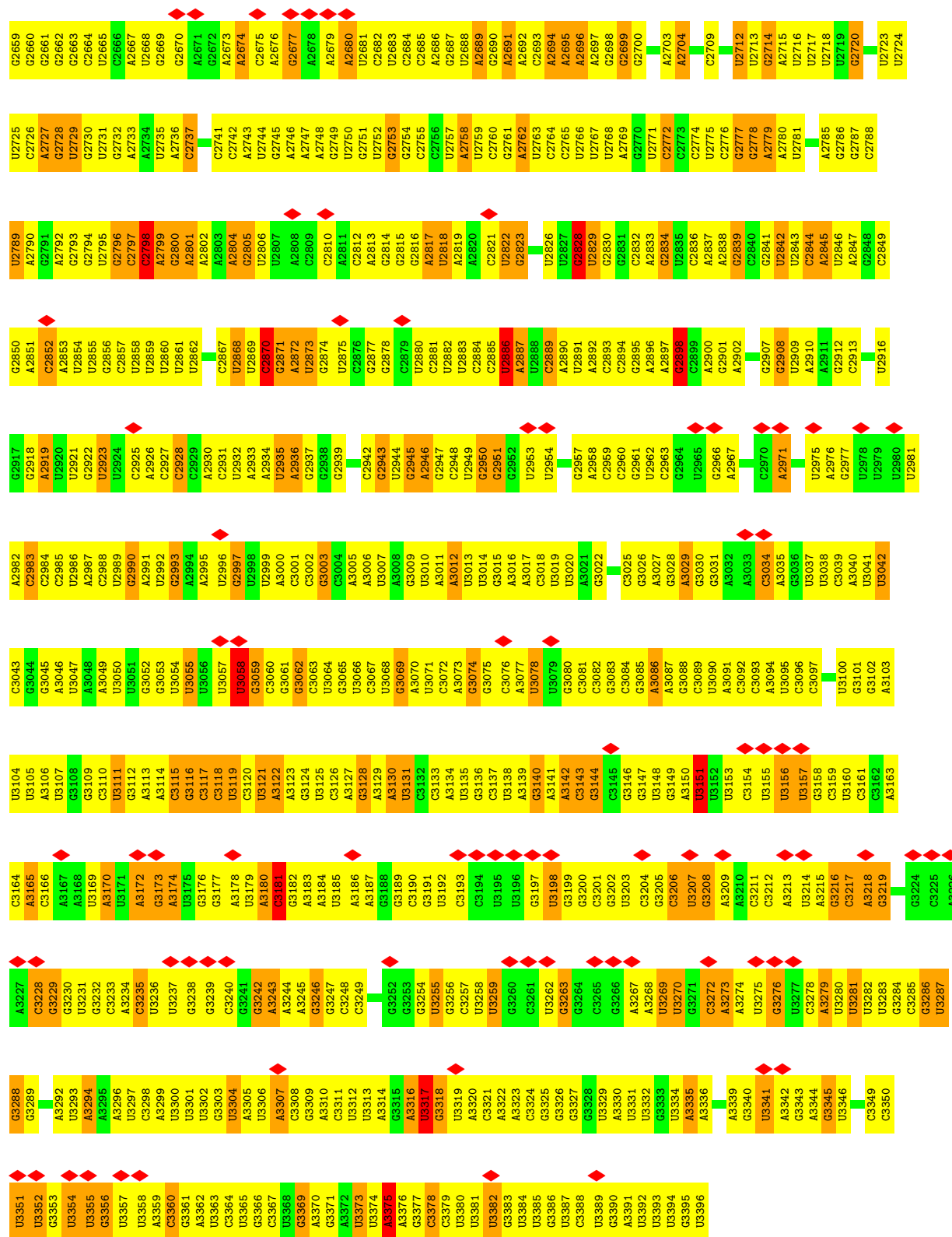


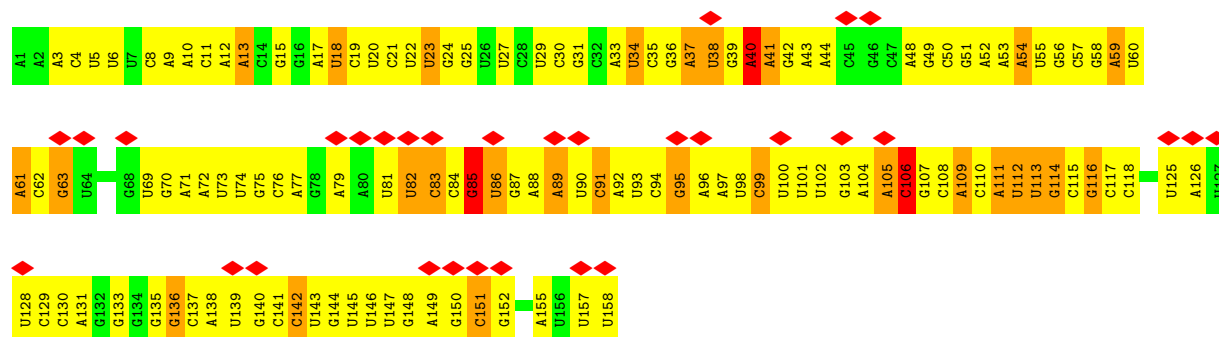




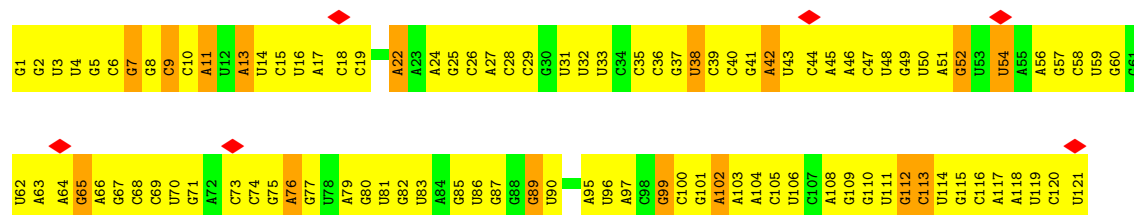
C1805	A1806	G1807	A1808	G1809	A1810	G1811	G1812	A1813	A1814	A1815	A1816	G1817	U1818	U1819	U1820	U1821	C1822	A1823	U1824	G1825	C1826	C1827	A1828	G1829	G1830	G1831	C1832	G1833	U1834	A1835	C1836	U1837	G1838	A1839	U1840	A1841	A1842	C1843	C1844	G1845	C1846	A1847	G1848	C1849	A1850	G1851	G1852	U1853	C1854	U1855	C1856	C1857	A1858	A1859	G1860	G1861	U1862	G1863	A1864
C1745	U1746	G1747	G1748	A1749	U1750	G1751	A1752	G1753	G1754	G1755	C1756	A1757	G1758	G1759	A1760	C1761	C1762	U1763	U1764	U1765	G1766	C1767	A1768	C1769	G1770	C1771	C1772	C1773	C1774	G1775	G1776	U1777	G1778	C1779	G1780	C1781	G1782	U1783	G1784	U1785	G1786	A1787	G1788	G1789	G1790	C1791	G1792	C1793	G1794	U1795	G1796	A1797	G1798	U1799	A1800	U1801	C1802	A1803	
C1685	U1686	U1687	U1688	C1689	C1690	U1691	U1692	C1693	U1694	A1695	A1696	A1697	C1698	A1699	G1700	C1701	U1702	U1703	A1704	U1705	C1706	A1707	C1708	C1709	C1710	C1711	G1712	G1713	U1714	A1715	U1716	U1717	G1718	G1719	U1720	U1721	U1722	U1723	U1724	C1725	C1726	G1727	U1728	A1729	G1730	A1731	U1732	G1733	G1734	G1735	G1736	U1737	C1738	U1739	U1740	A1741	U1742	G1743	G1744
G1623	G1624	A1625	U1626	C1627	C1628	U1629	U1630	C1631	A1632	U1636	A1637	A1638	C1639	G1640	U1641	A1642	A1643	C1644	U1645	C1646	U1647	A1648	A1649	U1650	U1651	G1652	C1653	A1654	G1655	A1656	C1657	G1658	U1659	U1660	G1661	G1662	C1663	C1664	C1665	G1666	A1667	G1668	C1669	C1670	C1671	U1672	G1673	G1674	G1675	U1676	G1677	G1678	U1679	U1682	A1683	U1684			
A1558	A1559	G1560	G1561	C1562	C1563	U1564	G1565	A1566	U1567	U1568	U1569	U1570	U1571	A1572	U1573	C1574	A1575	G1576	G1577	A1580	C1581	A1582	A1583	U1587	A1588	A1589	G1590	G1591	G1592	A1593	A1594	U1595	C1596	C1597	G1598	G1599	U1600	U1601	A1602	A1603	G1604	U1605	U1606	U1607	C1608	A1609	G1610	G1611	G1612	A1613	C1614	C1615	U1616	U1617	A1619	U1620			
C1497	A1498	C1499	G1500	U1501	C1502	A1503	A1504	C1505	A1506	G1507	C1508	A1509	G1510	U1511	U1512	G1513	G1514	G1517	U1518	A1519	G1520	G1521	U1522	U1523	A1524	G1525	C1526	G1527	G1528	A1529	C1530	C1531	C1532	U1533	A1534	A1535	G1536	A1537	G1538	A1539	U1540	U1541	G1542	G1543	G1544	A1545	A1546	G1547	C1548	U1549	C1550	C1551	G1552	U1553	U1554	U1555	C1556	A1557	
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G1375	C1376	U1377	U1378	C1379	G1380	A1381	U1384	C1385	A1386	G1387	U1388	U1389	A1390	C1391	G1392	A1393	A1394	G1395	C1396	C1397	U1398	A1399	G1400	A1401	G1404	U1405	A1406	A1407	G1408	G1409	U1410	C1411	G1412	G1413	G1414	U1415	C1416	G1417	A1418	A1419	C1420	G1421	G1422	C1423	C1424	U1425	C1426	U1427	A1428	G1429	U1430	A1431	C1432	A1433	G1434	U1435	U1436		
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C1255	G1256	C1257	U1258	A1259	A1260	G1261	G1262	A1263	G1264	U1265	G1266	U1267	G1268	U1269	A1270	C1271	C1272	A1273	A1274	C1275	C1276	C1277	A1278	C1279	C1280	G1281	G1282	C1283	C1284	G1285	A1286	A1287	U1288	G1289	A1290	A1291	C1292	U1293	A1294	G1295	C1296	C1297	C1298	U1299	G1300	A1301	A1302	A1303	A1304	U1305	G1306	C1307	A1308	U1309	G1310	G1311	C1312	G1313	C1314
C1192	A1193	G1194	A1195	C1196	U1197	C1198	C1199	A1200	C1201	A1202	A1203	A1204	A1205	U1208	G1209	U1210	U1211	A1212	G1213	U1214	U1215	C1219	U1220	A1221	G1222	A1223	C1224	A1225	G1226	C1227	C1228	G1229	G1230	A1231	G1232	G1233	G1234	U1235	G1236	G1237	C1238	C1239	A1240	U1241	G1242	A1243	U1244	A1245	G1246	U1247	C1248	G1249	G1250	A1251	A1252	U1253	C1254		
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G1066	U1067	C1068	G1072	U1073	U1074	A1075	C1076	U1077	U1078	A1079	A1080	U1081	U1082	G1083	A1084	A1085	C1091	C1092	A1093	U1094	U1095	U1096	G1097	A1098	A1099	U1100	G1101	A1102	A1103	G1104	A1105	C1106	C1107	U1108	U1109	U1110	U1111	A1112	A1113	U1114	G1115	G1116	G1117	A1118	C1119	A1120	U1121	U1122	U1123	U1124	U1125	G1126	G1127	U1128	A1129	A1130	G1131		



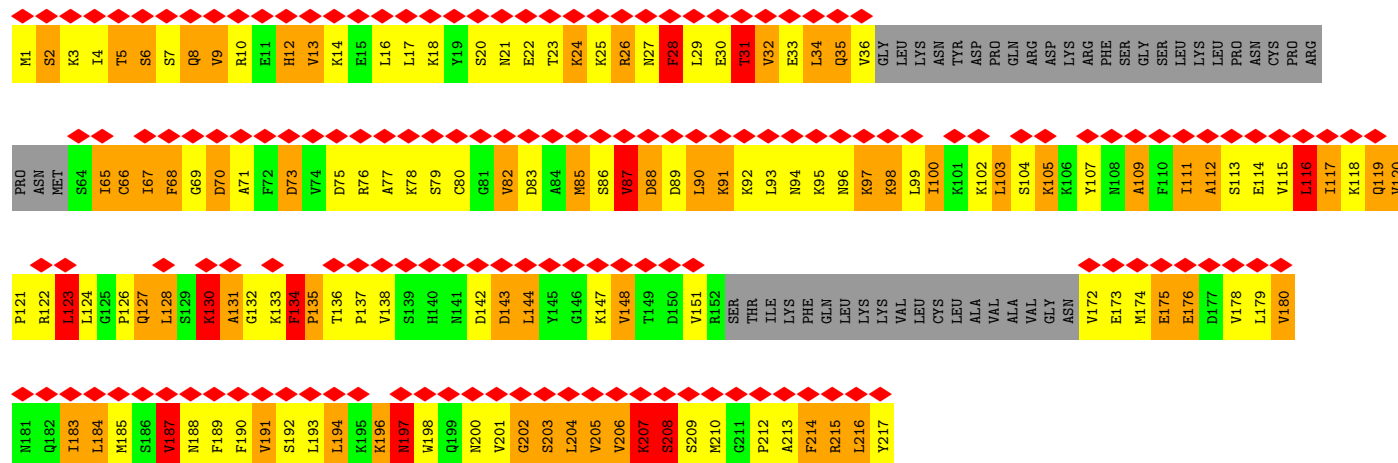




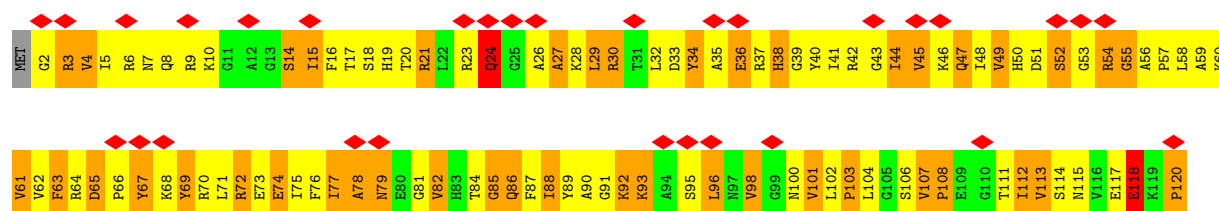
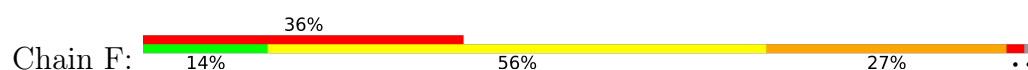
• Molecule 4: 5S ribosomal RNA

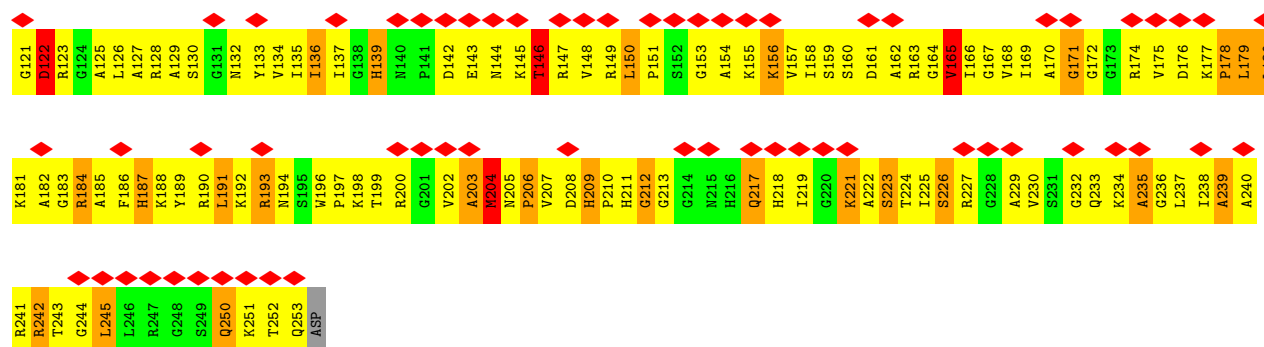


• Molecule 5: uL1 (yeast L1)

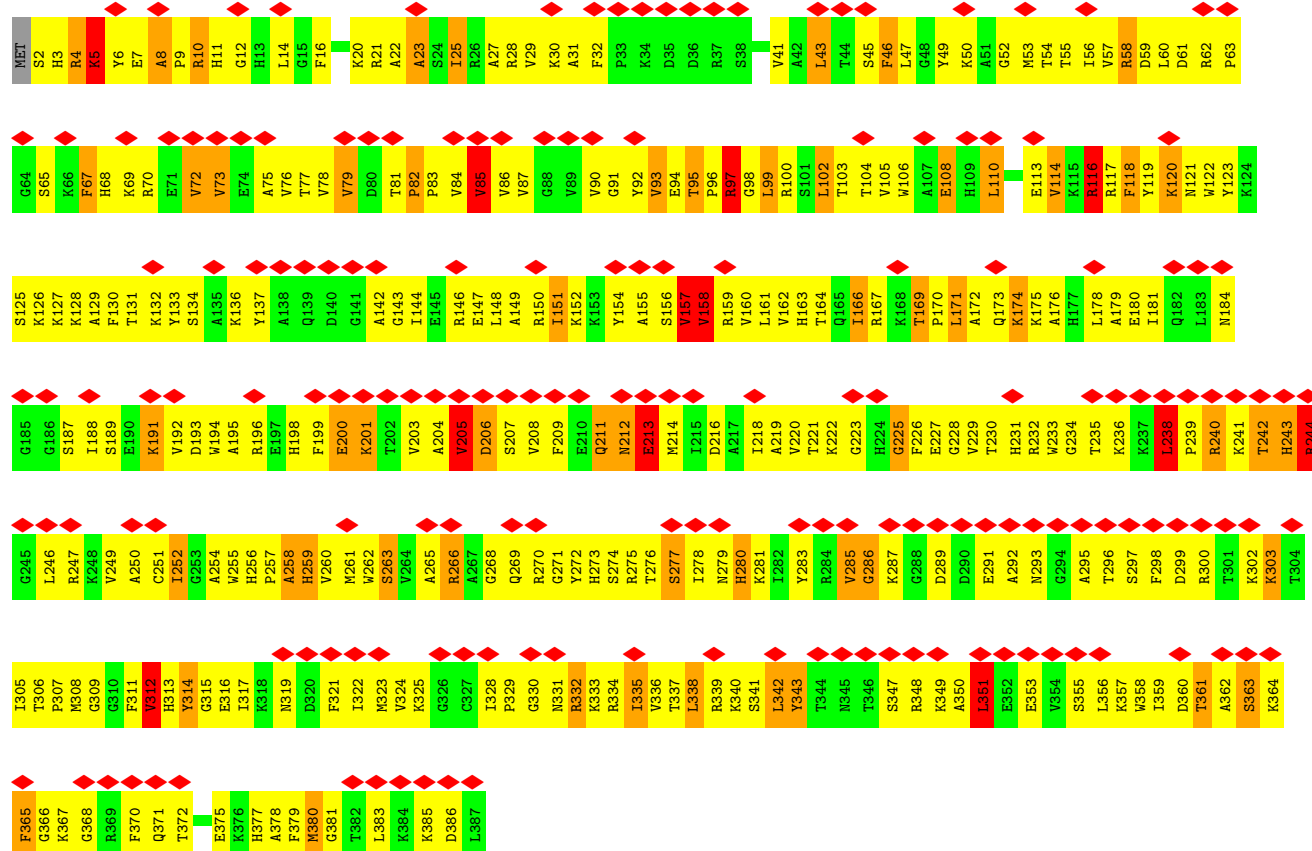


• Molecule 6: uL2 (yeast L2)

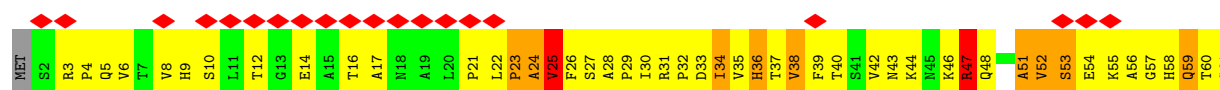


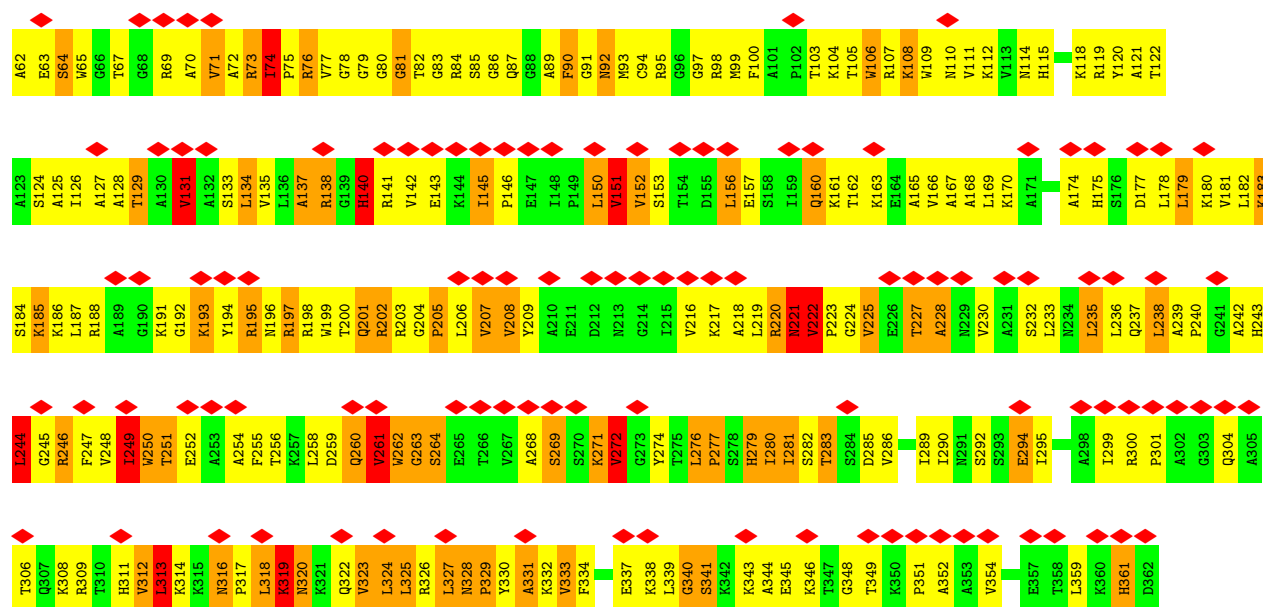


• Molecule 7: uL3 (yeast L3)

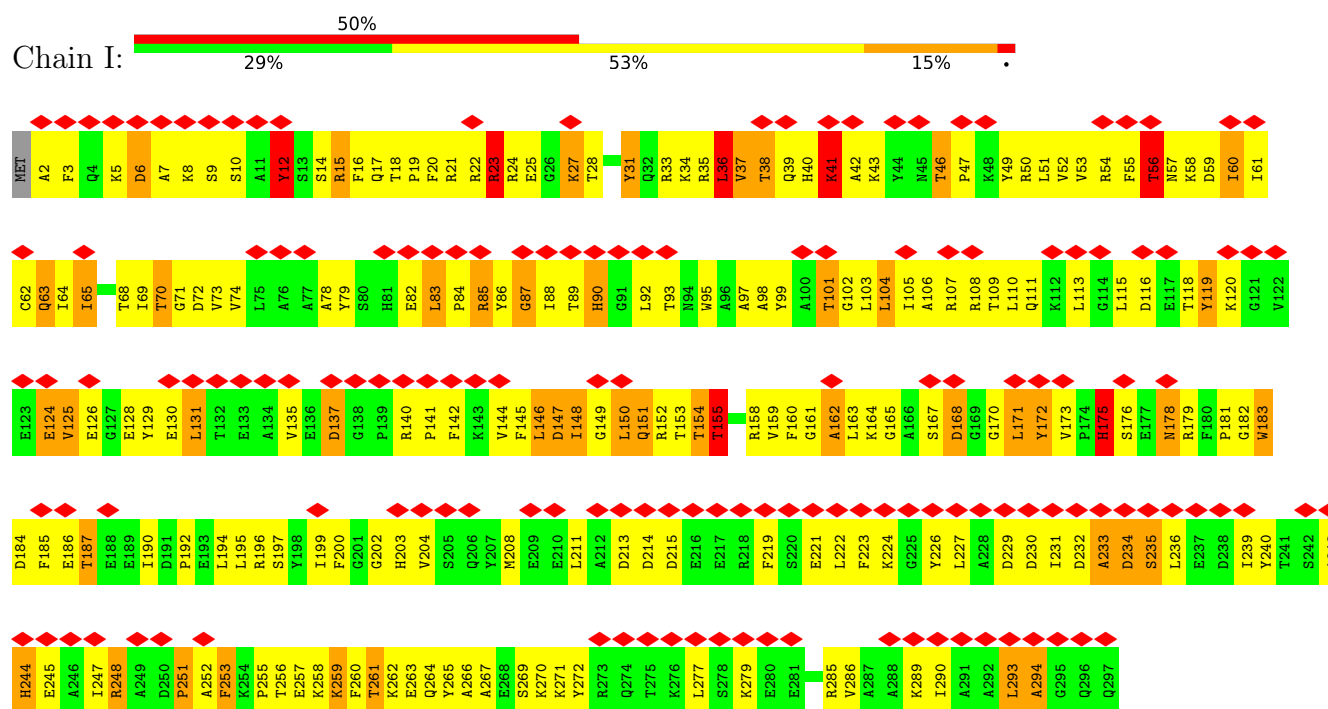


• Molecule 8: uL4 (yeast L4)

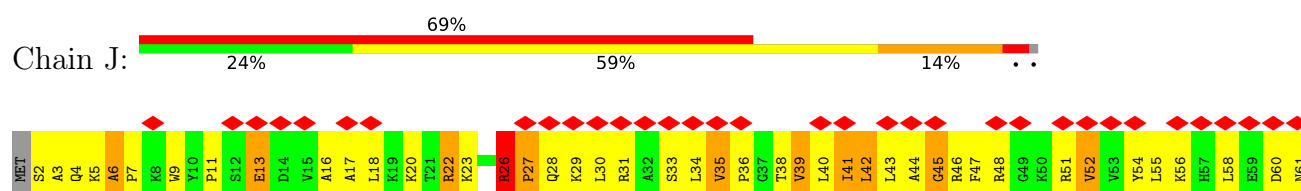


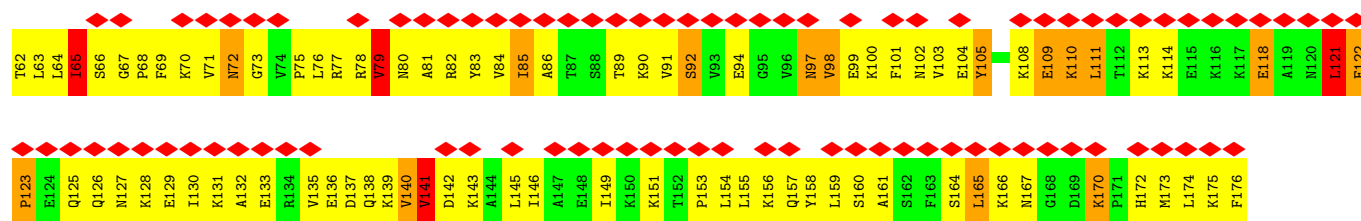


• Molecule 9: uL18 (yeast L5)

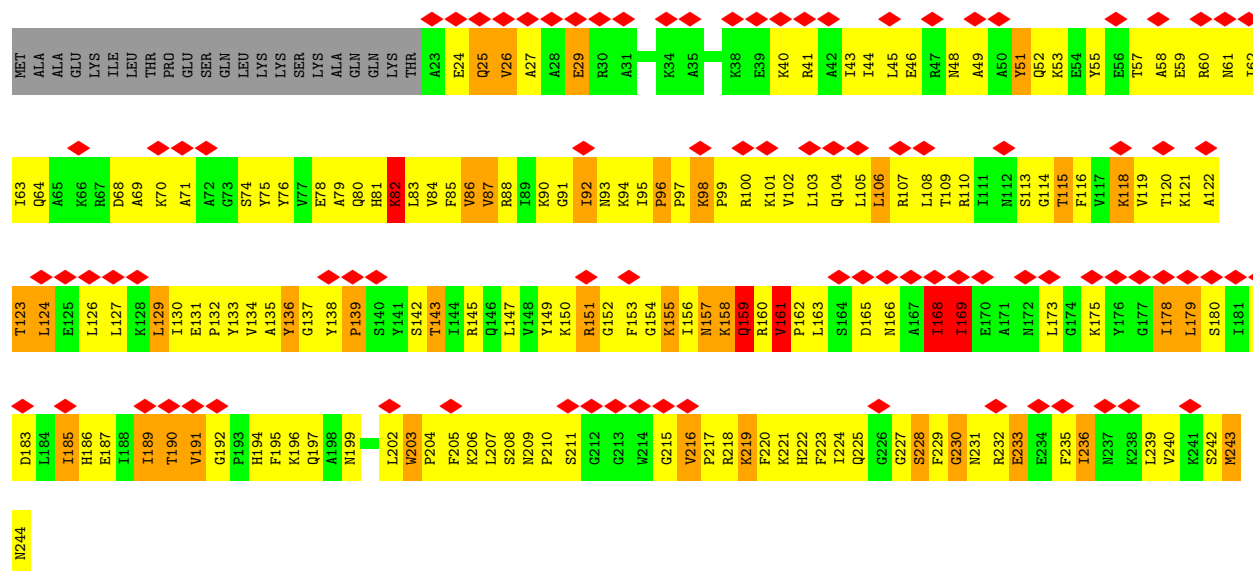


• Molecule 10: eL6 (yeast L6)

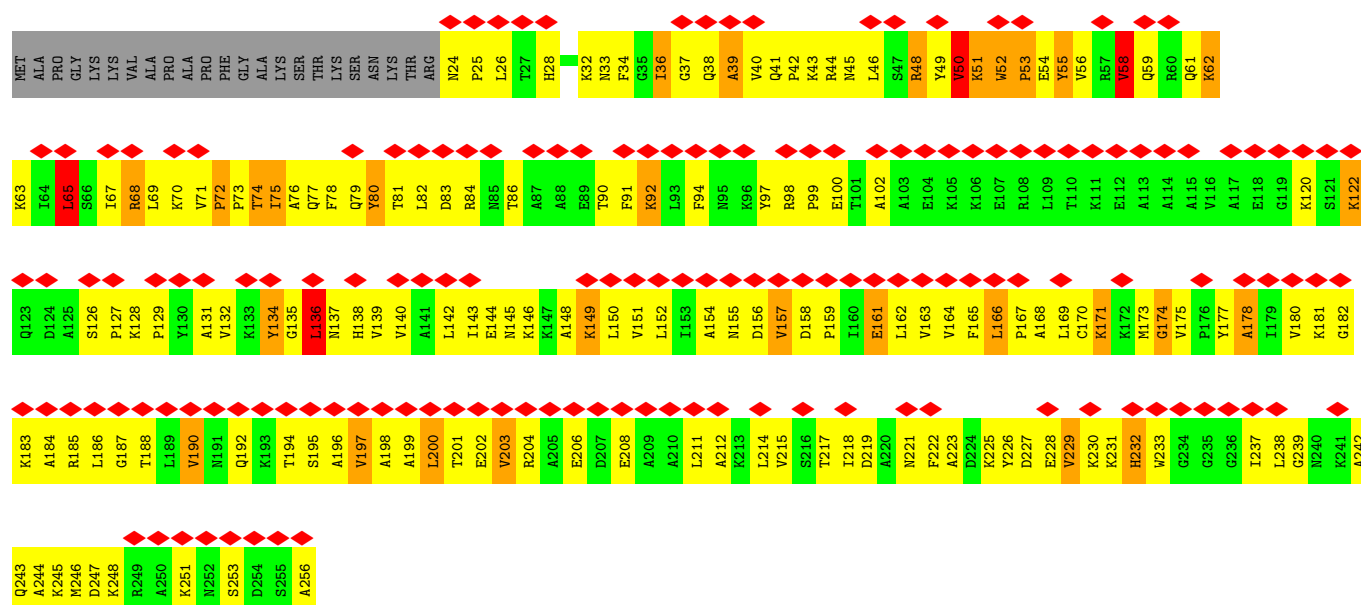




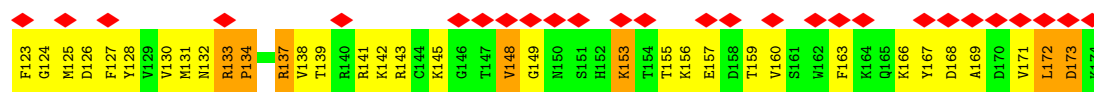
• Molecule 11: uL30 (yeast L7)



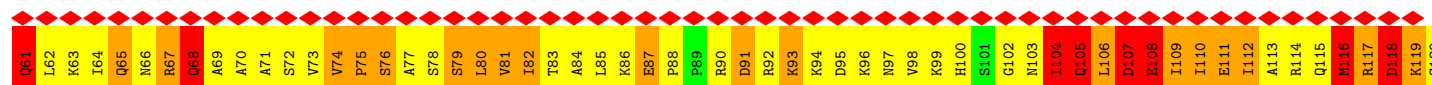
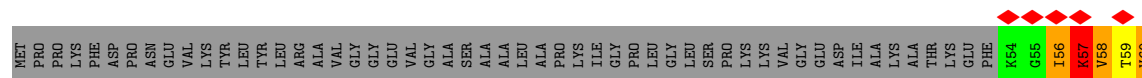
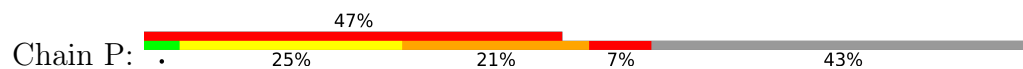
• Molecule 12: eL8 (yeast L8)



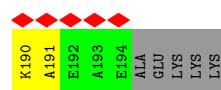
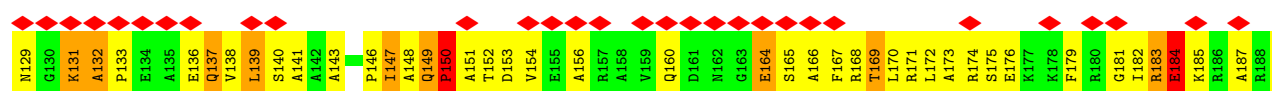
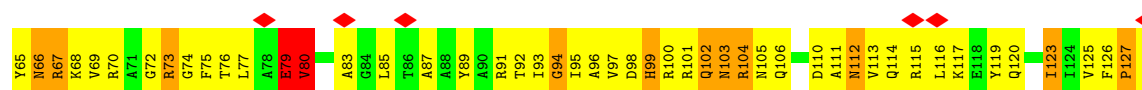
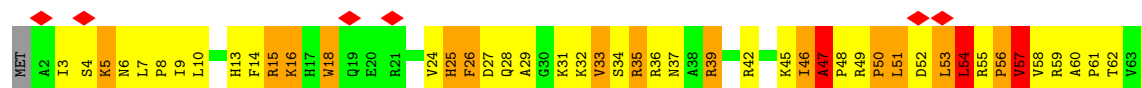




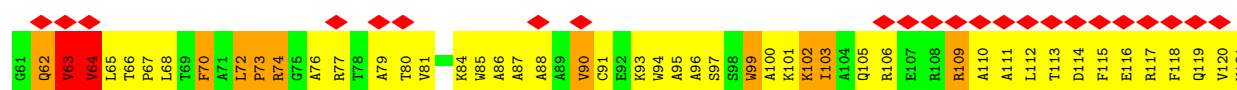
• Molecule 16: uL11 (yeast L12)

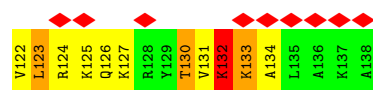


• Molecule 17: eL13 (yeast L13)

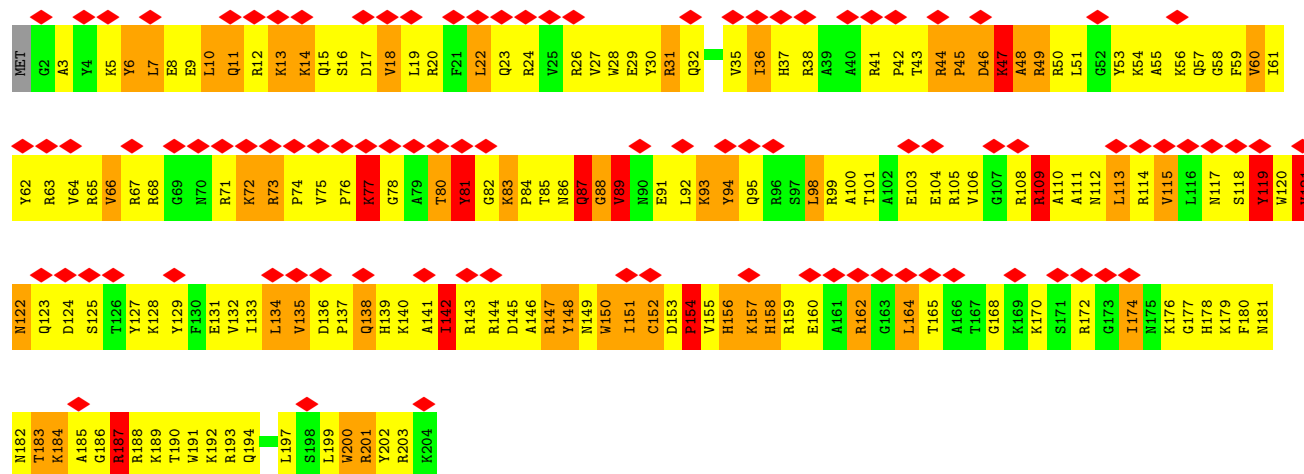
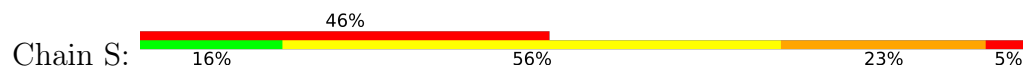


• Molecule 18: eL14 (yeast L14)

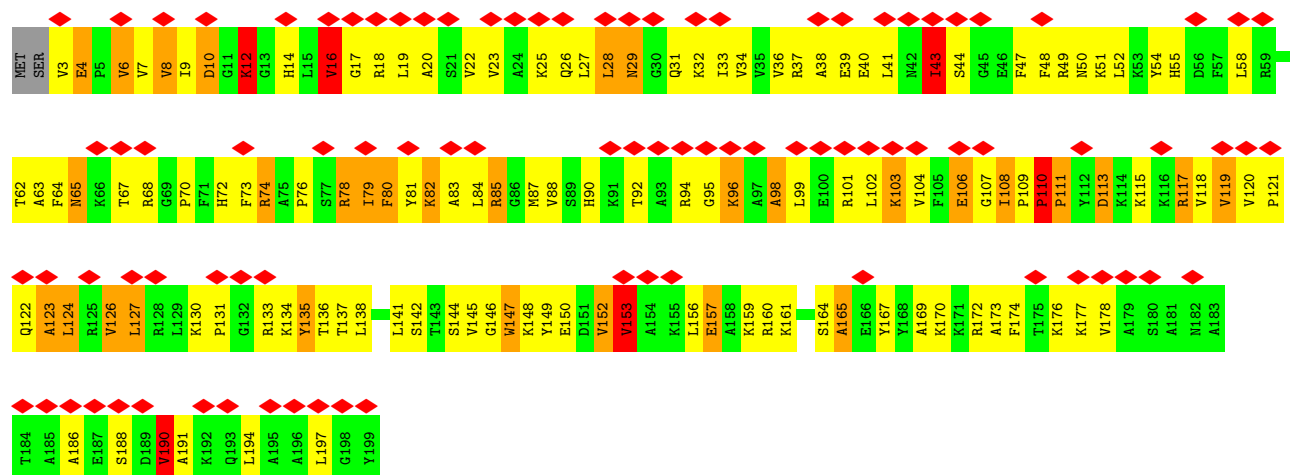




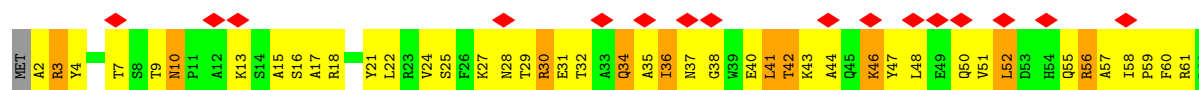
• Molecule 19: eL15 (yeast L15)

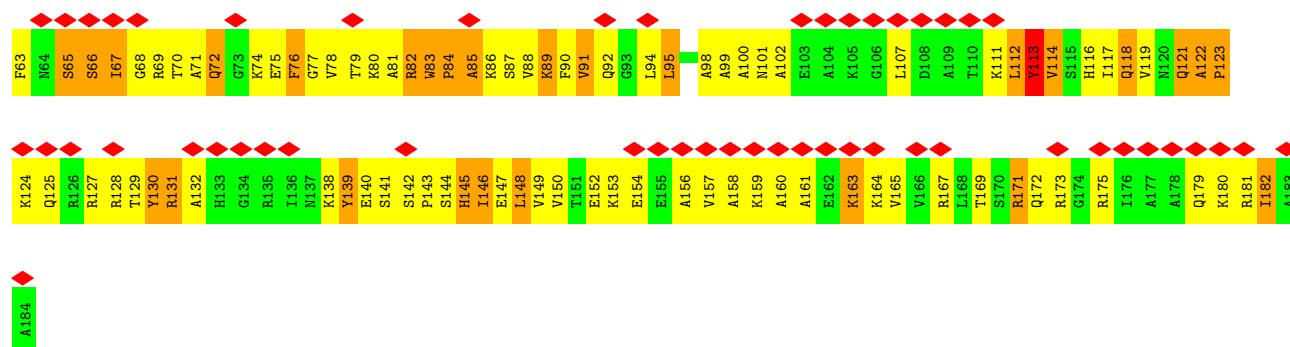


• Molecule 20: uL13 (yeast L16)

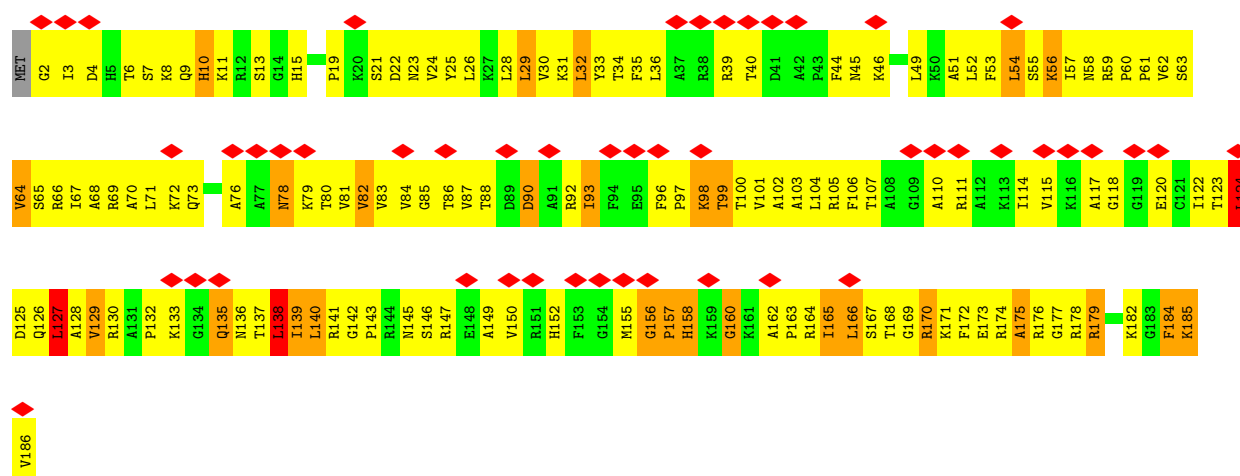


• Molecule 21: uL22 (yeast L17)

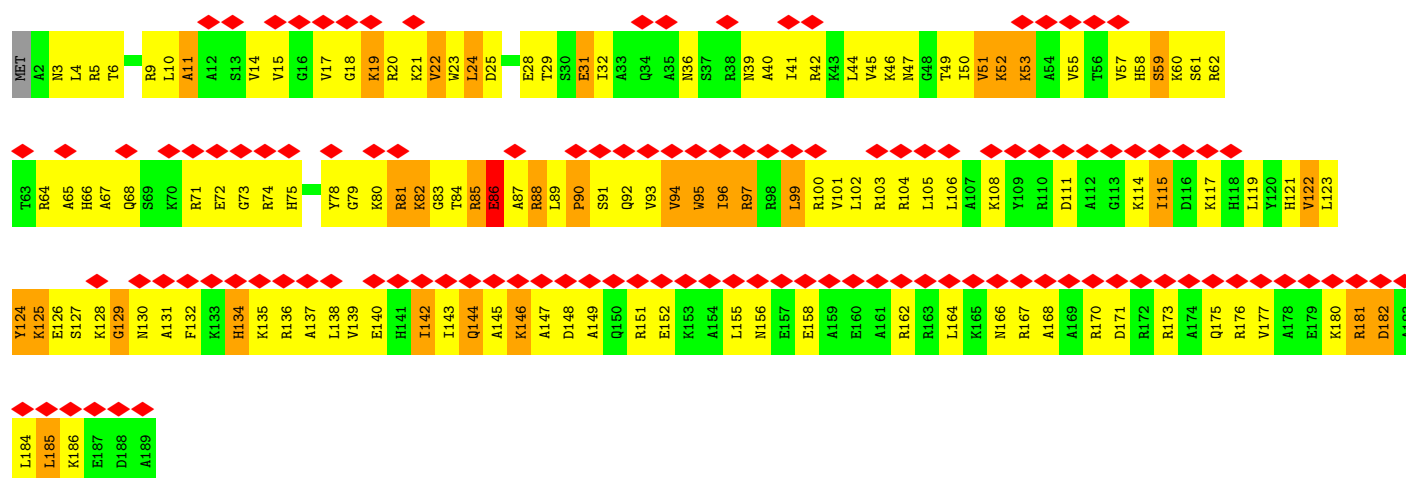




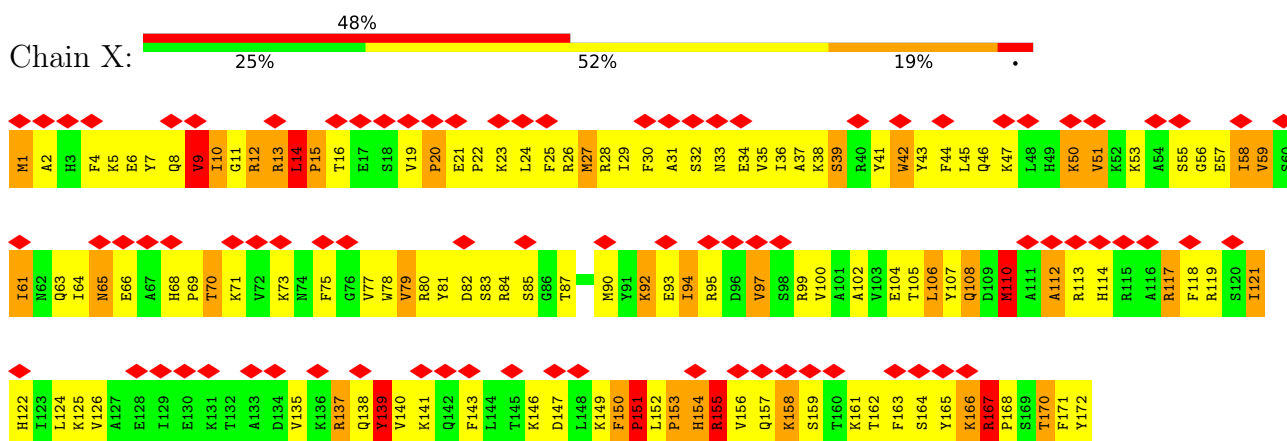
• Molecule 22: eL18 (yeast L18)



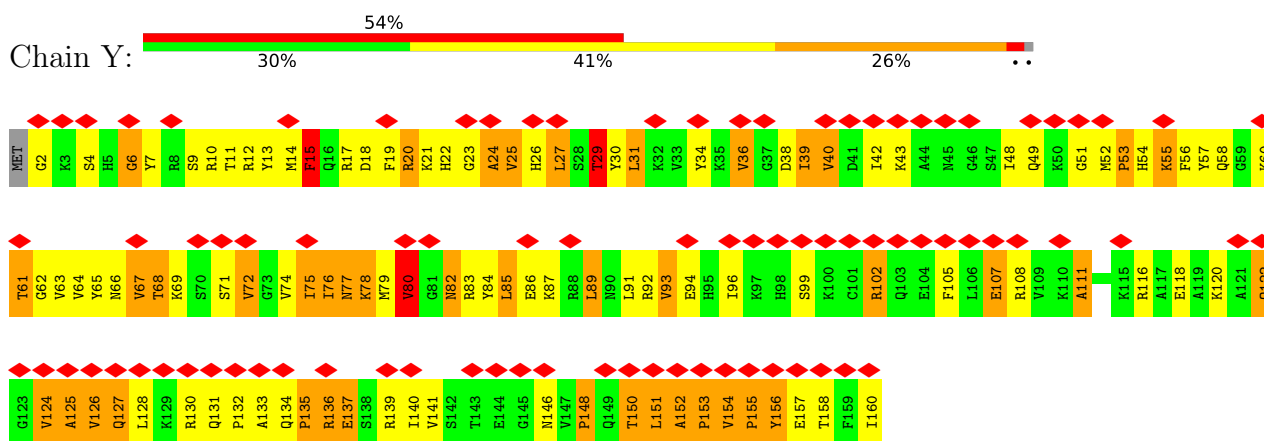
• Molecule 23: eL19 (yeast L19)



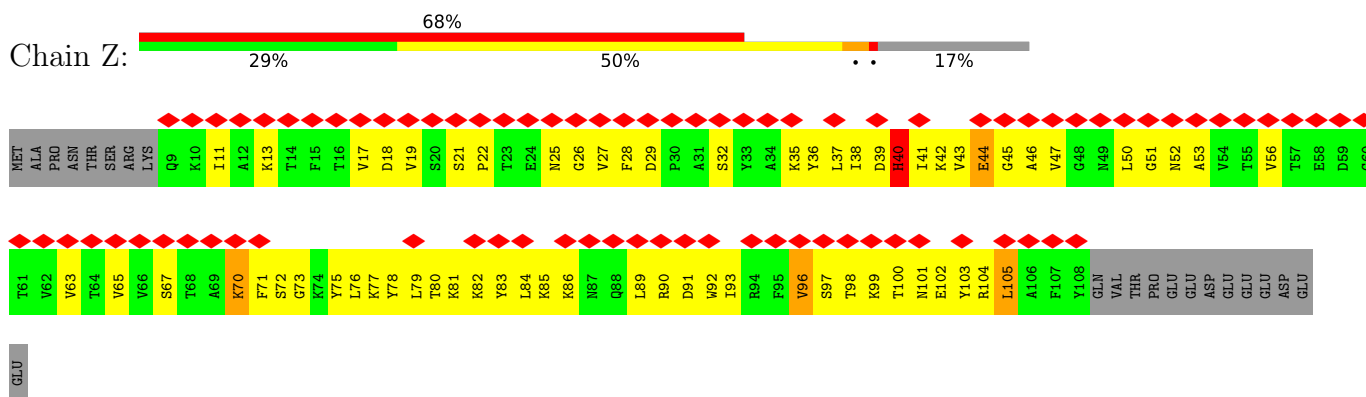
• Molecule 24: eL20 (yeast L20)



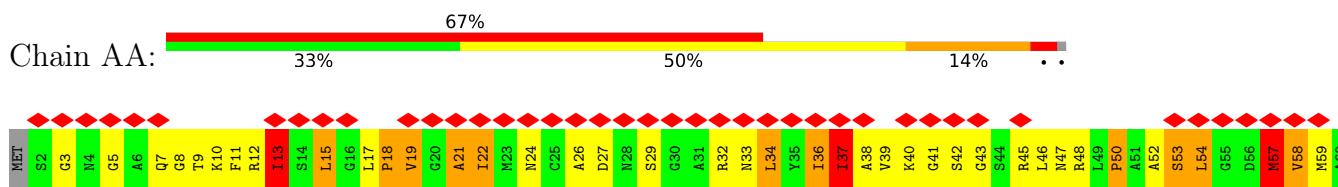
• Molecule 25: eL21 (yeast L21)

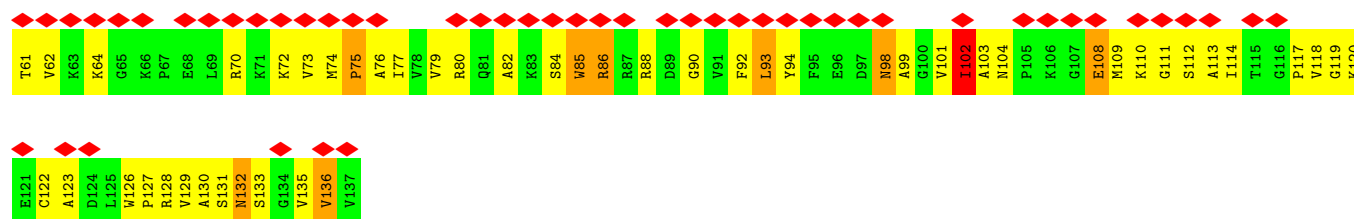


• Molecule 26: eL22 (yeast L22)

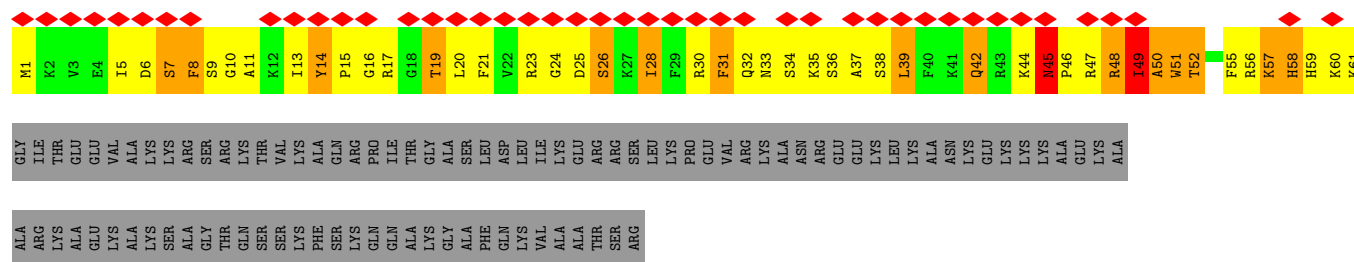


• Molecule 27: uL14 (yeast L23)

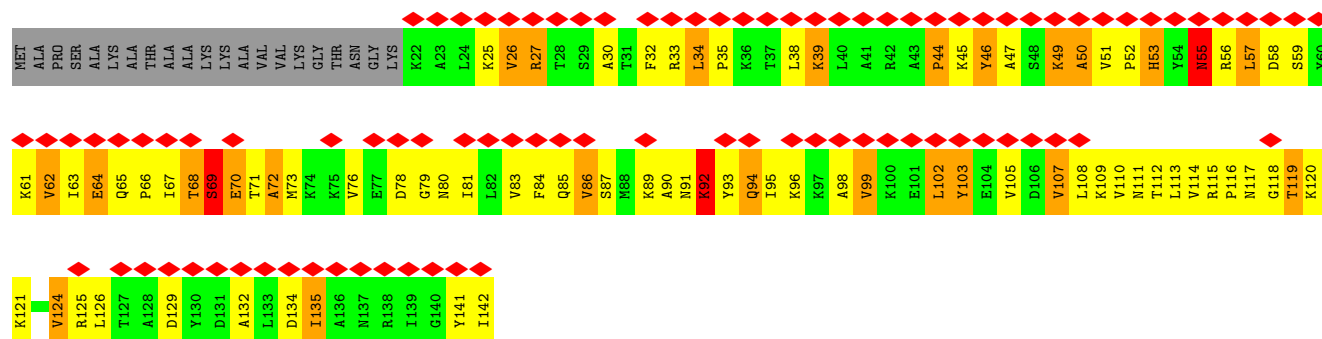




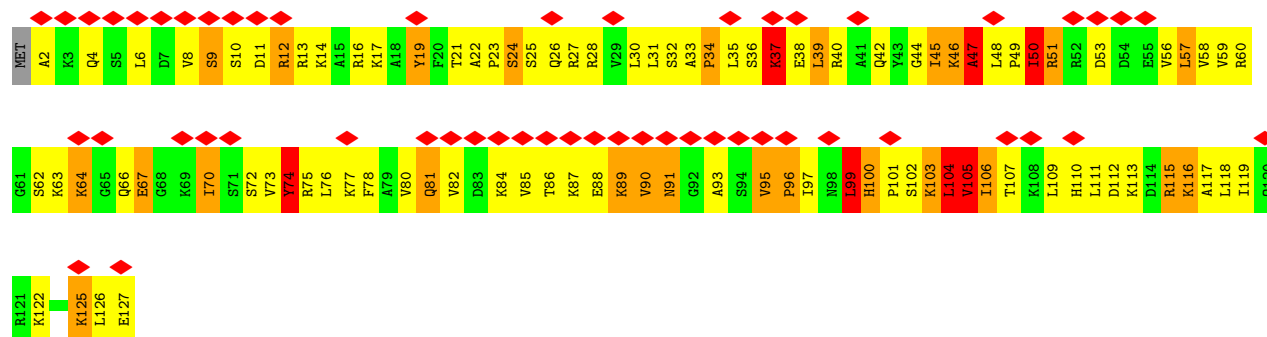
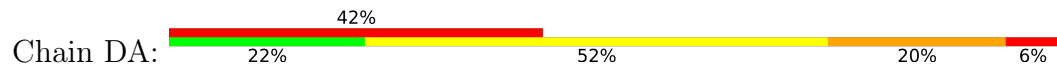
• Molecule 28: eL24 (yeast L24)



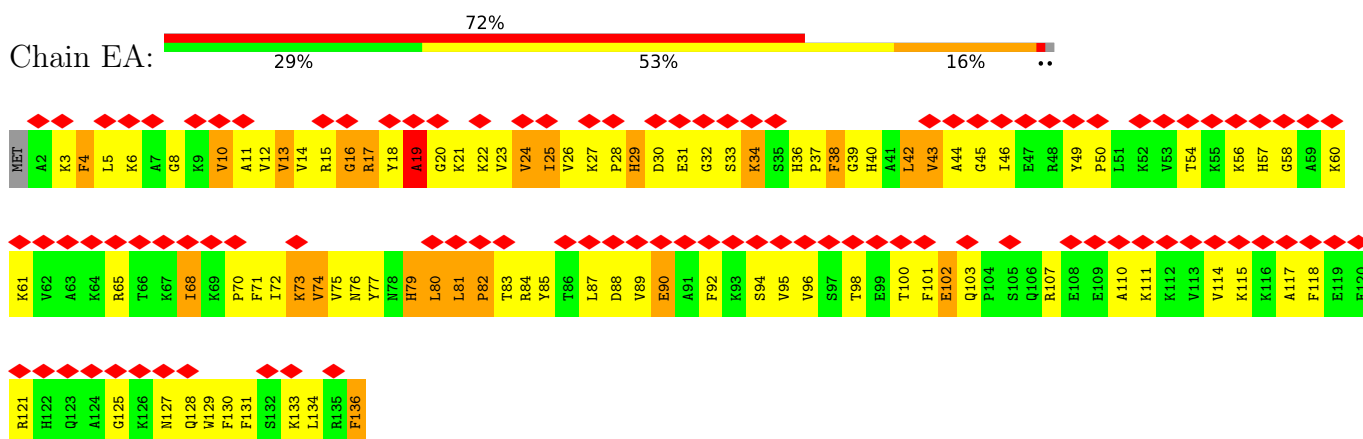
• Molecule 29: uL23 (yeast L25)



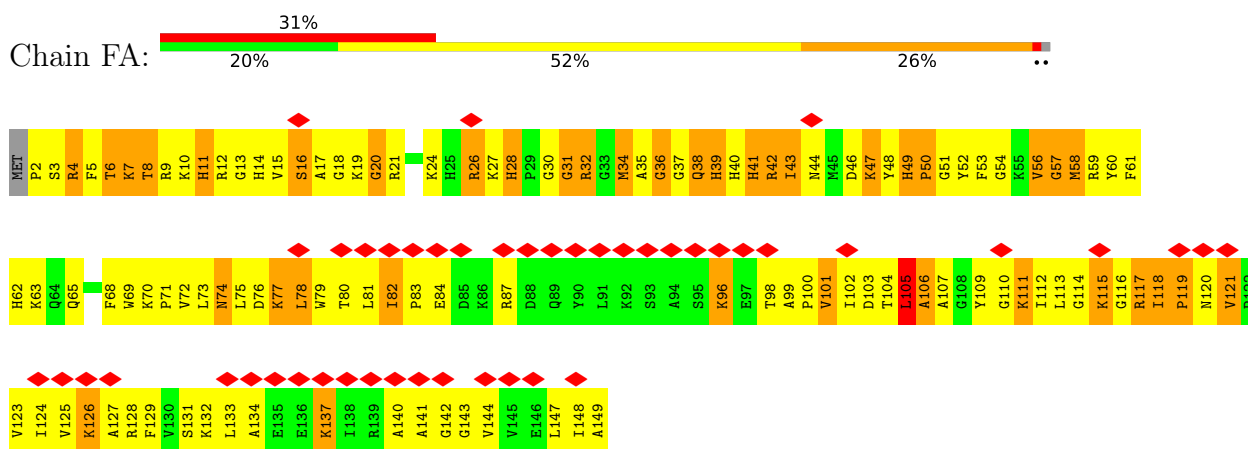
• Molecule 30: uL24 (yeast L26)



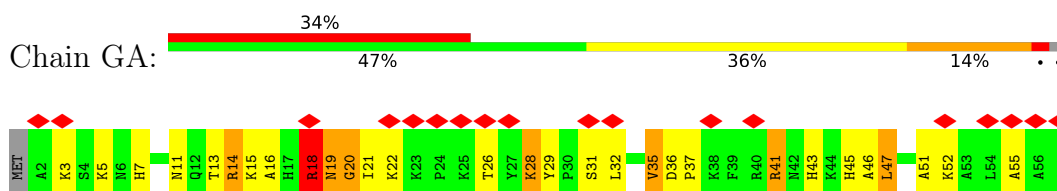
• Molecule 31: eL27 (yeast L27)



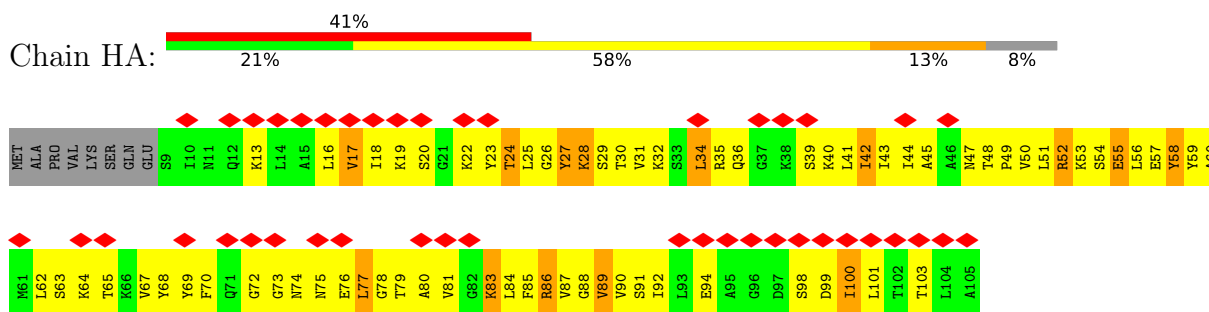
• Molecule 32: uL15 (yeast L28)



• Molecule 33: eL29 (yeast L29)

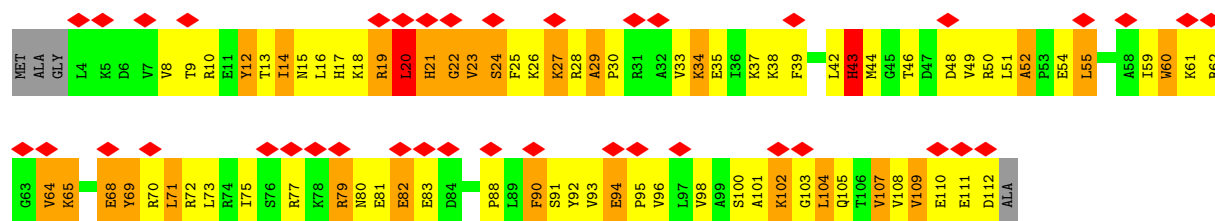


• Molecule 34: eL30 (yeast L30)

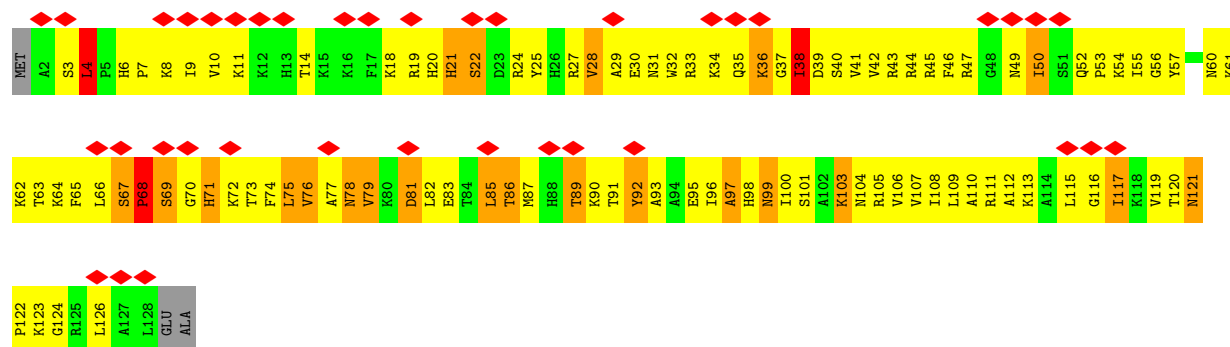


• Molecule 35: eL31 (yeast L31)

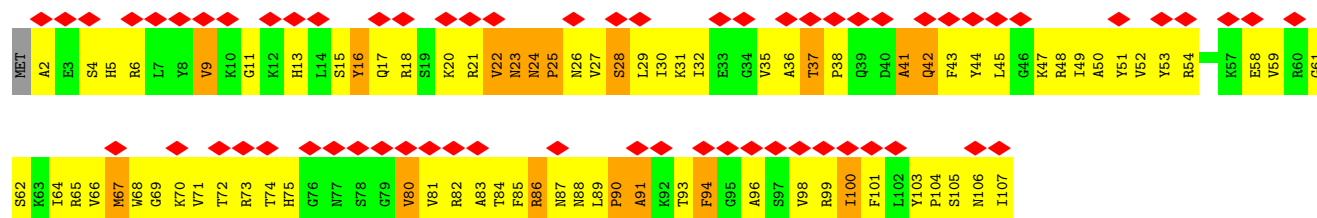




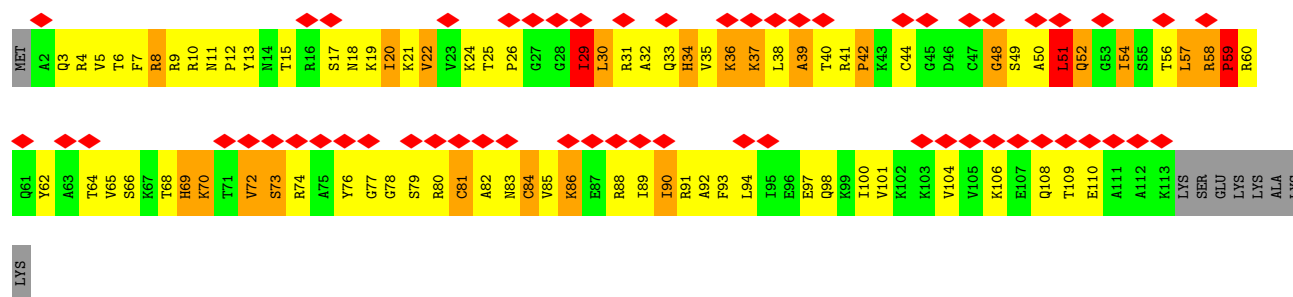
• Molecule 36: eL32 (yeast L32)



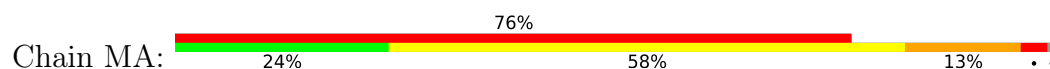
• Molecule 37: eL33 (yeast L33)

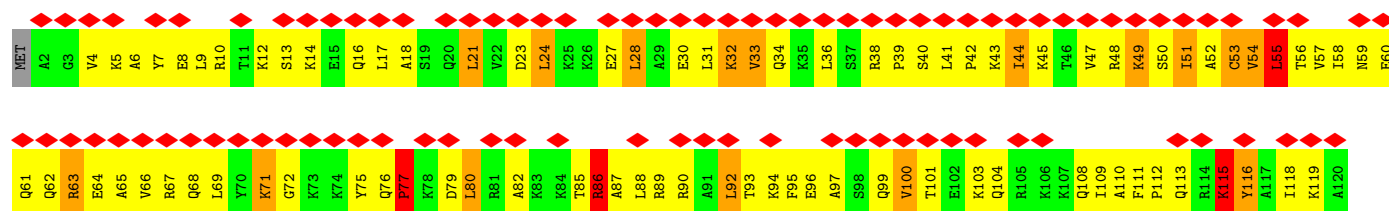


• Molecule 38: eL34 (yeast L34)

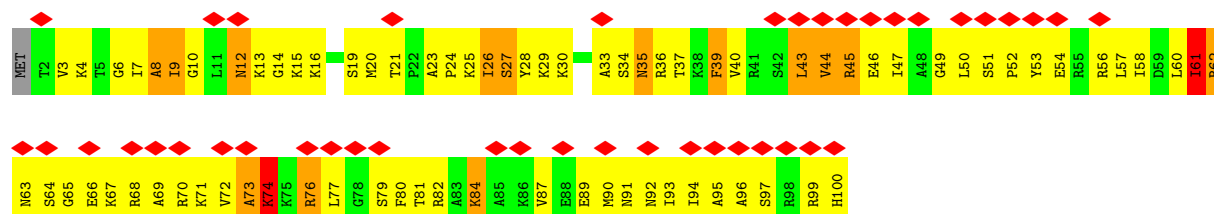


• Molecule 39: uL29 (yeast L35)

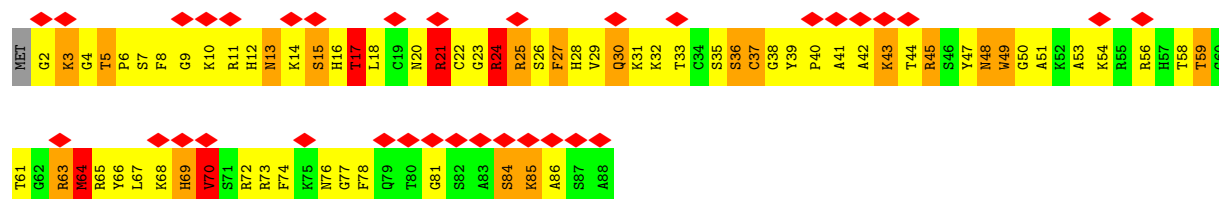




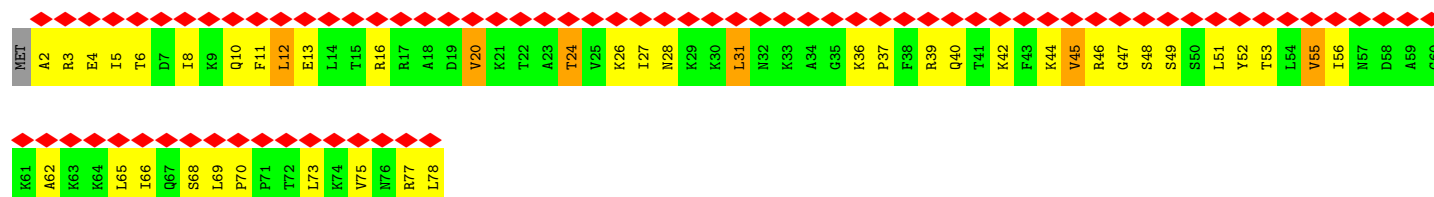
• Molecule 40: eL36 (yeast L36)



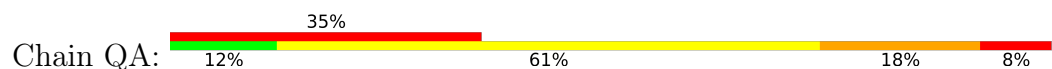
• Molecule 41: eL37 (yeast L37)



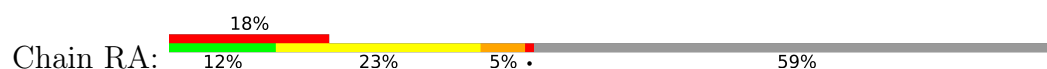
• Molecule 42: eL38 (yeast L38)

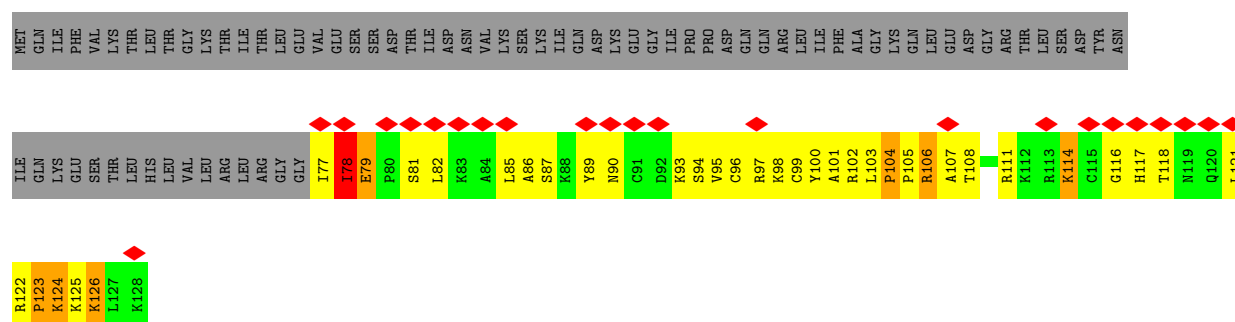


• Molecule 43: eL39 (yeast L39)

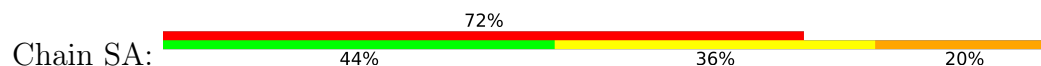


• Molecule 44: eL40 (yeast L40)





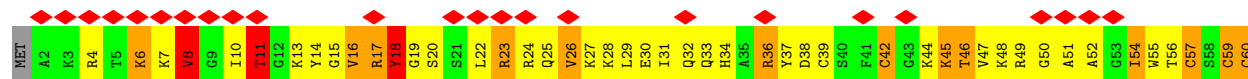
• Molecule 45: eL41 (yeast L41)



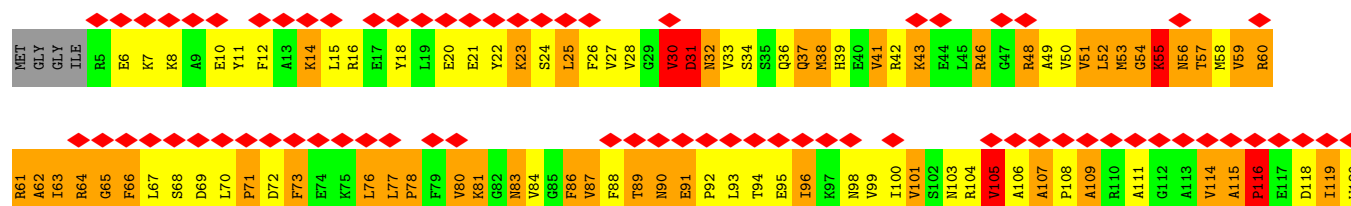
• Molecule 46: eL42 (yeast L42)

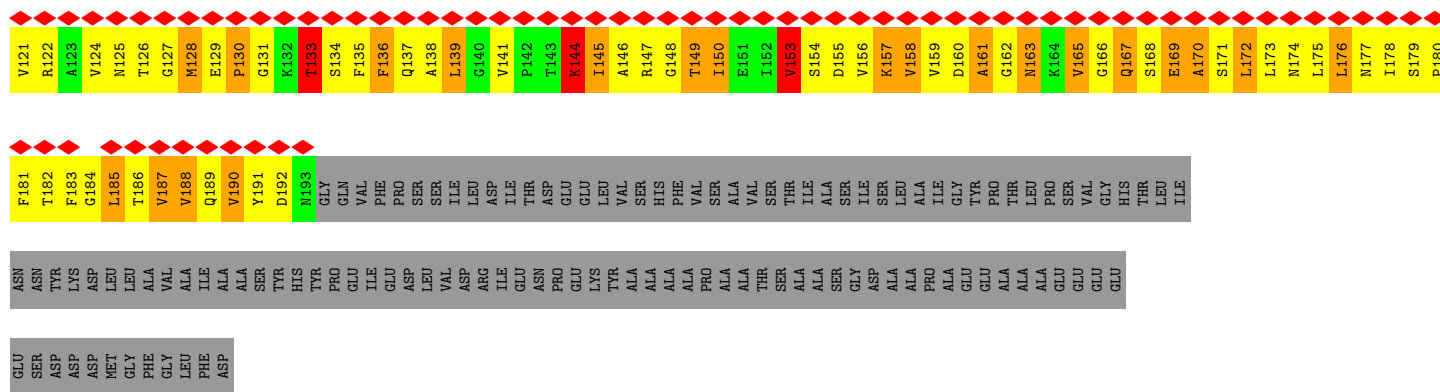


• Molecule 47: eL43 (yeast L43)

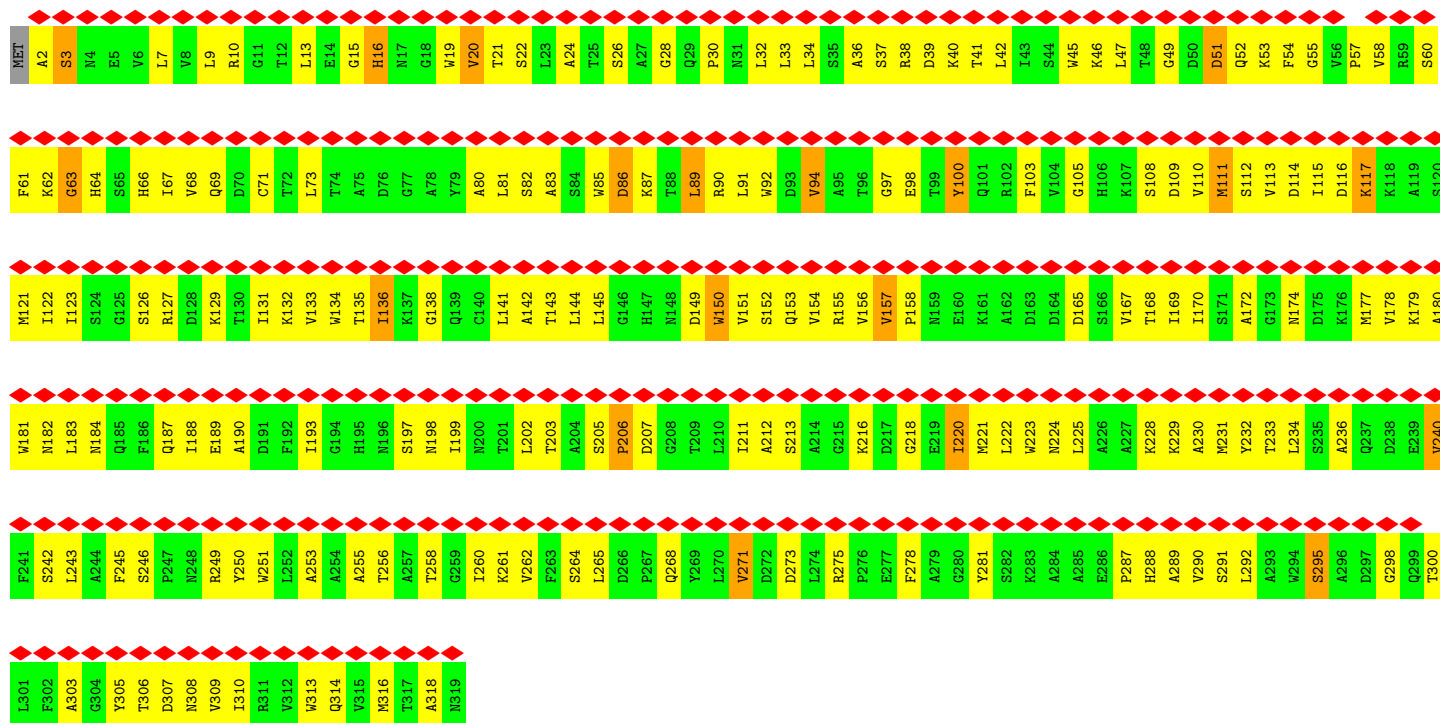


• Molecule 48: uL10 (yeast P0)

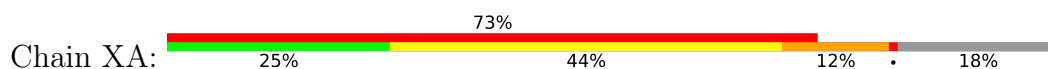


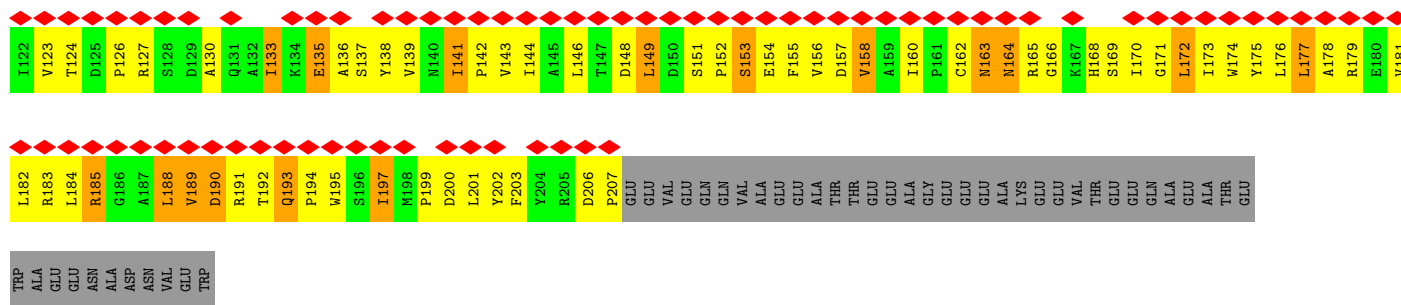


• Molecule 49: RACK1 (yeast Asc1)

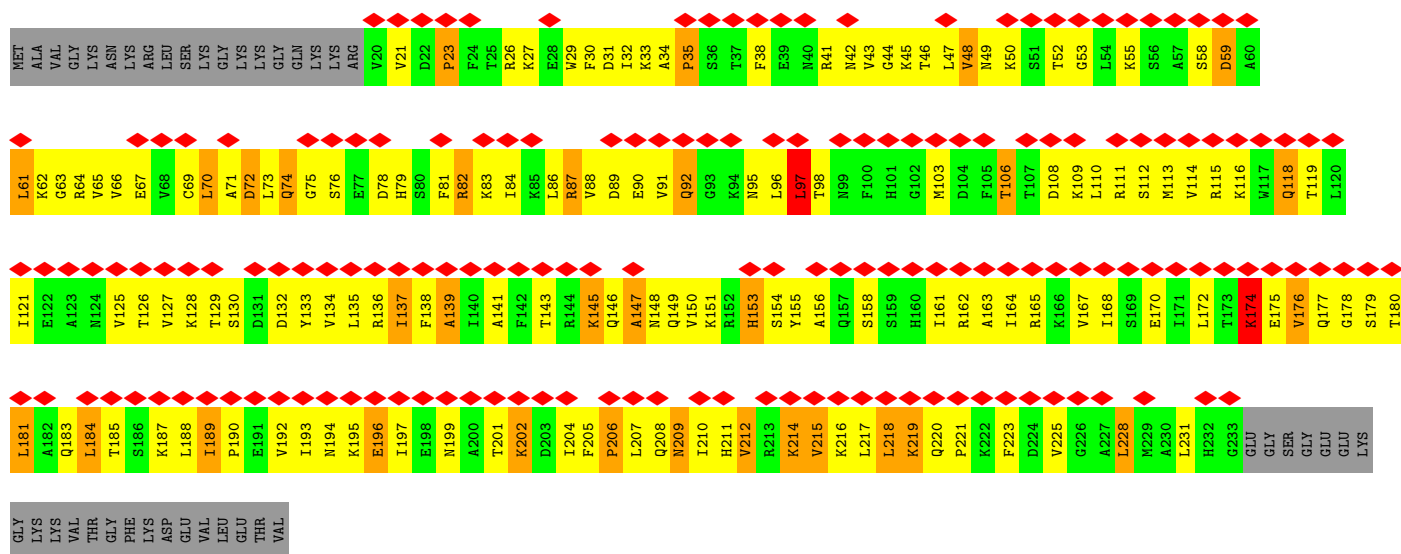


• Molecule 50: uS2 (yeast S0)

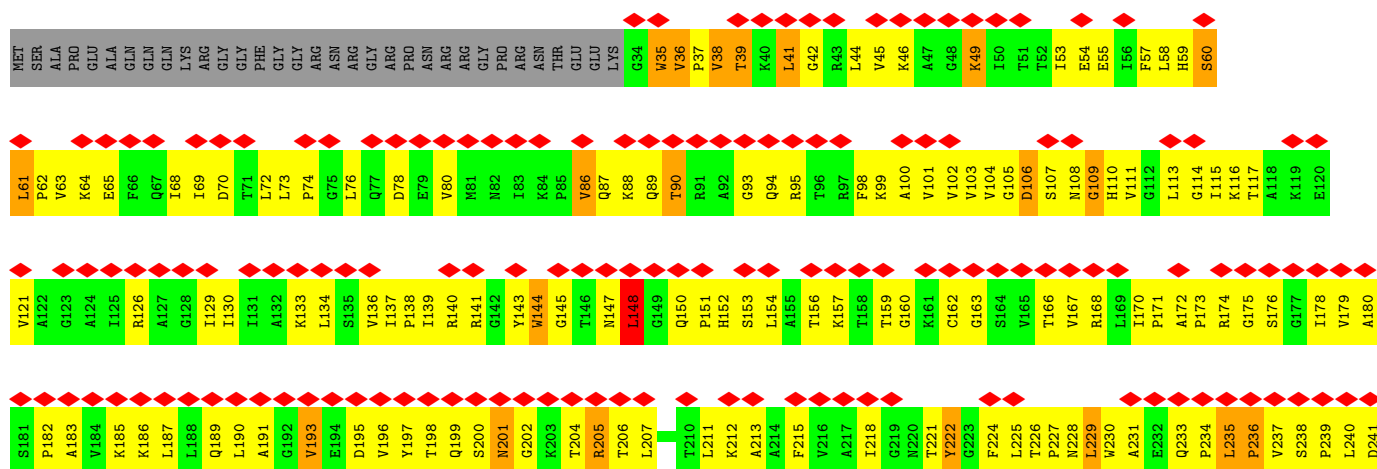


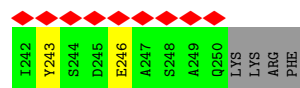


• Molecule 51: eS1 (yeast S1)

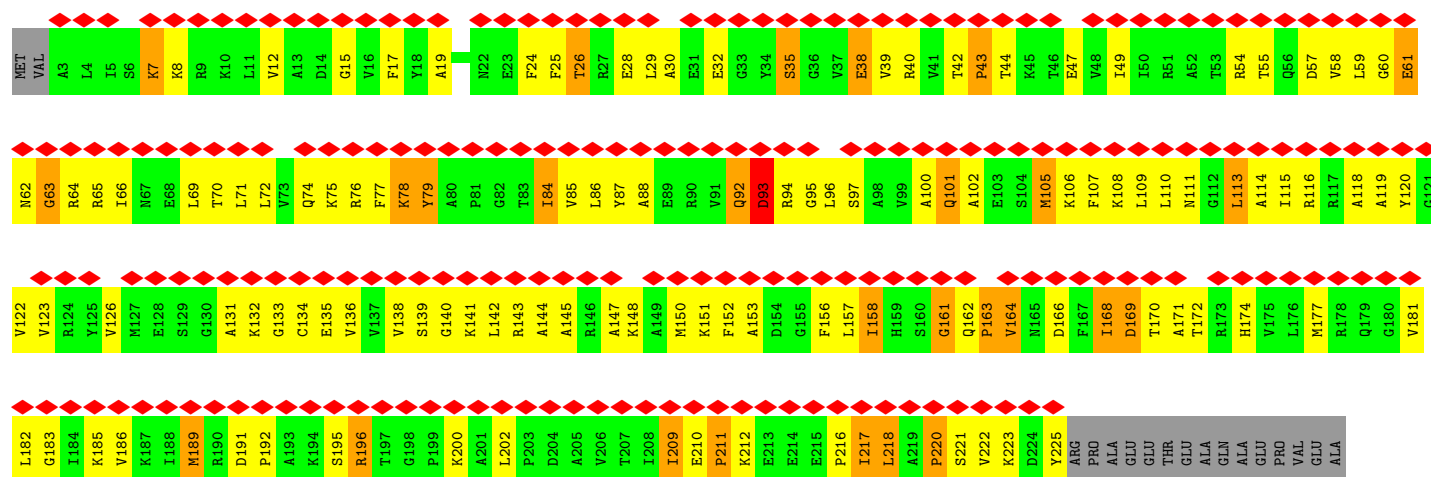
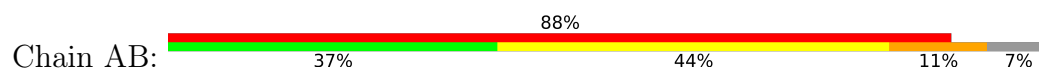


• Molecule 52: uS5 (yeast S2)

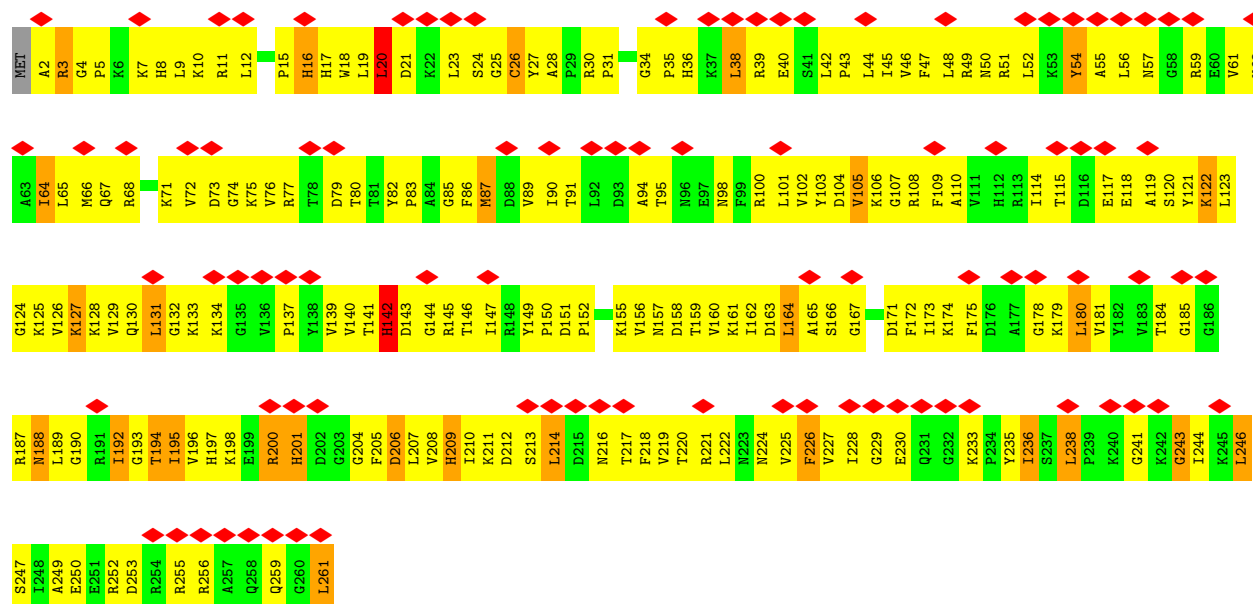




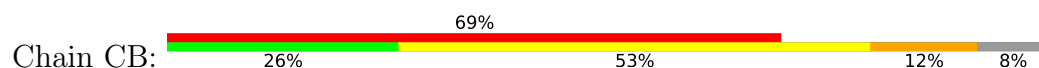
• Molecule 53: uS3 (yeast S3)

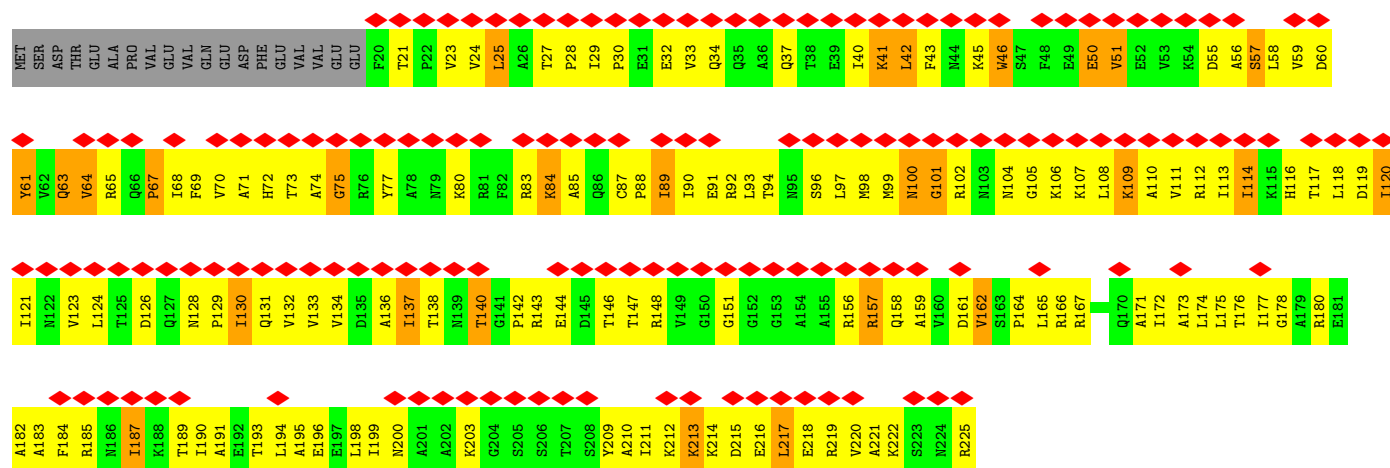


• Molecule 54: eS4 (yeast S4)

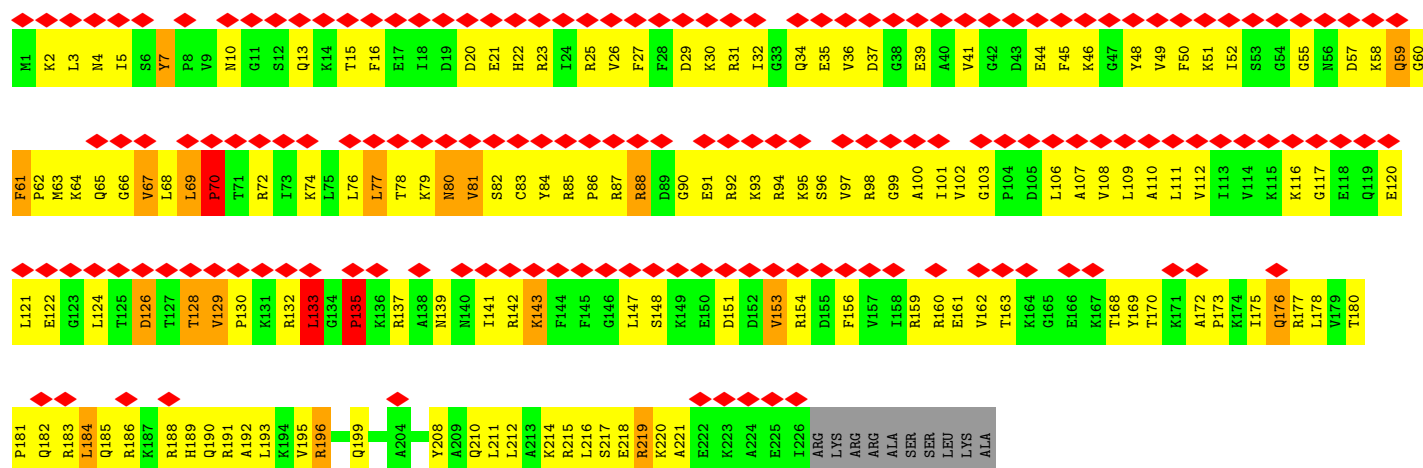


• Molecule 55: uS7 (yeast S5)

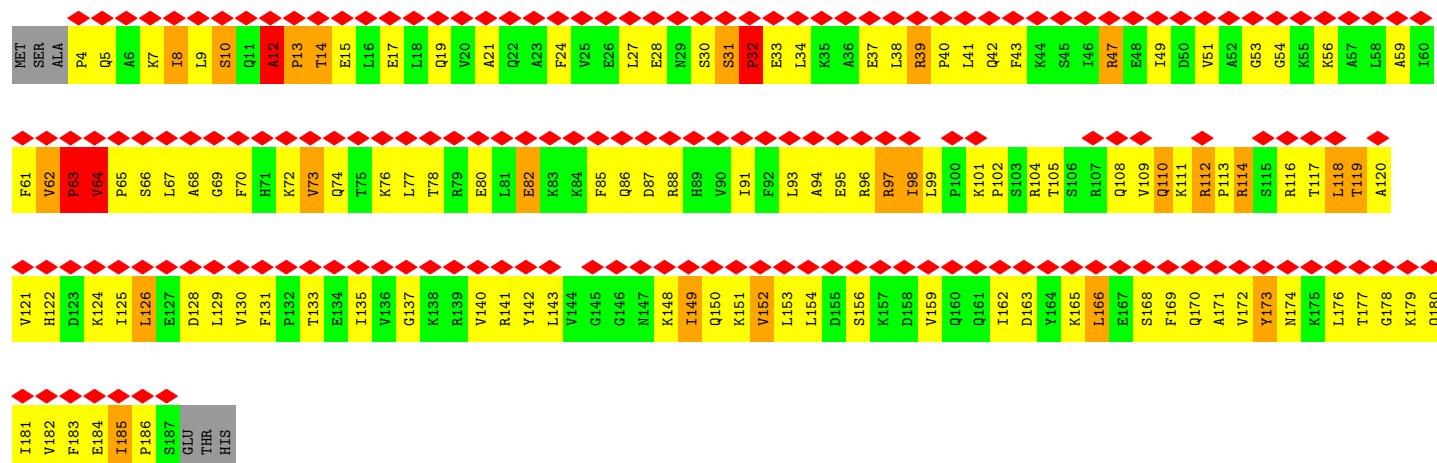




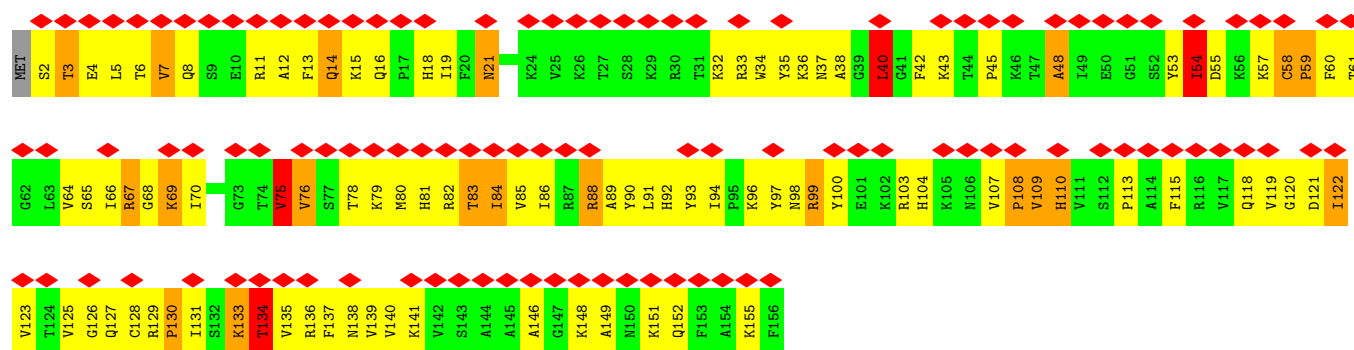
• Molecule 56: eS6 (yeast S6)



• Molecule 57: eS7 (yeast S7)

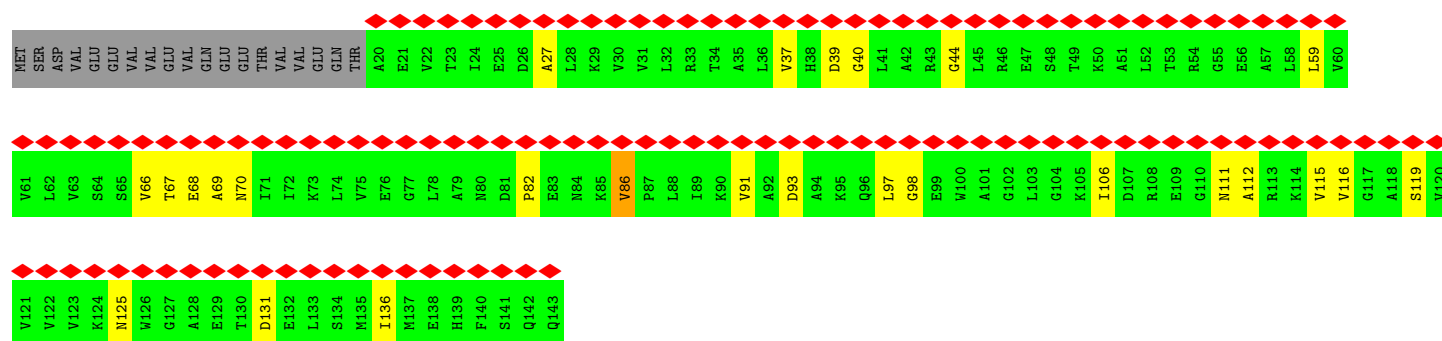


Chain IB: 



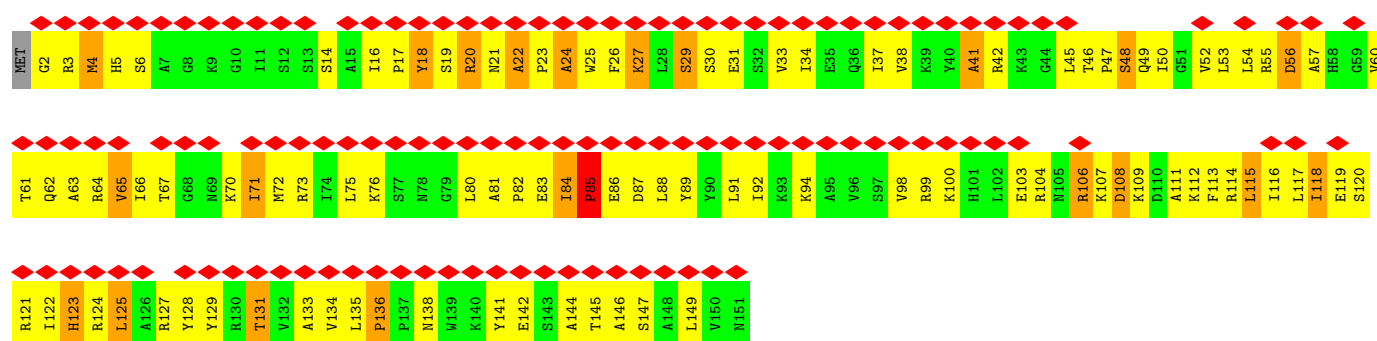
• Molecule 62: eS12 (yeast S12)

Chain JB: 



• Molecule 63: uS15 (yeast S13)

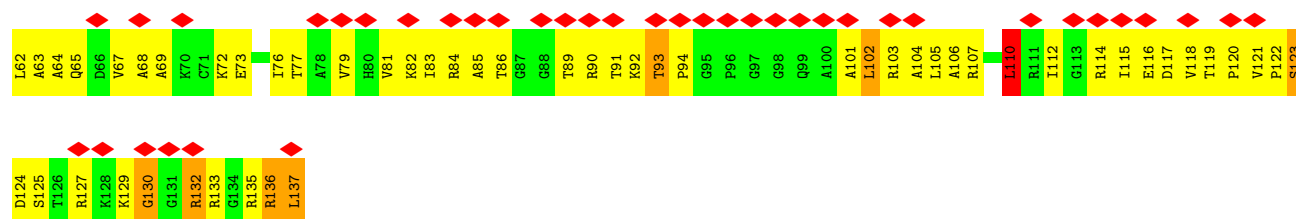
Chain KB: 



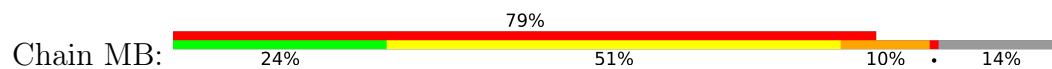
• Molecule 64: uS11 (yeast S14)

Chain LB: 

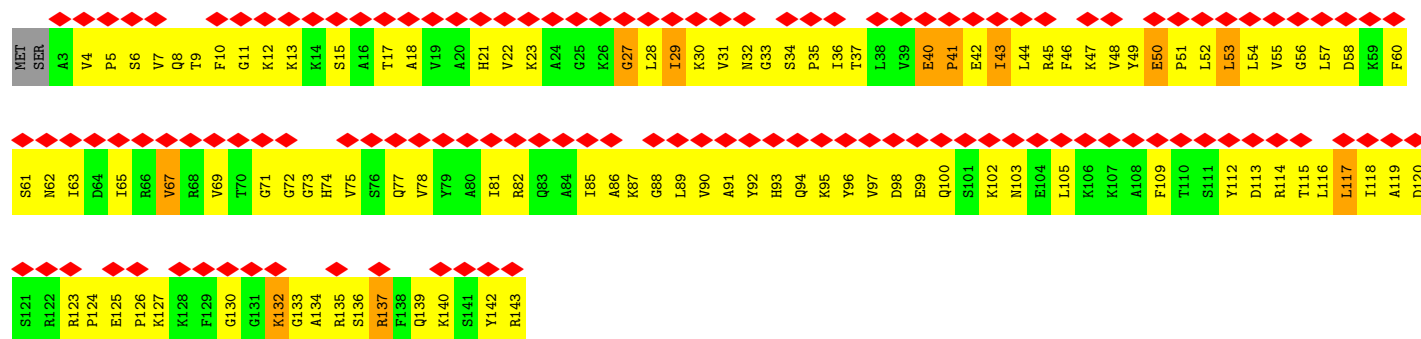
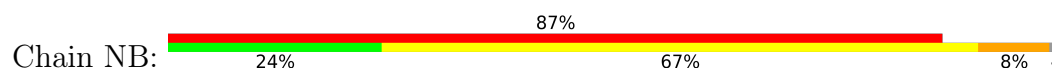




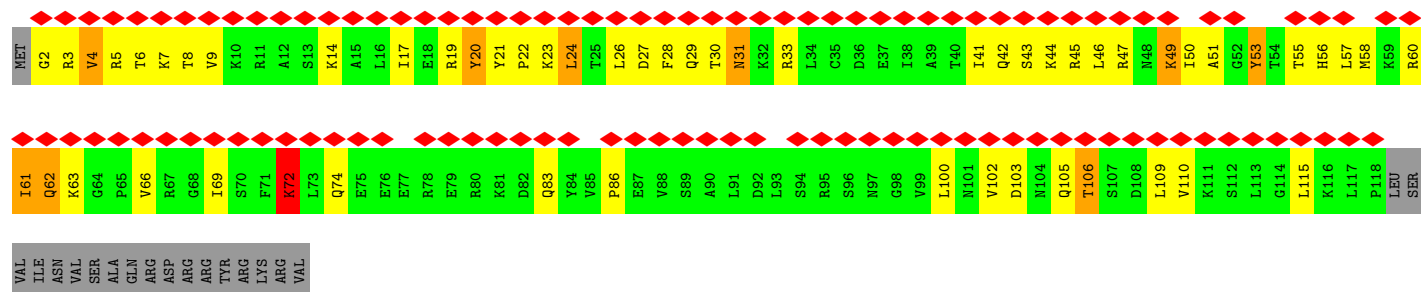
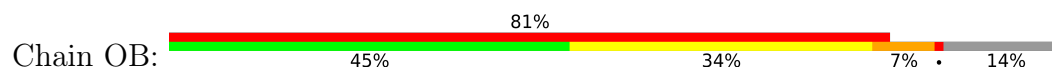
• Molecule 65: uS19 (yeast S15)



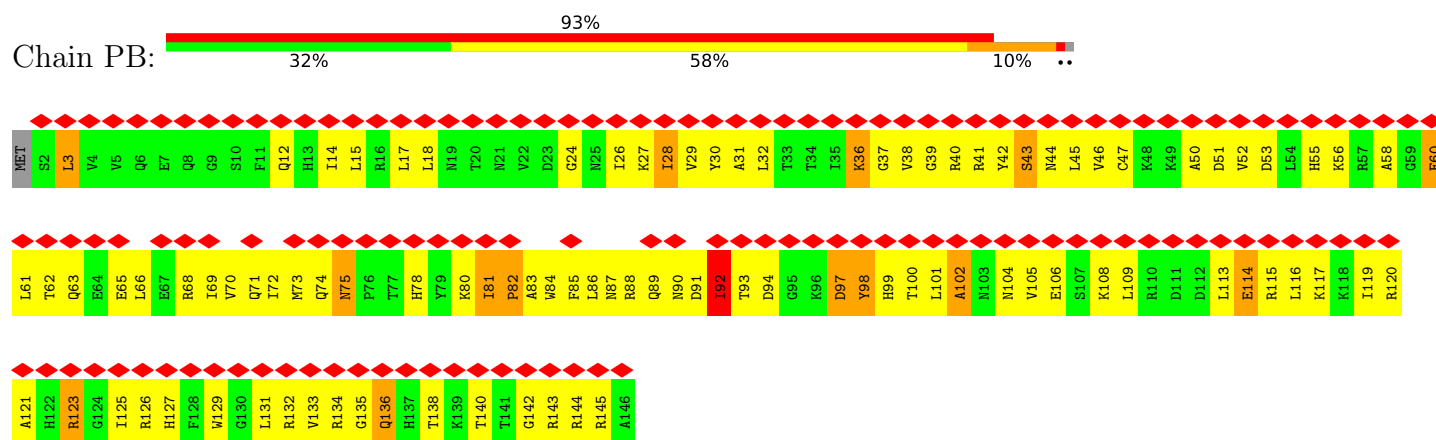
• Molecule 66: uS9 (yeast S16)



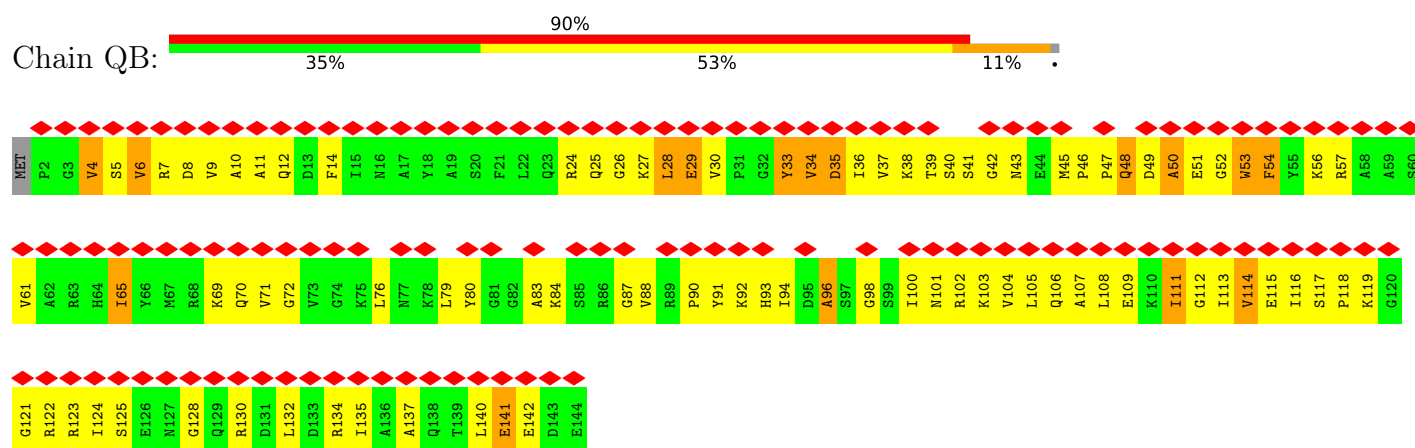
• Molecule 67: eS17 (yeast S17)



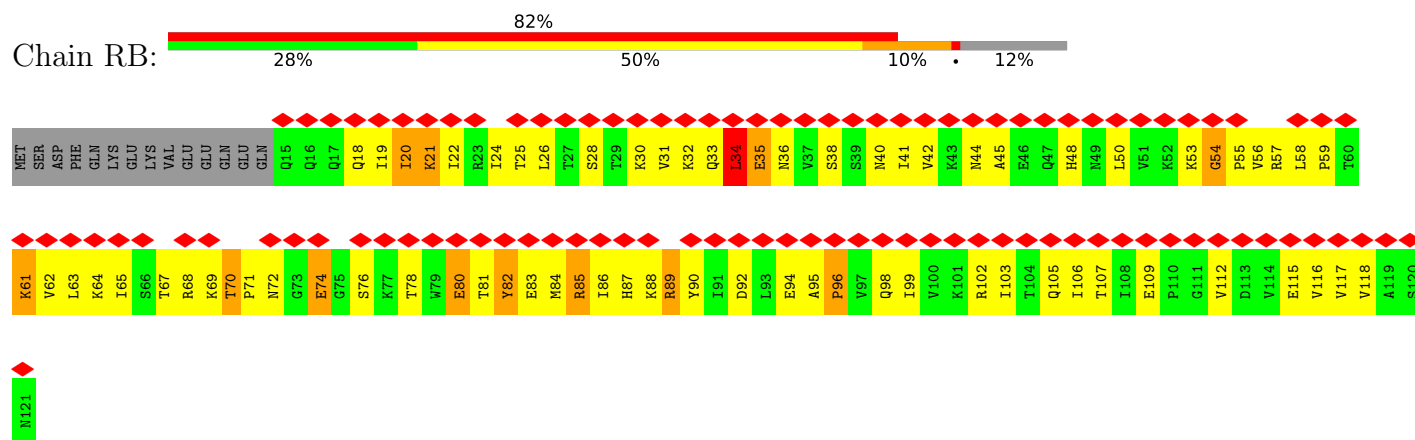
• Molecule 68: uS13 (yeast S18)



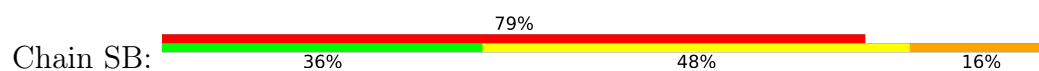
• Molecule 69: eS19 (yeast S19)

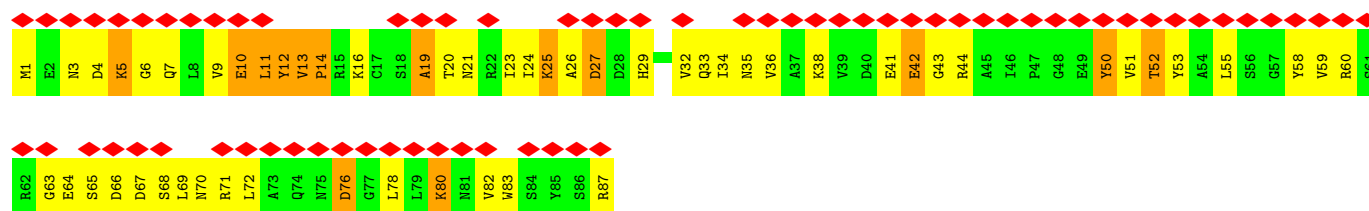


• Molecule 70: uS10 (yeast S20)

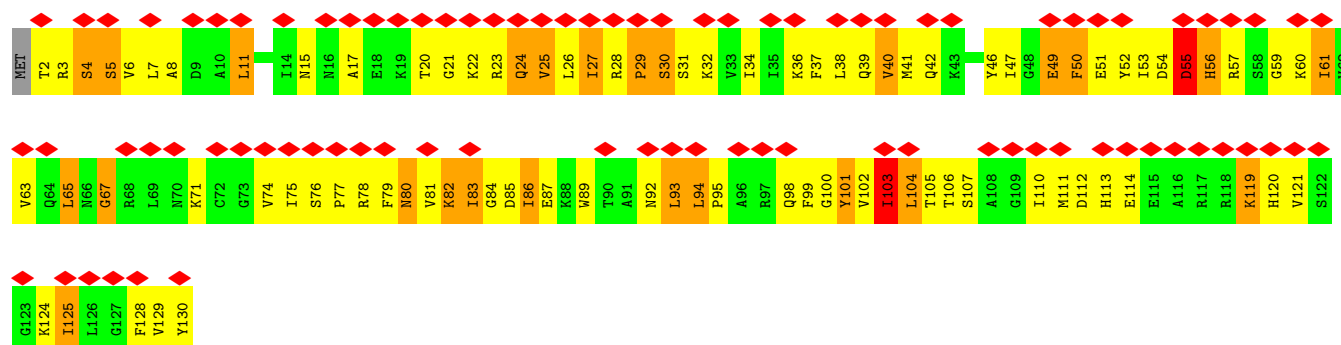


• Molecule 71: eS21 (yeast S21)

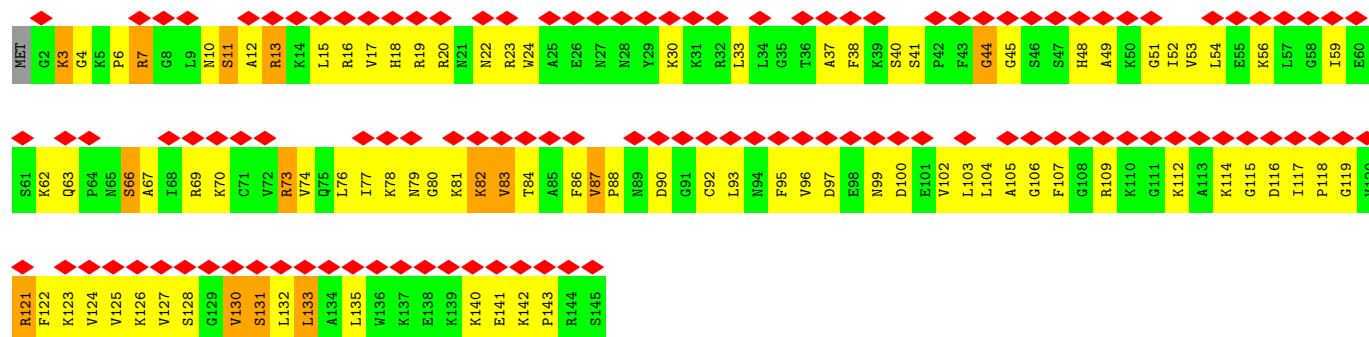
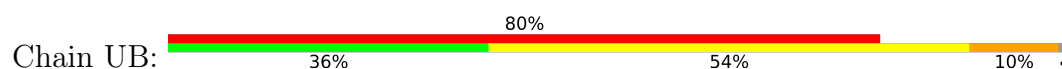




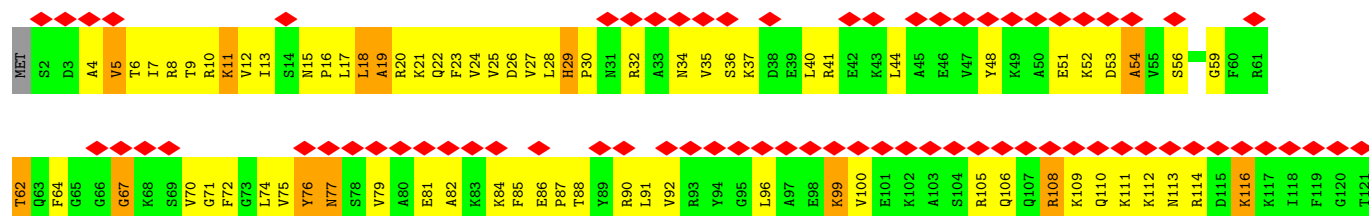
• Molecule 72: uS8 (yeast S22)

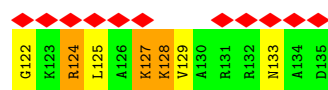


• Molecule 73: uS12 (yeast S23)

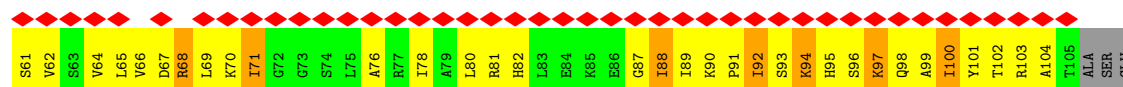
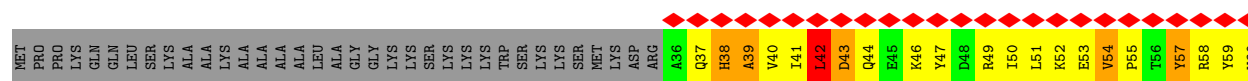


• Molecule 74: eS24 (yeast S24)

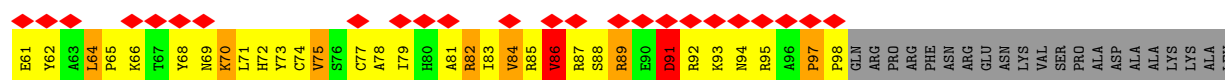
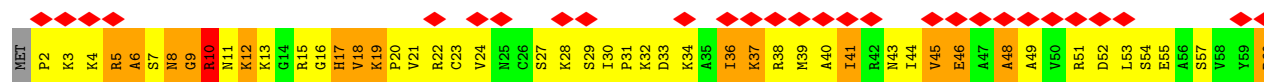
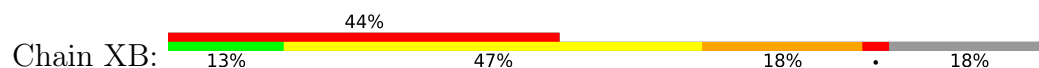




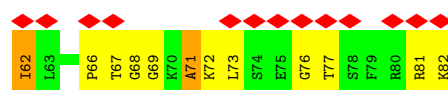
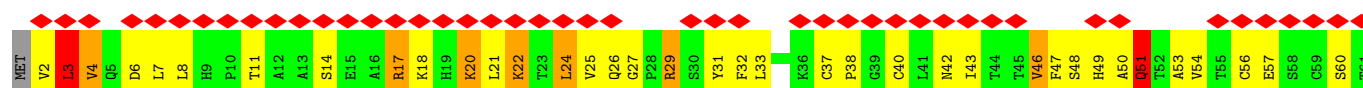
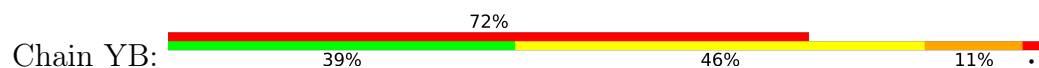
• Molecule 75: eS25 (yeast S25)



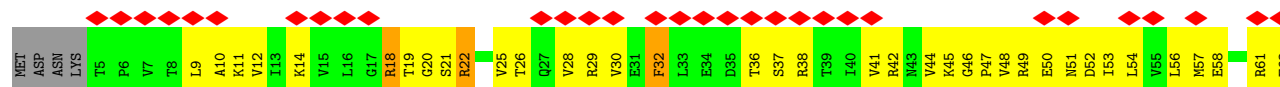
• Molecule 76: eS26 (yeast S26)



• Molecule 77: eS27 (yeast S27)



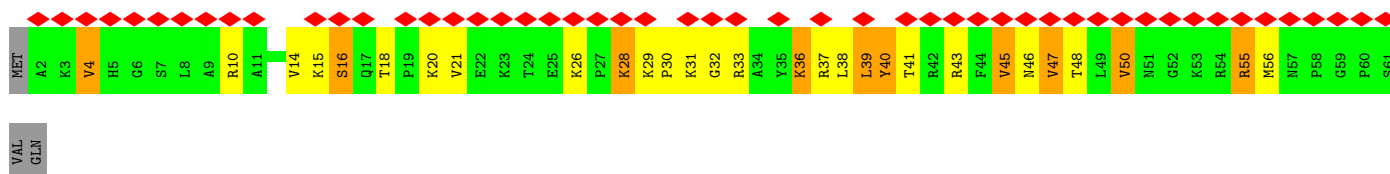
• Molecule 78: eS28 (yeast S28)



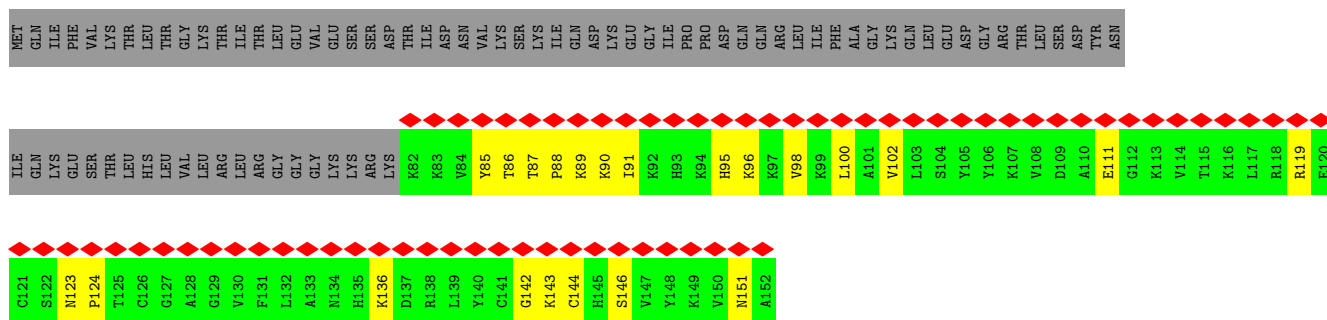
• Molecule 79: uS14 (yeast S29)



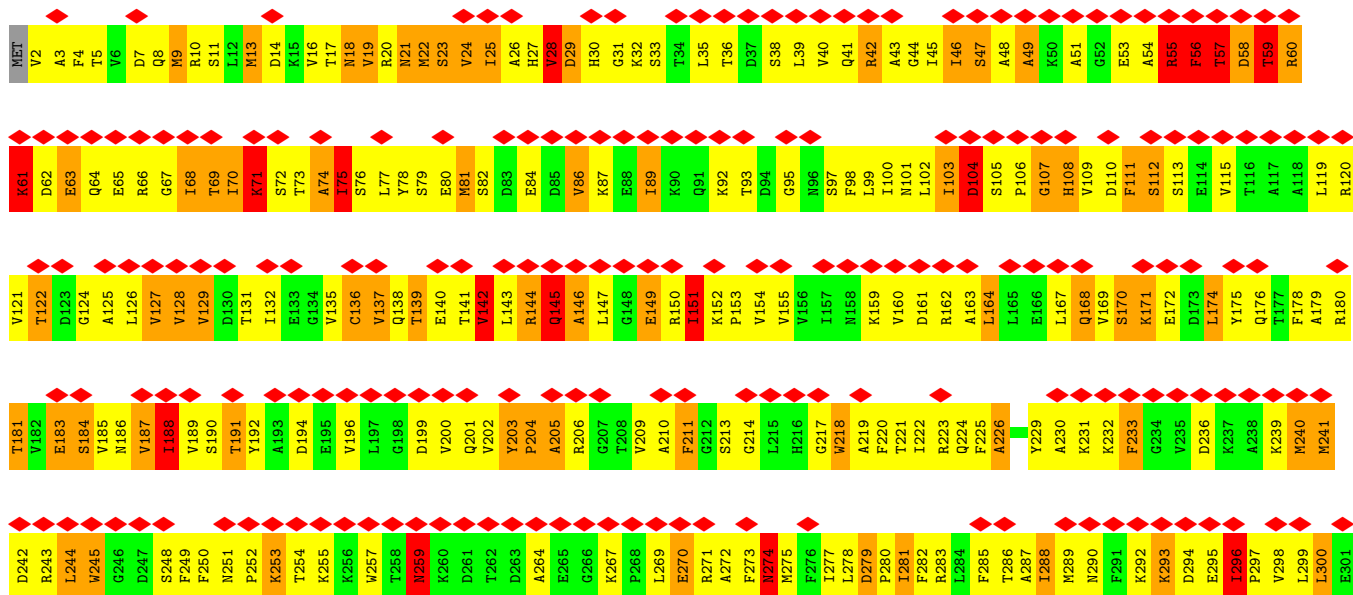
Chain BC:

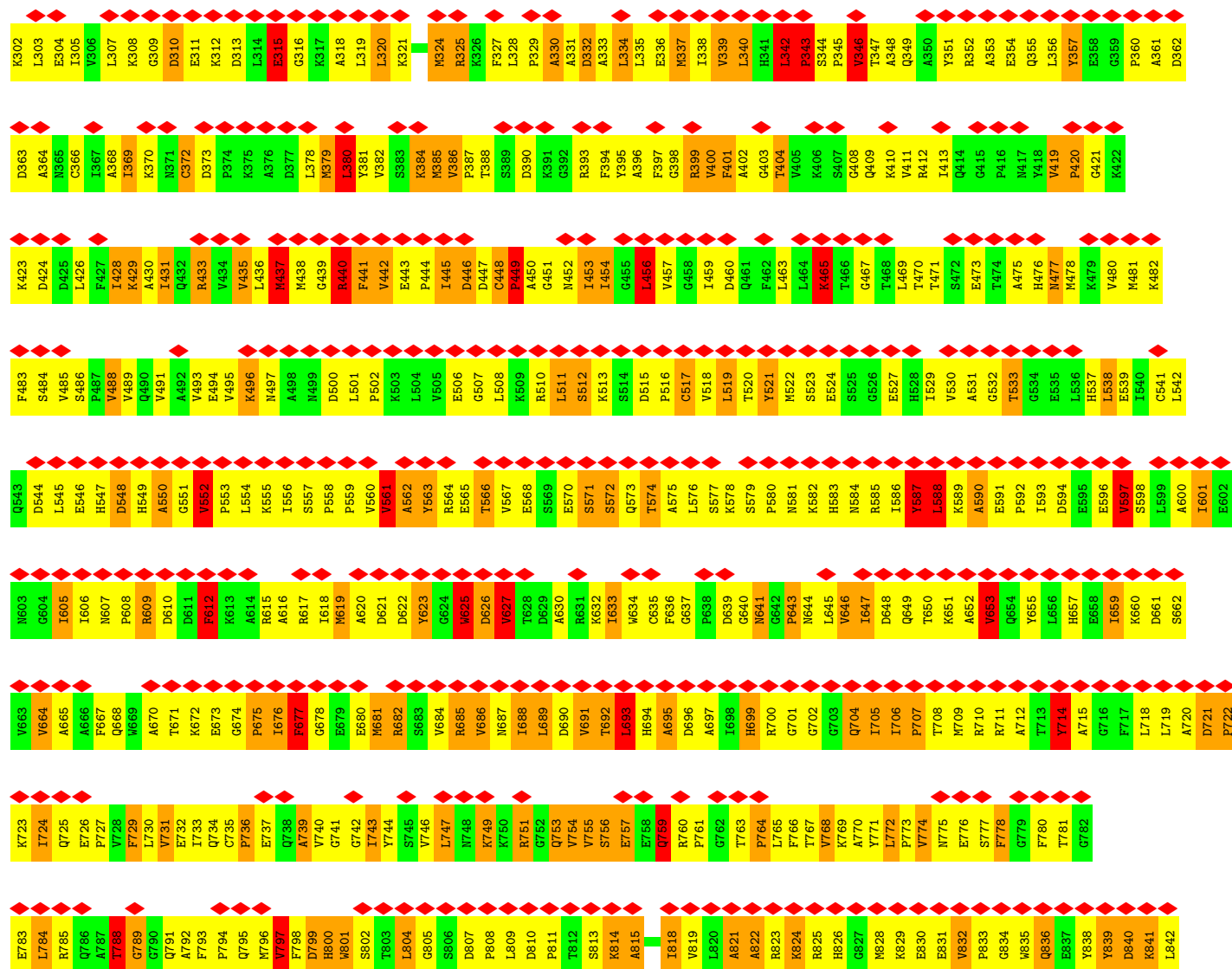


Chain CC:

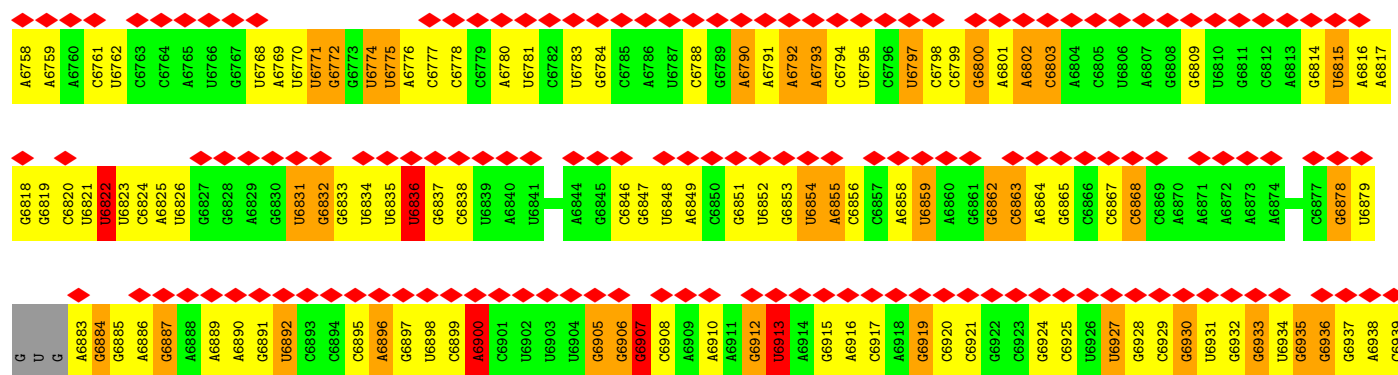
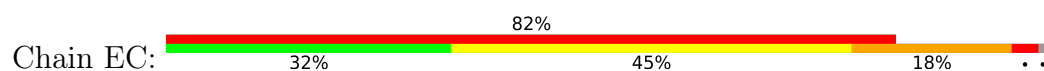


Chain DC:





• Molecule 83: IRES



U6940	U6941	A6942	A6943	U6944	U6945	A6946	A6947	U6948	C6949	C6950	C6951	U6952	C6953	C6954	U6955	A6956	A6957	C6958
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38047	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	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.130	Depositor
Minimum map value	-0.063	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.032	Depositor
Map size (Å)	419.84, 419.84, 419.84	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.64, 1.64, 1.64	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO1, MG, GDP, 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	0.76	0/42096	0.67	29/65570 (0.0%)
2	B	0.96	1/78631 (0.0%)	0.74	107/122552 (0.1%)
3	C	1.01	0/3747	0.74	4/5832 (0.1%)
4	D	0.88	0/2884	0.69	1/4491 (0.0%)
5	E	2.60	124/1377 (9.0%)	1.11	2/1844 (0.1%)
6	F	1.77	30/1952 (1.5%)	1.06	7/2622 (0.3%)
7	G	1.61	27/3153 (0.9%)	1.00	14/4239 (0.3%)
8	H	1.80	46/2802 (1.6%)	1.10	14/3792 (0.4%)
9	I	1.51	16/2426 (0.7%)	1.03	8/3271 (0.2%)
10	J	1.58	10/1425 (0.7%)	1.07	5/1912 (0.3%)
11	K	1.79	18/1822 (1.0%)	1.13	12/2451 (0.5%)
12	L	1.58	11/1850 (0.6%)	1.03	8/2495 (0.3%)
13	M	1.70	19/1540 (1.2%)	0.98	6/2073 (0.3%)
14	N	1.68	15/1754 (0.9%)	1.01	9/2350 (0.4%)
15	O	1.37	4/1375 (0.3%)	0.93	6/1842 (0.3%)
16	P	2.65	73/728 (10.0%)	1.19	5/975 (0.5%)
17	Q	1.61	10/1568 (0.6%)	1.12	9/2106 (0.4%)
18	R	1.82	21/1069 (2.0%)	1.09	6/1438 (0.4%)
19	S	1.79	32/1758 (1.8%)	1.17	10/2354 (0.4%)
20	T	1.69	21/1586 (1.3%)	1.08	8/2128 (0.4%)
21	U	1.85	29/1466 (2.0%)	1.13	14/1968 (0.7%)
22	V	1.76	12/1466 (0.8%)	1.09	6/1965 (0.3%)
23	W	1.49	5/1539 (0.3%)	1.13	13/2050 (0.6%)
24	X	1.77	19/1482 (1.3%)	0.96	7/1990 (0.4%)
25	Y	1.90	29/1301 (2.2%)	1.05	10/1743 (0.6%)
26	Z	1.32	0/812	0.89	1/1099 (0.1%)
27	AA	1.78	20/1019 (2.0%)	1.01	4/1369 (0.3%)
28	BA	1.88	10/521 (1.9%)	1.03	3/691 (0.4%)
29	CA	1.84	14/984 (1.4%)	1.00	5/1325 (0.4%)
30	DA	1.86	25/1005 (2.5%)	1.07	3/1341 (0.2%)
31	EA	1.53	11/1119 (1.0%)	0.90	1/1497 (0.1%)
32	FA	1.74	21/1205 (1.7%)	1.05	10/1612 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	GA	1.54	1/474 (0.2%)	1.15	3/629 (0.5%)
34	HA	1.38	1/751 (0.1%)	1.16	8/1008 (0.8%)
35	IA	1.68	9/904 (1.0%)	1.09	7/1213 (0.6%)
36	JA	1.86	19/1041 (1.8%)	1.01	5/1394 (0.4%)
37	KA	1.72	11/869 (1.3%)	0.93	2/1168 (0.2%)
38	LA	1.70	15/891 (1.7%)	1.06	7/1191 (0.6%)
39	MA	1.67	6/979 (0.6%)	1.10	8/1301 (0.6%)
40	NA	1.54	7/779 (0.9%)	1.14	9/1034 (0.9%)
41	OA	1.98	19/697 (2.7%)	1.04	4/923 (0.4%)
42	PA	1.62	6/619 (1.0%)	0.90	2/826 (0.2%)
43	QA	1.83	7/444 (1.6%)	1.13	3/588 (0.5%)
44	RA	1.72	1/424 (0.2%)	1.15	4/562 (0.7%)
45	SA	1.53	1/235 (0.4%)	1.08	1/300 (0.3%)
46	TA	1.65	12/861 (1.4%)	0.91	1/1136 (0.1%)
47	UA	1.64	8/702 (1.1%)	0.98	2/934 (0.2%)
48	VA	2.32	87/1498 (5.8%)	1.26	20/2025 (1.0%)
49	WA	1.38	5/2498 (0.2%)	0.76	3/3398 (0.1%)
50	XA	1.15	1/1651 (0.1%)	1.00	8/2257 (0.4%)
51	YA	1.33	6/1735 (0.3%)	0.91	3/2335 (0.1%)
52	ZA	1.31	1/1665 (0.1%)	0.96	3/2263 (0.1%)
53	AB	1.42	2/1759 (0.1%)	0.93	5/2368 (0.2%)
54	BB	1.23	1/2110 (0.0%)	0.90	6/2839 (0.2%)
55	CB	1.27	1/1630 (0.1%)	0.97	5/2202 (0.2%)
56	DB	1.22	2/1844 (0.1%)	0.94	7/2464 (0.3%)
57	EB	1.37	4/1506 (0.3%)	0.94	3/2028 (0.1%)
58	FB	1.41	4/1515 (0.3%)	0.96	5/2021 (0.2%)
59	GB	1.13	2/1519 (0.1%)	0.96	4/2035 (0.2%)
60	HB	1.46	1/837 (0.1%)	0.92	4/1131 (0.4%)
61	IB	1.62	10/1273 (0.8%)	0.89	1/1712 (0.1%)
62	JB	1.94	4/495 (0.8%)	1.20	1/617 (0.2%)
63	KB	1.47	2/1216 (0.2%)	1.09	10/1638 (0.6%)
64	LB	1.18	1/953 (0.1%)	0.96	2/1279 (0.2%)
65	MB	1.59	6/996 (0.6%)	0.99	2/1335 (0.1%)
66	NB	1.37	3/1126 (0.3%)	0.94	2/1510 (0.1%)
67	OB	1.33	2/844 (0.2%)	1.02	2/1120 (0.2%)
68	PB	1.45	4/1212 (0.3%)	0.95	5/1628 (0.3%)
69	QB	1.40	2/1131 (0.2%)	1.06	5/1517 (0.3%)
70	RB	1.53	3/866 (0.3%)	0.92	2/1169 (0.2%)
71	SB	1.26	0/694	0.90	2/935 (0.2%)
72	TB	1.40	3/1039 (0.3%)	0.95	4/1395 (0.3%)
73	UB	1.42	5/1140 (0.4%)	0.91	0/1518
74	VB	1.16	0/1088	0.94	3/1449 (0.2%)
75	WB	1.41	3/571 (0.5%)	0.98	2/768 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	XB	1.34	3/782 (0.4%)	0.90	2/1047 (0.2%)
77	YB	1.39	1/621 (0.2%)	0.89	1/838 (0.1%)
78	ZB	1.26	1/500 (0.2%)	0.78	1/670 (0.1%)
79	AC	1.50	2/454 (0.4%)	0.91	1/602 (0.2%)
80	BC	1.33	0/483	0.90	1/643 (0.2%)
81	CC	1.93	2/283 (0.7%)	1.00	2/352 (0.6%)
82	DC	2.15	268/6665 (4.0%)	1.13	43/9022 (0.5%)
83	EC	1.38	0/4579	0.91	18/7119 (0.3%)
All	All	1.28	1238/230910 (0.5%)	0.85	601/338443 (0.2%)

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	21
2	B	0	92
3	C	0	4
4	D	0	3
6	F	0	1
83	EC	0	8
All	All	0	129

The worst 5 of 1238 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	DC	61	LYS	CA-C	16.90	1.61	1.52
11	K	96	PRO	CA-C	15.57	1.60	1.51
82	DC	799	ASP	CA-C	12.16	1.60	1.53
63	KB	136	PRO	CA-C	12.06	1.58	1.51
29	CA	64	GLU	CA-C	11.10	1.59	1.53

The worst 5 of 601 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	126	GLN	N-CA-C	-14.71	95.95	112.57
19	S	109	ARG	N-CA-C	-11.87	101.09	114.62
14	N	117	GLY	N-CA-C	-10.91	99.25	115.72
48	VA	103	ASN	N-CA-C	-10.66	100.57	112.72
12	L	80	TYR	N-CA-C	-9.61	102.79	112.97

There are no chirality outliers.

5 of 129 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	203	U	Sidechain
1	A	309	C	Sidechain
1	A	322	G	Sidechain
1	A	324	U	Sidechain
1	A	98	U	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	37658	0	18908	1686	0
2	B	70288	0	35262	4090	0
3	C	3354	0	1695	203	0
4	D	2580	0	1304	168	0
5	E	1359	0	1425	95	0
6	F	1918	0	1987	417	0
7	G	3082	0	3165	424	0
8	H	2750	0	2863	441	0
9	I	2376	0	2325	310	0
10	J	1401	0	1500	275	0
11	K	1785	0	1862	253	0
12	L	1818	0	1908	238	0
13	M	1519	0	1587	191	0
14	N	1718	0	1754	201	0
15	O	1354	0	1383	141	0
16	P	723	0	774	104	0
17	Q	1543	0	1608	199	0
18	R	1054	0	1149	192	0
19	S	1721	0	1779	306	0
20	T	1556	0	1659	188	0
21	U	1443	0	1485	182	0
22	V	1442	0	1543	239	0
23	W	1522	0	1617	215	0
24	X	1446	0	1487	219	0
25	Y	1277	0	1323	152	0
26	Z	796	0	812	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	AA	1004	0	1048	111	0
28	BA	509	0	537	74	0
29	CA	969	0	1036	103	0
30	DA	994	0	1081	152	0
31	EA	1093	0	1155	133	0
32	FA	1174	0	1215	165	0
33	GA	463	0	491	40	0
34	HA	743	0	797	136	0
35	IA	890	0	938	116	0
36	JA	1020	0	1090	168	0
37	KA	851	0	880	172	0
38	LA	881	0	949	135	0
39	MA	970	0	1078	96	0
40	NA	772	0	849	104	0
41	OA	682	0	687	88	0
42	PA	613	0	682	40	0
43	QA	437	0	475	78	0
44	RA	418	0	459	60	0
45	SA	234	0	284	28	0
46	TA	848	0	918	96	0
47	UA	695	0	738	114	0
48	VA	1473	0	1514	151	0
49	WA	2445	0	2401	201	0
50	XA	1611	0	1618	169	0
51	YA	1709	0	1784	217	0
52	ZA	1635	0	1723	202	0
53	AB	1734	0	1817	139	0
54	BB	2069	0	2154	273	0
55	CB	1610	0	1675	195	0
56	DB	1820	0	1918	174	0
57	EB	1481	0	1572	153	0
58	FB	1490	0	1525	184	0
59	GB	1494	0	1573	168	0
60	HB	817	0	804	70	0
61	IB	1245	0	1314	158	0
62	JB	496	0	141	4	0
63	KB	1193	0	1255	155	0
64	LB	942	0	979	116	0
65	MB	975	0	1017	89	0
66	NB	1106	0	1166	135	0
67	OB	836	0	827	56	0
68	PB	1193	0	1222	99	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	QB	1113	0	1124	104	0
70	RB	856	0	917	108	0
71	SB	685	0	672	85	0
72	TB	1022	0	1060	152	0
73	UB	1122	0	1196	116	0
74	VB	1074	0	1132	89	0
75	WB	563	0	603	72	0
76	XB	769	0	818	124	0
77	YB	611	0	633	58	0
78	ZB	498	0	535	54	0
79	AC	444	0	436	55	0
80	BC	475	0	525	33	0
81	CC	284	0	76	0	0
82	DC	6561	0	6629	677	0
83	EC	4105	0	2063	82	0
84	DC	28	0	12	3	0
85	DC	1	0	0	0	0
86	DC	35	0	40	6	0
All	All	215363	0	160021	15614	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 42.

The worst 5 of 15614 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)
10:J:31:ARG:CD	37:KA:107:ILE:HA	1.38	1.53
10:J:158:TYR:CE1	18:R:115:PHE:HA	1.45	1.50
10:J:165:LEU:HG	37:KA:6:ARG:O	1.26	1.33
10:J:31:ARG:HD3	37:KA:107:ILE:CA	1.57	1.33
10:J:165:LEU:O	37:KA:6:ARG:CB	1.80	1.28

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%)	125 (76%)	32 (19%)	8 (5%)	2	19
6	F	250/254 (98%)	152 (61%)	66 (26%)	32 (13%)	0	4
7	G	384/387 (99%)	268 (70%)	80 (21%)	36 (9%)	0	10
8	H	359/362 (99%)	239 (67%)	79 (22%)	41 (11%)	0	5
9	I	294/297 (99%)	213 (72%)	57 (19%)	24 (8%)	0	11
10	J	173/176 (98%)	124 (72%)	33 (19%)	16 (9%)	0	10
11	K	220/244 (90%)	165 (75%)	46 (21%)	9 (4%)	2	21
12	L	231/256 (90%)	165 (71%)	52 (22%)	14 (6%)	1	15
13	M	189/191 (99%)	134 (71%)	41 (22%)	14 (7%)	1	13
14	N	207/221 (94%)	150 (72%)	42 (20%)	15 (7%)	1	13
15	O	167/174 (96%)	118 (71%)	32 (19%)	17 (10%)	0	8
16	P	92/165 (56%)	61 (66%)	23 (25%)	8 (9%)	0	10
17	Q	191/199 (96%)	138 (72%)	36 (19%)	17 (9%)	0	10
18	R	134/138 (97%)	102 (76%)	23 (17%)	9 (7%)	1	15
19	S	201/204 (98%)	130 (65%)	58 (29%)	13 (6%)	1	15
20	T	195/199 (98%)	164 (84%)	23 (12%)	8 (4%)	2	21
21	U	181/184 (98%)	137 (76%)	36 (20%)	8 (4%)	2	20
22	V	183/186 (98%)	130 (71%)	42 (23%)	11 (6%)	1	16
23	W	186/189 (98%)	140 (75%)	35 (19%)	11 (6%)	1	16
24	X	170/172 (99%)	116 (68%)	42 (25%)	12 (7%)	1	14
25	Y	157/160 (98%)	107 (68%)	34 (22%)	16 (10%)	0	8
26	Z	98/121 (81%)	70 (71%)	24 (24%)	4 (4%)	2	21
27	AA	134/137 (98%)	103 (77%)	27 (20%)	4 (3%)	3	26
28	BA	59/155 (38%)	38 (64%)	14 (24%)	7 (12%)	0	5
29	CA	119/142 (84%)	83 (70%)	23 (19%)	13 (11%)	0	7
30	DA	124/127 (98%)	95 (77%)	19 (15%)	10 (8%)	1	11
31	EA	133/136 (98%)	92 (69%)	32 (24%)	9 (7%)	1	14
32	FA	146/149 (98%)	89 (61%)	40 (27%)	17 (12%)	0	5
33	GA	56/59 (95%)	46 (82%)	9 (16%)	1 (2%)	6	34
34	HA	95/105 (90%)	70 (74%)	21 (22%)	4 (4%)	2	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	IA	107/113 (95%)	78 (73%)	19 (18%)	10 (9%)	0	10
36	JA	125/130 (96%)	88 (70%)	34 (27%)	3 (2%)	4	30
37	KA	104/107 (97%)	72 (69%)	27 (26%)	5 (5%)	2	19
38	LA	110/121 (91%)	70 (64%)	28 (26%)	12 (11%)	0	7
39	MA	117/120 (98%)	93 (80%)	16 (14%)	8 (7%)	1	14
40	NA	97/100 (97%)	72 (74%)	21 (22%)	4 (4%)	2	21
41	OA	85/88 (97%)	45 (53%)	27 (32%)	13 (15%)	0	3
42	PA	75/78 (96%)	64 (85%)	11 (15%)	0	100	100
43	QA	48/51 (94%)	29 (60%)	12 (25%)	7 (15%)	0	3
44	RA	50/128 (39%)	30 (60%)	15 (30%)	5 (10%)	0	8
45	SA	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
46	TA	103/106 (97%)	67 (65%)	29 (28%)	7 (7%)	1	14
47	UA	89/92 (97%)	55 (62%)	25 (28%)	9 (10%)	0	8
48	VA	187/312 (60%)	137 (73%)	34 (18%)	16 (9%)	0	10
49	WA	316/319 (99%)	236 (75%)	67 (21%)	13 (4%)	2	21
50	XA	204/252 (81%)	141 (69%)	45 (22%)	18 (9%)	0	10
51	YA	212/255 (83%)	142 (67%)	51 (24%)	19 (9%)	0	10
52	ZA	215/254 (85%)	160 (74%)	41 (19%)	14 (6%)	1	15
53	AB	221/240 (92%)	169 (76%)	35 (16%)	17 (8%)	1	12
54	BB	258/261 (99%)	188 (73%)	53 (20%)	17 (7%)	1	15
55	CB	204/225 (91%)	156 (76%)	32 (16%)	16 (8%)	1	12
56	DB	224/236 (95%)	169 (75%)	42 (19%)	13 (6%)	1	16
57	EB	182/190 (96%)	118 (65%)	44 (24%)	20 (11%)	0	6
58	FB	184/200 (92%)	130 (71%)	36 (20%)	18 (10%)	0	9
59	GB	183/197 (93%)	132 (72%)	35 (19%)	16 (9%)	0	10
60	HB	94/105 (90%)	63 (67%)	22 (23%)	9 (10%)	0	9
61	IB	153/156 (98%)	102 (67%)	41 (27%)	10 (6%)	1	15
62	JB	122/143 (85%)	87 (71%)	20 (16%)	15 (12%)	0	4
63	KB	148/151 (98%)	114 (77%)	25 (17%)	9 (6%)	1	15
64	LB	125/137 (91%)	90 (72%)	28 (22%)	7 (6%)	1	17
65	MB	120/142 (84%)	81 (68%)	30 (25%)	9 (8%)	1	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	NB	139/143 (97%)	106 (76%)	24 (17%)	9 (6%)	1	15
67	OB	115/136 (85%)	90 (78%)	19 (16%)	6 (5%)	1	18
68	PB	143/146 (98%)	99 (69%)	34 (24%)	10 (7%)	1	14
69	QB	141/144 (98%)	108 (77%)	23 (16%)	10 (7%)	1	14
70	RB	105/121 (87%)	77 (73%)	25 (24%)	3 (3%)	3	26
71	SB	85/87 (98%)	64 (75%)	13 (15%)	8 (9%)	0	10
72	TB	127/130 (98%)	89 (70%)	28 (22%)	10 (8%)	1	12
73	UB	142/145 (98%)	102 (72%)	31 (22%)	9 (6%)	1	15
74	VB	132/135 (98%)	94 (71%)	31 (24%)	7 (5%)	1	18
75	WB	68/108 (63%)	48 (71%)	11 (16%)	9 (13%)	0	3
76	XB	95/119 (80%)	60 (63%)	19 (20%)	16 (17%)	0	2
77	YB	79/82 (96%)	50 (63%)	24 (30%)	5 (6%)	1	15
78	ZB	61/67 (91%)	42 (69%)	19 (31%)	0	100	100
79	AC	51/56 (91%)	41 (80%)	7 (14%)	3 (6%)	1	16
80	BC	58/63 (92%)	41 (71%)	13 (22%)	4 (7%)	1	14
81	CC	69/152 (45%)	37 (54%)	14 (20%)	18 (26%)	0	1
82	DC	838/842 (100%)	629 (75%)	153 (18%)	56 (7%)	1	15
All	All	12226/13416 (91%)	8741 (72%)	2555 (21%)	930 (8%)	1	13

5 of 930 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	21	ARG
6	F	77	ILE
6	F	93	LYS
6	F	120	PRO
6	F	203	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	157/198 (79%)	133 (85%)	24 (15%)	3	15
6	F	194/196 (99%)	170 (88%)	24 (12%)	4	20
7	G	322/323 (100%)	284 (88%)	38 (12%)	5	21
8	H	288/289 (100%)	247 (86%)	41 (14%)	3	17
9	I	244/245 (100%)	213 (87%)	31 (13%)	4	20
10	J	152/153 (99%)	140 (92%)	12 (8%)	11	35
11	K	186/205 (91%)	168 (90%)	18 (10%)	8	27
12	L	191/208 (92%)	174 (91%)	17 (9%)	9	31
13	M	171/171 (100%)	151 (88%)	20 (12%)	5	21
14	N	180/187 (96%)	159 (88%)	21 (12%)	5	21
15	O	147/150 (98%)	135 (92%)	12 (8%)	10	34
16	P	81/136 (60%)	63 (78%)	18 (22%)	1	6
17	Q	154/159 (97%)	131 (85%)	23 (15%)	3	16
18	R	107/109 (98%)	95 (89%)	12 (11%)	6	22
19	S	175/176 (99%)	143 (82%)	32 (18%)	2	12
20	T	160/162 (99%)	144 (90%)	16 (10%)	7	26
21	U	145/146 (99%)	131 (90%)	14 (10%)	8	27
22	V	150/151 (99%)	135 (90%)	15 (10%)	7	26
23	W	153/154 (99%)	138 (90%)	15 (10%)	7	27
24	X	156/156 (100%)	130 (83%)	26 (17%)	2	13
25	Y	136/137 (99%)	116 (85%)	20 (15%)	3	16
26	Z	87/107 (81%)	82 (94%)	5 (6%)	18	43
27	AA	104/105 (99%)	90 (86%)	14 (14%)	4	18
28	BA	54/129 (42%)	48 (89%)	6 (11%)	6	23
29	CA	105/118 (89%)	89 (85%)	16 (15%)	3	15
30	DA	109/110 (99%)	93 (85%)	16 (15%)	3	16
31	EA	115/116 (99%)	104 (90%)	11 (10%)	8	28
32	FA	118/119 (99%)	107 (91%)	11 (9%)	8	29
33	GA	46/47 (98%)	38 (83%)	8 (17%)	2	13
34	HA	81/88 (92%)	72 (89%)	9 (11%)	6	23
35	IA	96/97 (99%)	80 (83%)	16 (17%)	2	13
36	JA	109/111 (98%)	92 (84%)	17 (16%)	2	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	KA	90/91 (99%)	86 (96%)	4 (4%)	25	48
38	LA	95/103 (92%)	84 (88%)	11 (12%)	5	21
39	MA	104/105 (99%)	88 (85%)	16 (15%)	2	15
40	NA	81/82 (99%)	72 (89%)	9 (11%)	6	23
41	OA	70/71 (99%)	65 (93%)	5 (7%)	13	38
42	PA	68/69 (99%)	65 (96%)	3 (4%)	25	48
43	QA	45/46 (98%)	40 (89%)	5 (11%)	6	23
44	RA	47/116 (40%)	44 (94%)	3 (6%)	16	40
45	SA	23/23 (100%)	19 (83%)	4 (17%)	2	13
46	TA	90/91 (99%)	70 (78%)	20 (22%)	1	6
47	UA	71/72 (99%)	57 (80%)	14 (20%)	1	9
48	VA	160/254 (63%)	144 (90%)	16 (10%)	7	26
49	WA	261/262 (100%)	250 (96%)	11 (4%)	26	49
50	XA	172/210 (82%)	156 (91%)	16 (9%)	8	29
51	YA	191/224 (85%)	172 (90%)	19 (10%)	7	27
52	ZA	176/205 (86%)	166 (94%)	10 (6%)	18	43
53	AB	182/195 (93%)	166 (91%)	16 (9%)	9	32
54	BB	221/222 (100%)	202 (91%)	19 (9%)	10	33
55	CB	173/191 (91%)	160 (92%)	13 (8%)	12	36
56	DB	193/201 (96%)	182 (94%)	11 (6%)	18	43
57	EB	165/170 (97%)	150 (91%)	15 (9%)	9	30
58	FB	150/161 (93%)	137 (91%)	13 (9%)	9	32
59	GB	158/166 (95%)	151 (96%)	7 (4%)	25	48
60	HB	89/98 (91%)	85 (96%)	4 (4%)	24	47
61	IB	136/137 (99%)	123 (90%)	13 (10%)	8	28
63	KB	127/128 (99%)	114 (90%)	13 (10%)	7	25
64	LB	96/105 (91%)	92 (96%)	4 (4%)	26	49
65	MB	103/118 (87%)	96 (93%)	7 (7%)	14	39
66	NB	117/119 (98%)	111 (95%)	6 (5%)	21	45
67	OB	82/124 (66%)	75 (92%)	7 (8%)	10	33
68	PB	128/129 (99%)	115 (90%)	13 (10%)	7	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	QB	115/116 (99%)	110 (96%)	5 (4%)	26	48
70	RB	100/114 (88%)	92 (92%)	8 (8%)	11	35
71	SB	74/74 (100%)	67 (90%)	7 (10%)	8	28
72	TB	110/111 (99%)	93 (84%)	17 (16%)	2	15
73	UB	119/120 (99%)	111 (93%)	8 (7%)	15	39
74	VB	112/113 (99%)	104 (93%)	8 (7%)	13	38
75	WB	61/89 (68%)	57 (93%)	4 (7%)	15	40
76	XB	83/101 (82%)	71 (86%)	12 (14%)	3	16
77	YB	70/71 (99%)	63 (90%)	7 (10%)	7	26
78	ZB	56/60 (93%)	53 (95%)	3 (5%)	20	44
79	AC	47/49 (96%)	41 (87%)	6 (13%)	4	20
80	BC	51/54 (94%)	44 (86%)	7 (14%)	3	17
82	DC	713/714 (100%)	626 (88%)	87 (12%)	5	21
All	All	10248/11032 (93%)	9164 (89%)	1084 (11%)	9	24

5 of 1084 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
72	TB	24	GLN
74	VB	77	ASN
72	TB	11	LEU
82	DC	435	VAL
23	W	14	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 352 such sidechains are listed below:

Mol	Chain	Res	Type
53	AB	67	ASN
66	NB	100	GLN
54	BB	98	ASN
58	FB	64	ASN
70	RB	18	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1753/1798 (97%)	368 (20%)	5 (0%)
2	B	3265/3396 (96%)	680 (20%)	26 (0%)
3	C	157/158 (99%)	36 (22%)	2 (1%)
4	D	120/121 (99%)	17 (14%)	0
83	EC	185/201 (92%)	73 (39%)	3 (1%)
All	All	5480/5674 (96%)	1174 (21%)	36 (0%)

5 of 1174 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	42	G

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	3242	G
83	EC	6949	G
2	B	3269	U
3	C	85	G
2	B	1064	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	18,20,21	2.84	8 (44%)	17,28,30	2.31	6 (35%)

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	-	4/20/21/23	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	DC	699	DDE	CD2-CG	7.98	1.53	1.36
82	DC	699	DDE	CBW-CBI	4.56	1.61	1.53
82	DC	699	DDE	CAT-CE1	3.88	1.56	1.49
82	DC	699	DDE	CB-CG	3.16	1.58	1.49
82	DC	699	DDE	CBW-NCB	3.04	1.60	1.54

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	DC	699	DDE	CAU-CAT-CE1	7.21	141.28	114.38
82	DC	699	DDE	CD2-NE2-CE1	3.11	110.15	107.55
82	DC	699	DDE	CAU-CBW-CBI	-2.79	105.77	111.22
82	DC	699	DDE	CD2-CG-ND1	-2.36	104.11	108.87
82	DC	699	DDE	OAG-CBI-NAD	2.11	126.76	123.04

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
82	DC	699	DDE	OAG-CBI-CBW-NCB
82	DC	699	DDE	CE1-CAT-CAU-CBW
82	DC	699	DDE	CA-CB-CG-ND1
82	DC	699	DDE	CA-CB-CG-CD2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	DC	699	DDE	2	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides 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
86	SO1	DC	903	-	34,39,39	2.52	16 (47%)	38,64,64	2.04	10 (26%)
84	GDP	DC	901	85	29,30,30	2.18	6 (20%)	45,47,47	1.76	11 (24%)

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
86	SO1	DC	903	-	-	3/21/104/104	0/7/5/5
84	GDP	DC	901	85	-	3/16/32/32	0/3/3/3

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	DC	901	GDP	PA-O3A	8.29	1.68	1.59
86	DC	903	SO1	O56-C52	-4.42	1.30	1.41
86	DC	903	SO1	O17-C52	4.41	1.47	1.40
86	DC	903	SO1	C8-C2	3.88	1.60	1.53
86	DC	903	SO1	C7-C2	3.81	1.60	1.54

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	DC	903	SO1	C12-C6-C10	-5.57	103.56	107.92
84	DC	901	GDP	C2-N3-C4	5.52	121.81	112.30
84	DC	901	GDP	C5-C4-N3	-5.35	119.88	128.39
86	DC	903	SO1	C25-C22-C24	5.33	130.59	113.64
84	DC	901	GDP	N9-C4-N3	4.10	134.14	125.95

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

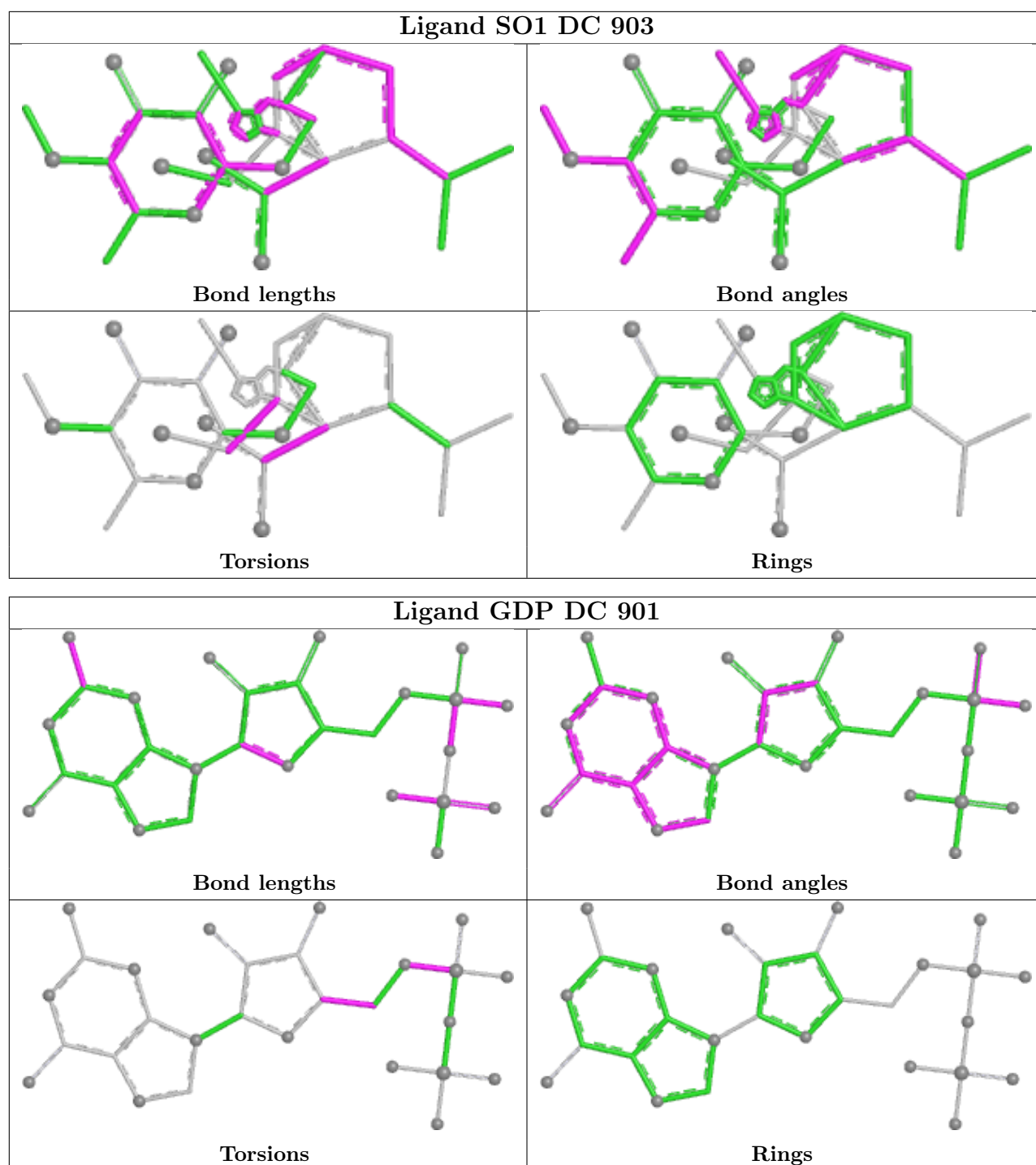
Mol	Chain	Res	Type	Atoms
84	DC	901	GDP	O4'-C4'-C5'-O5'
86	DC	903	SO1	C2-C1-C5-O14
86	DC	903	SO1	C2-C1-C5-O15
84	DC	901	GDP	C3'-C4'-C5'-O5'
84	DC	901	GDP	C5'-O5'-PA-O1A

There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	DC	903	SO1	6	0
84	DC	901	GDP	3	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 than 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.



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.

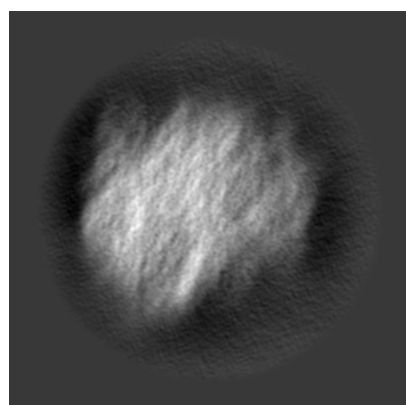
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6643. These allow visual inspection of the internal detail of the map and identification of artifacts.

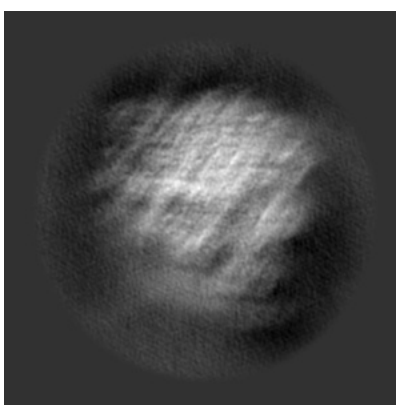
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

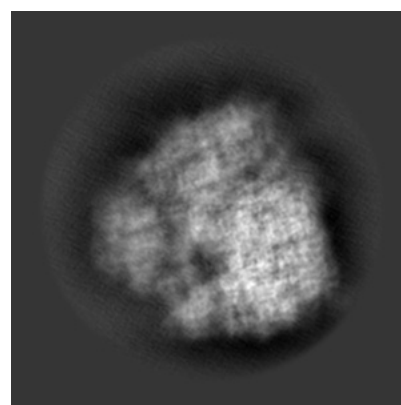
6.1.1 Primary map



X



Y

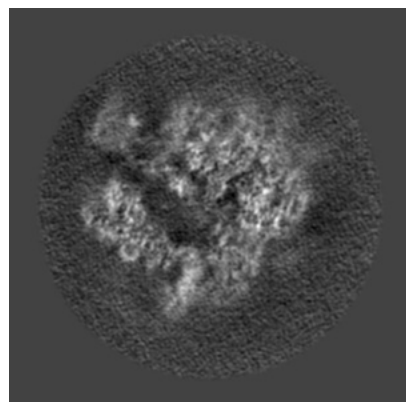


Z

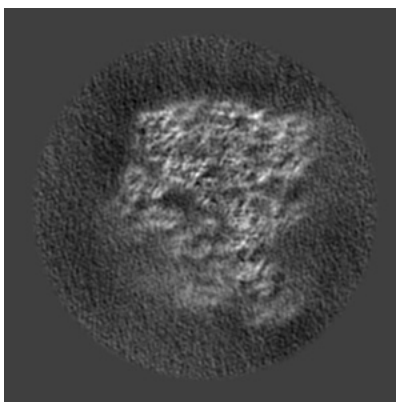
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

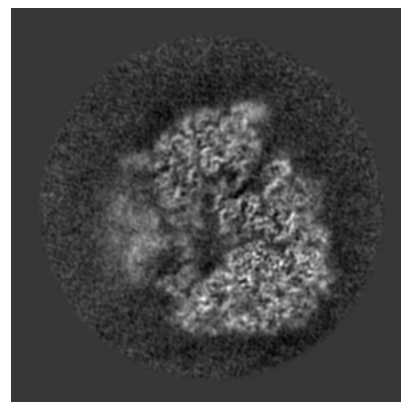
6.2.1 Primary map



X Index: 128



Y Index: 128

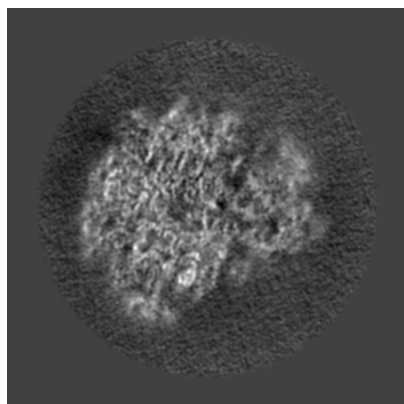


Z Index: 128

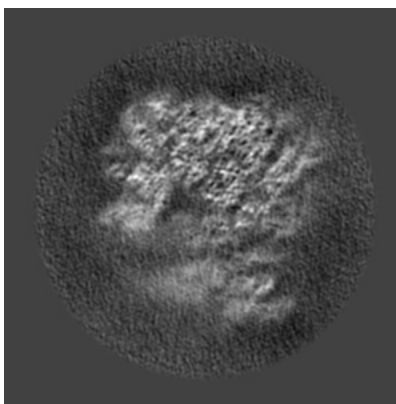
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

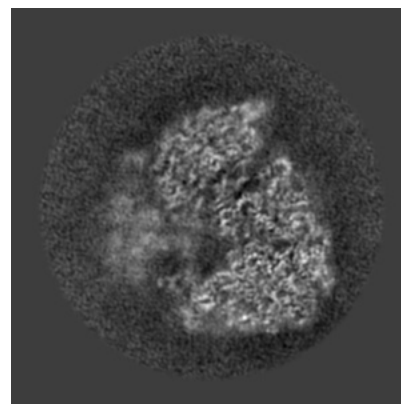
6.3.1 Primary map



X Index: 146



Y Index: 117

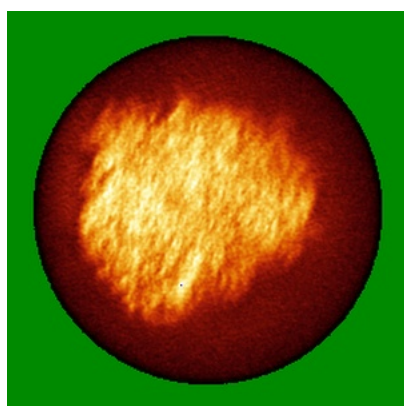


Z Index: 130

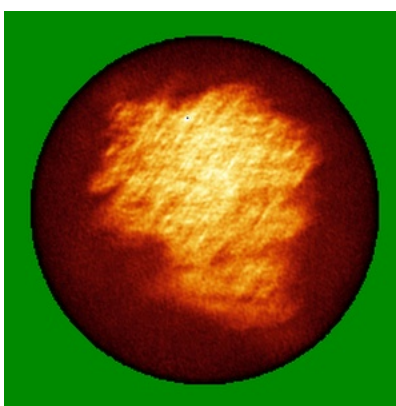
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

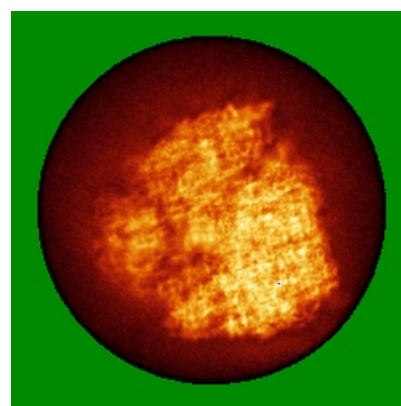
6.4.1 Primary map



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

This section was not generated.

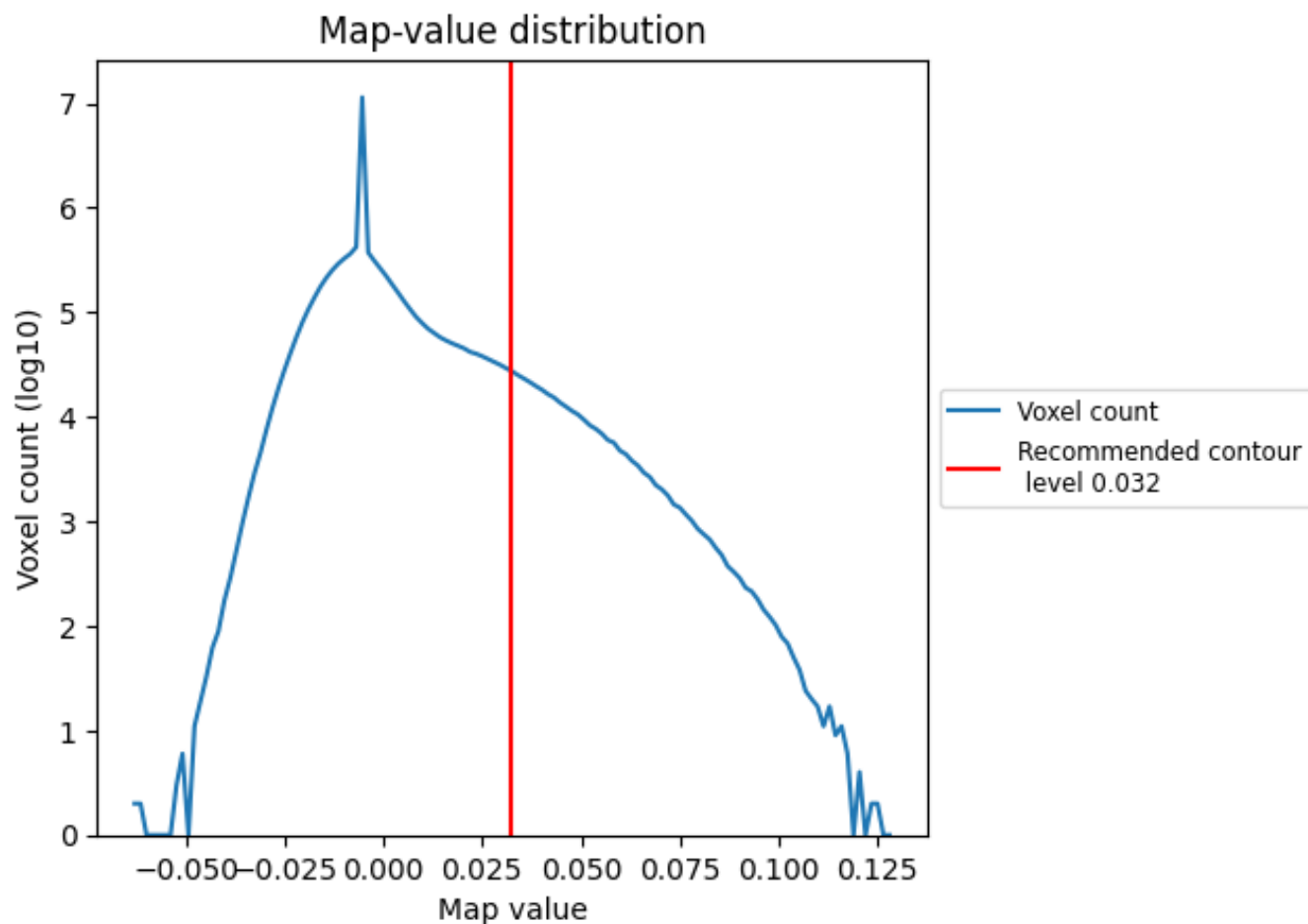
6.6 Mask visualisation

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

7 Map analysis [i](#)

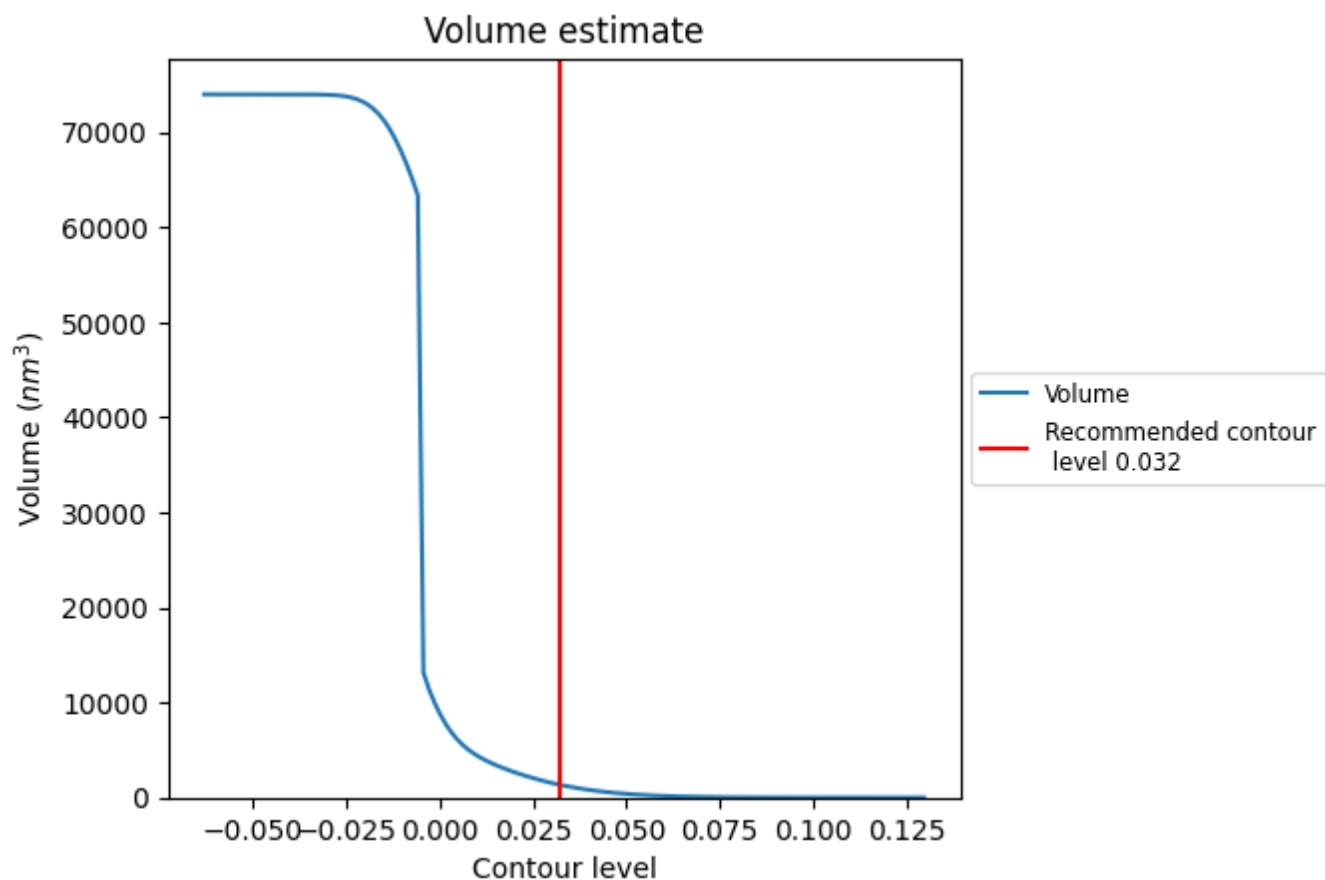
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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.

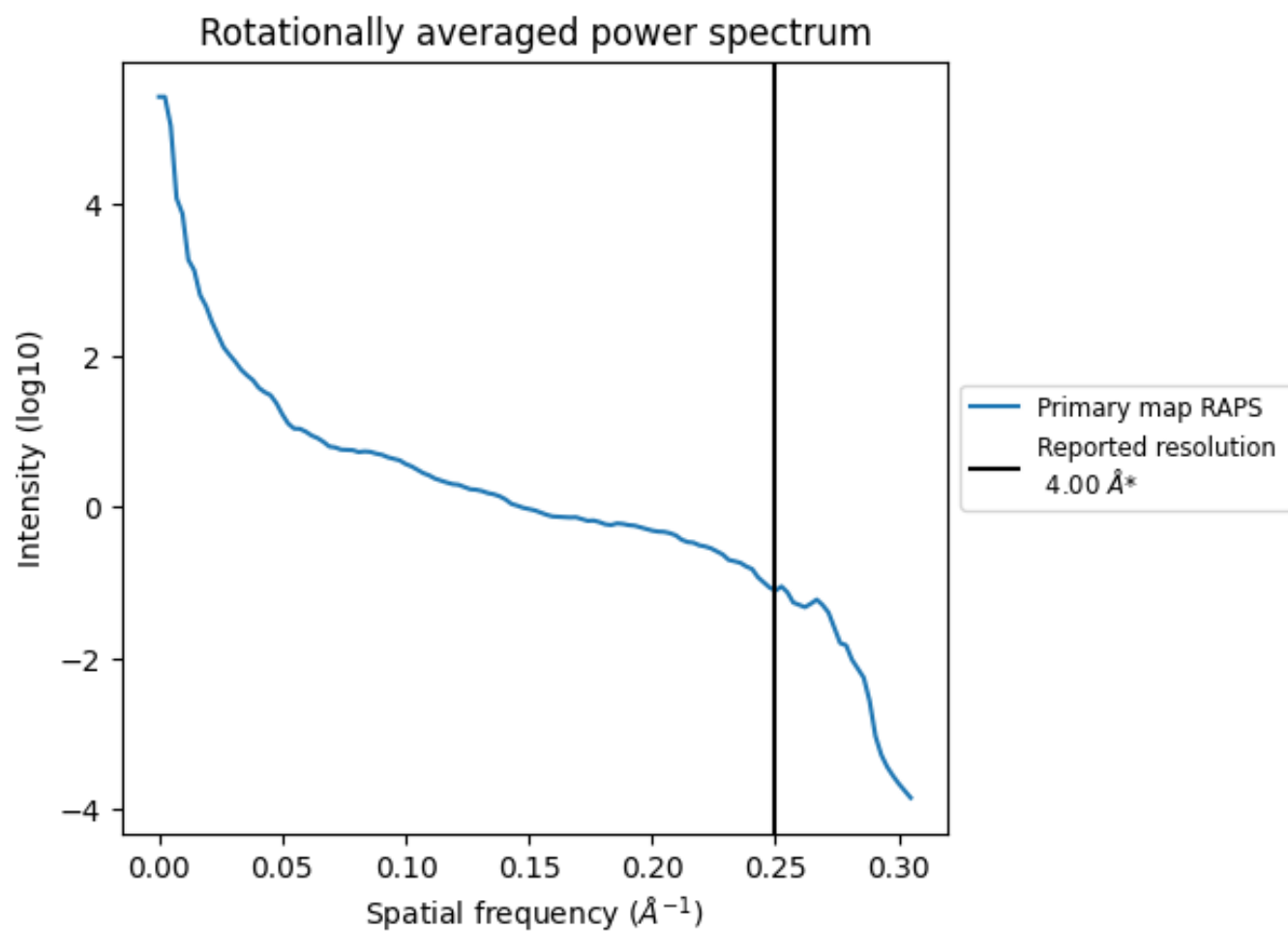
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1358 nm³; this corresponds to an approximate mass of 1227 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6643 and PDB model 5JUO. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

This section was not generated.

9.2 Q-score mapped to coordinate model [i](#)

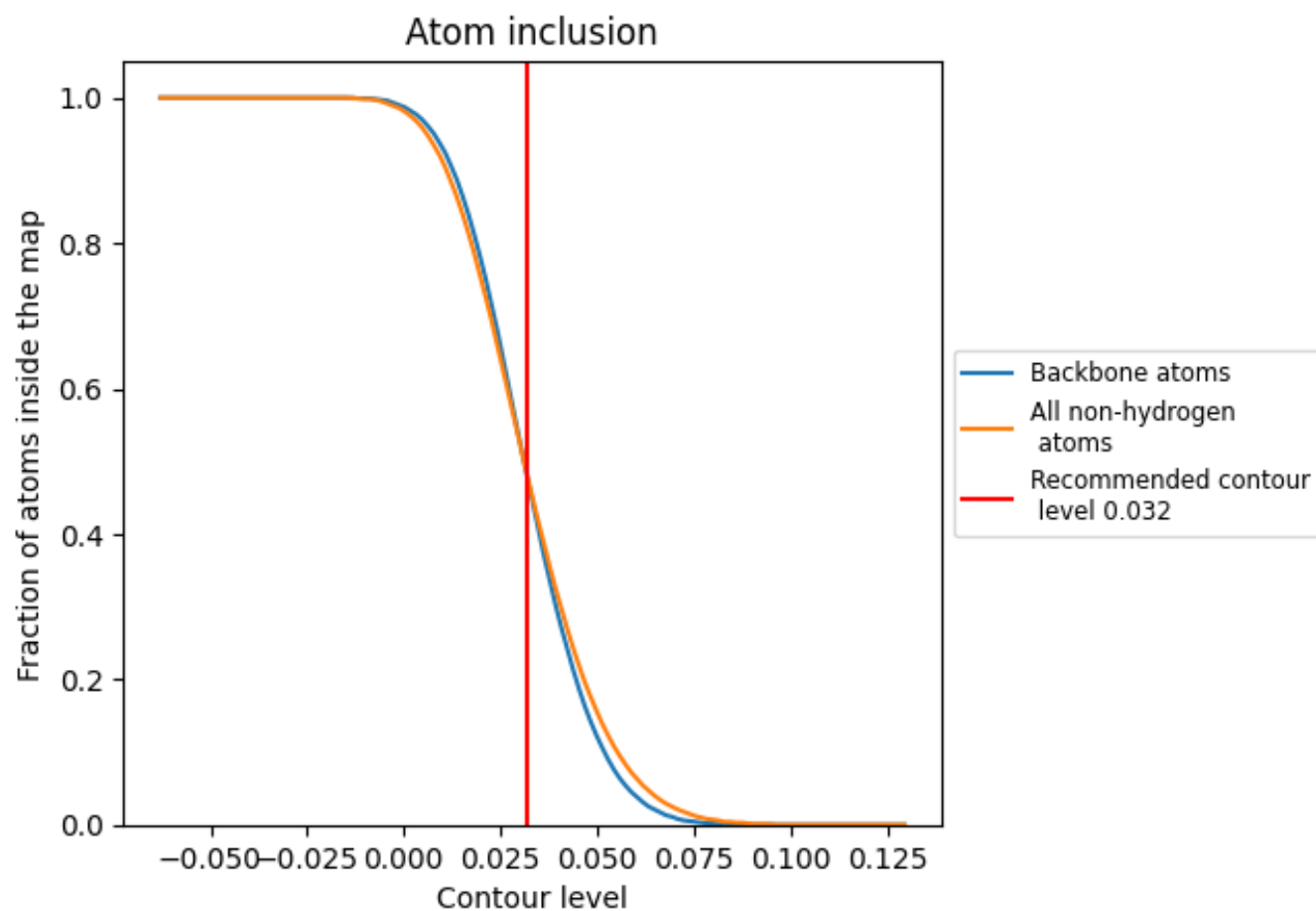


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 48% 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 (0.032) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4790	0.2040
A	0.5020	0.1890
AA	0.2860	0.2560
AB	0.0840	0.1120
AC	0.2730	0.0780
B	0.6760	0.2440
BA	0.2490	0.2340
BB	0.5170	0.2050
BC	0.1370	0.1810
C	0.6460	0.2300
CA	0.2220	0.1680
CB	0.2280	0.1330
CC	0.0040	0.0250
D	0.7830	0.2300
DA	0.4960	0.1870
DB	0.2600	0.1630
DC	0.2620	0.1730
E	0.0780	0.0830
EA	0.2580	0.1320
EB	0.0630	0.1030
EC	0.1850	0.0860
F	0.5130	0.2250
FA	0.5830	0.2770
FB	0.3170	0.1660
G	0.4450	0.2470
GA	0.5470	0.2670
GB	0.4620	0.2120
H	0.5310	0.2540
HA	0.4980	0.1840
HB	0.2070	0.0580
I	0.4220	0.1740
IA	0.4830	0.2370
IB	0.2400	0.1850
J	0.2760	0.2090
JA	0.5340	0.2640



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Chain	Atom inclusion	Q-score
JB	 0.0000	 -0.0160
K	 0.4580	 0.2370
KA	 0.3270	 0.2730
KB	 0.1760	 0.1510
L	 0.2940	 0.1830
LA	 0.4690	 0.1970
LB	 0.4510	 0.2010
M	 0.3530	 0.2500
MA	 0.2290	 0.1810
MB	 0.0910	 0.0360
N	 0.3750	 0.2290
NA	 0.4760	 0.2190
NB	 0.1380	 0.1110
O	 0.3620	 0.1810
OA	 0.5350	 0.2400
OB	 0.0860	 0.1320
P	 0.1850	 0.0540
PA	 0.0120	 0.0860
PB	 0.0730	 0.0680
Q	 0.6390	 0.2500
QA	 0.5480	 0.2280
QB	 0.0830	 0.0800
R	 0.4670	 0.2300
RA	 0.5070	 0.2640
RB	 0.0790	 0.0760
S	 0.4480	 0.2420
SA	 0.2820	 0.2650
SB	 0.1970	 0.1990
T	 0.4520	 0.2620
TA	 0.5670	 0.2180
TB	 0.3050	 0.2100
U	 0.5480	 0.2400
UA	 0.5120	 0.2050
UB	 0.2210	 0.2240
V	 0.6090	 0.2550
VA	 0.2270	 0.1130
VB	 0.2730	 0.2120
W	 0.3260	 0.1760
WA	 0.0130	 0.1100
WB	 0.0550	 0.1060
X	 0.4410	 0.2430
XA	 0.1060	 0.1600

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Chain	Atom inclusion	Q-score
XB	 0.3990	 0.2400
Y	 0.3970	 0.2310
YA	 0.2160	 0.1710
YB	 0.2130	 0.1690
Z	 0.1920	 0.1390
ZA	 0.2460	 0.2020
ZB	 0.3740	 0.1580