



## wwPDB EM Validation Summary Report ⓘ

Nov 26, 2022 – 09:12 PM EST

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

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

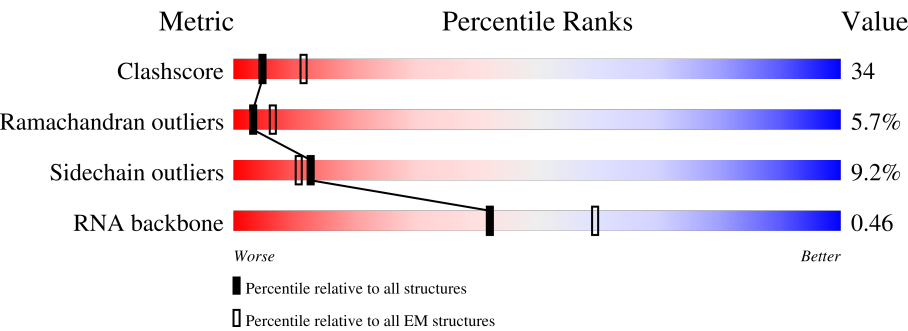
EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 4.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	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  $\geq 3$ , 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	<div><div>43%</div><div><div>30%</div><div>57%</div><div>12%</div><div>.</div></div></div>
2	B	3396	<div><div>18%</div><div><div>21%</div><div>56%</div><div>19%</div><div>..</div></div></div>
3	C	158	<div><div>23%</div><div><div>20%</div><div>62%</div><div>18%</div><div>.</div></div></div>
4	D	121	<div><div>.</div><div><div>26%</div><div>63%</div><div>11%</div><div>.</div></div></div>
5	E	217	<div><div>77%</div><div><div>30%</div><div>40%</div><div>8%</div><div>21%</div></div></div>
6	F	254	<div><div>41%</div><div><div>26%</div><div>62%</div><div>10%</div><div>..</div></div></div>
7	G	387	<div><div>45%</div><div><div>29%</div><div>61%</div><div>9%</div></div></div>

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

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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	<div><div></div><div>89%</div><div>22%41%25%11%</div></div>

## 2 Entry composition

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

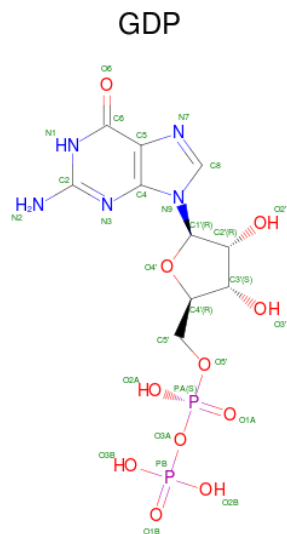
- Molecule 82 is a protein called yeast eEF2.

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

- Molecule 83 is a RNA chain called IRES.

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

- Molecule 84 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>11</sub>P<sub>2</sub>).

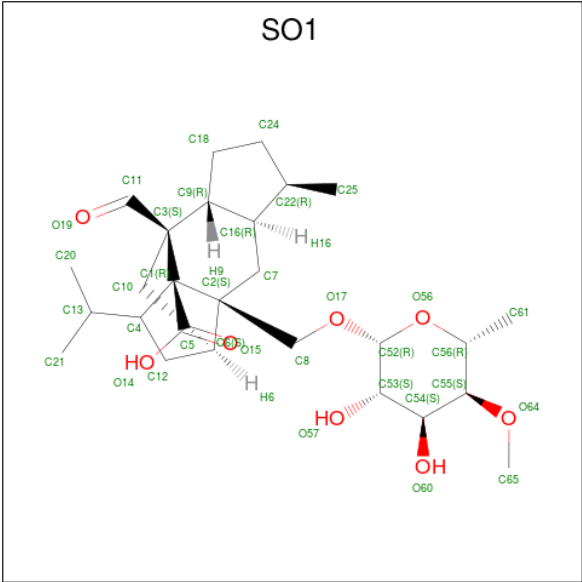


Mol	Chain	Residues	Atoms					AltConf
84	DC	1	Total	C	N	O	P	0
			28	10	5	11	2	

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

Mol	Chain	Residues	Atoms	AltConf
85	DC	1	Total Mg 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<sub>27</sub>H<sub>42</sub>O<sub>8</sub>).

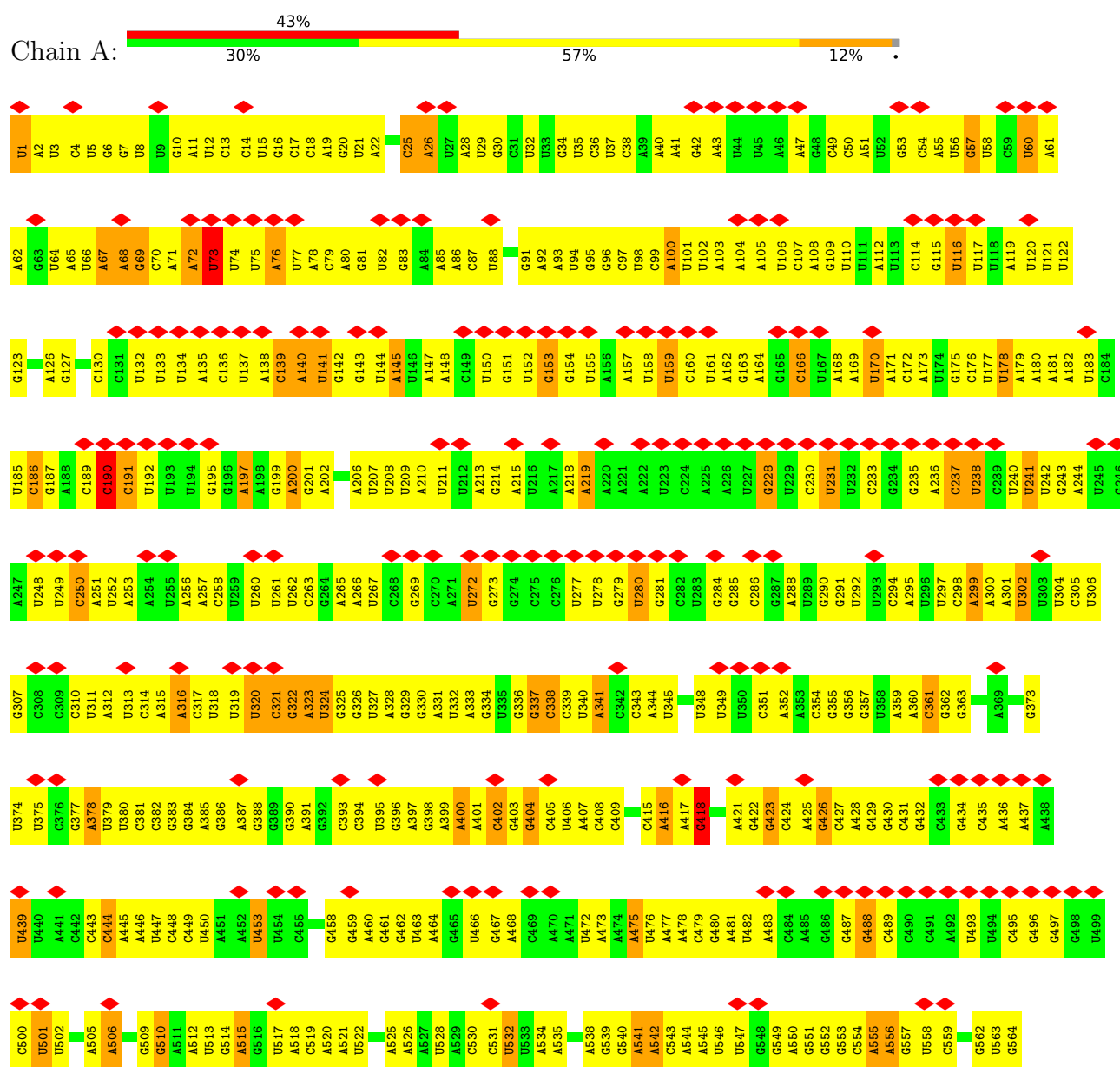


Mol	Chain	Residues	Atoms			AltConf
86	DC	1	Total	C	O	0
			35	27	8	

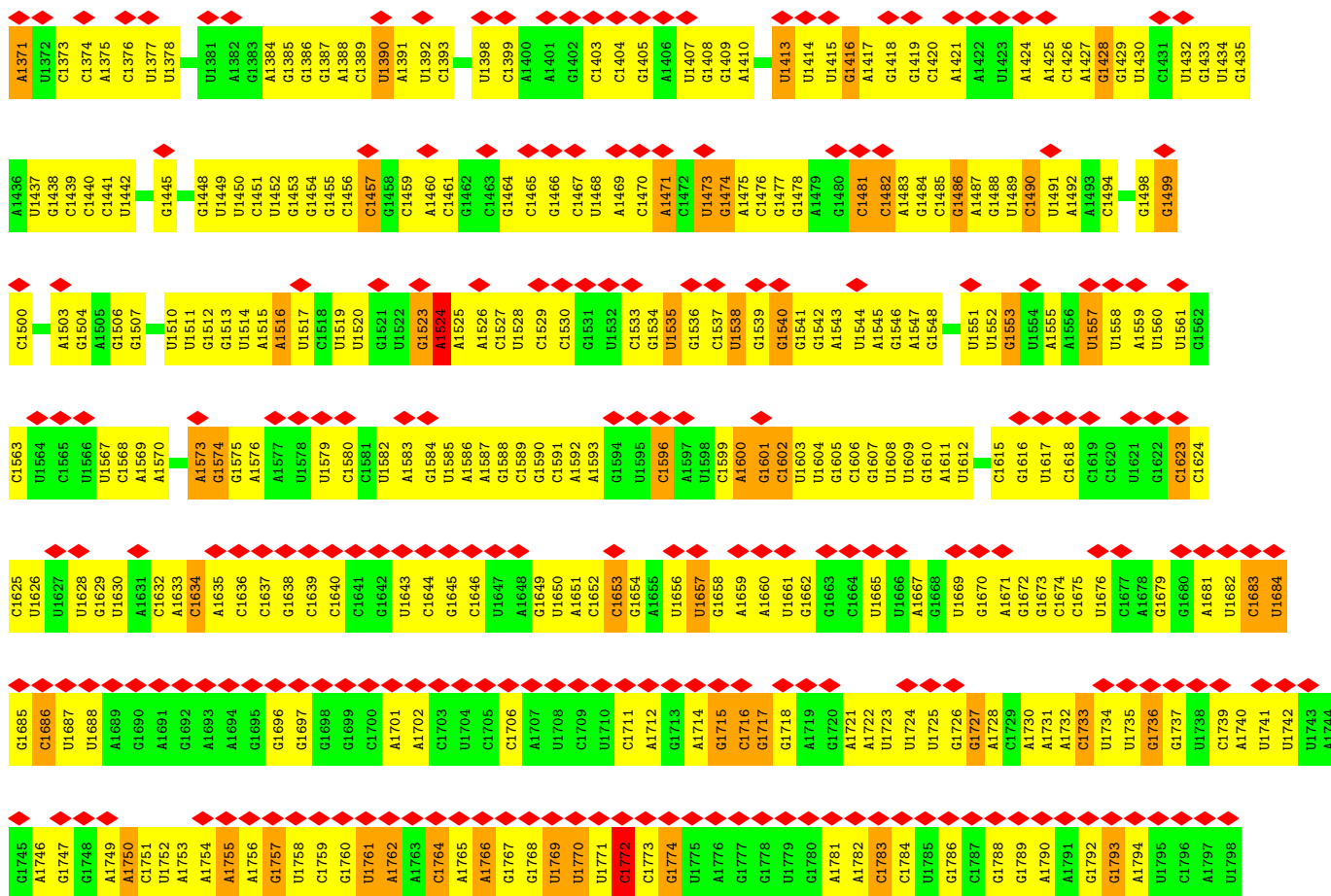
### 3 Residue-property plots

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.

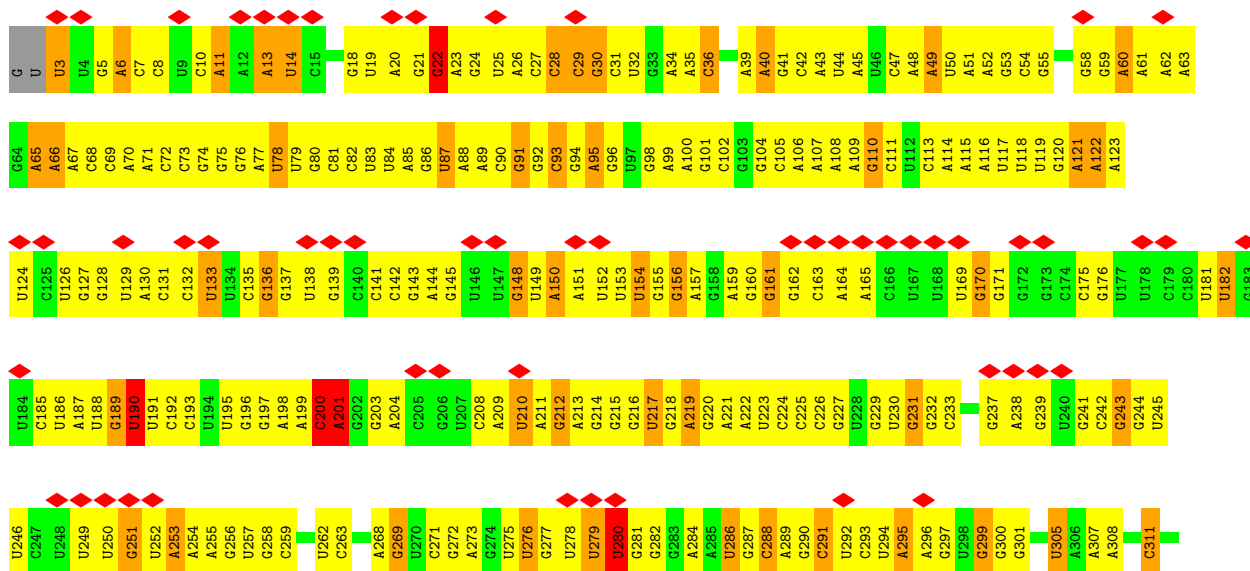
#### • Molecule 1: 18S ribosomal RNA



U1305	C1306	U1307	A1313	U1314	U1315	G1316	C1317	G1318	A1319	U1320	A1321	A1322	G1323	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	C1358	C1359	A1360	U1361	C1362	U1363	G1364	C1365	G1366	G1367	U1368	U1369	U1370																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
G1241	A1242	G1243	A1244	G1245	C1246	U1247	A1248	U1249	U1250	U1251	C1252	U1253	U1254	G1255	A1256	U1257	U1258	U1259	U1260	G1261	U1262	G1263	G1264	G1265	U1269	U1270	G1271	U1272	G1273	C1274	A1275	U1276	G1277	G1278	C1279	C1280	G1281	U1282	U1283	C1284	U1285	U1286	A1287	G1288	U1289	U1290	G1291	C1292	U1293	G1294	U1298	G1299	A1300	U1301	U1302	U1303	G1304																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
C1177	G1178	G1179	U1180	U1181	U1182	A1183	A1184	U1185	U1186	U1187	G1188	A1189	C1190	U1191	C1192	A1193	A1194	C1195	A1196	C1197	U1198	G1199	G1200	G1201	A1202	A1203	A1204	C1205	A1208	C1209	C1210	A1211	G1212	G1213	U1214	C1215	C1216	A1217	G1218	A1219	A1223	A1224	U1225	A1226	A1227	G1228	G1229	A1230	U1231	U1232	C1235	A1236	G1237	A1238	U1239	U1240																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
U1115	A1116	U1117	G1118	U1119	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	G1163	G1164	G1165	A1166	G1167	U1168	G1169	G1170	A1171	G1172	C1173	G1174	U1175	G1176																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
U1054	U1055	U1056	U1057	U1058	U1059	U1060	A1061	A1062	U1063	G1064	A1065	C1066	C1067	C1068	A1069	C1070	U1071	C1072	G1073	G1074	C1075	A1076	C1077	C1078	U1080	A1081	C1082	G1083	A1086	A1087	U1088	U1089	C1090	A1091	A1092	A1093	G1094	U1095	C1096	U1097	U1098	U1099	G1100	G1101	G1102	U1103	U1104	C1105	U1106	G1107	G1108	G1109	G1110	G1111	G1112	A1113	G1114																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
G994	A995	U996	U997	A998	U999	C1000	A1001	G1002	A1003	U1004	A1005	C1006	C1007	G1008	U1009	C1010	G1011	U1012	A1013	G1014	U1015	C1016	U1017	U1018	A1019	A1020	C1021	C1022	A1023	U1024	A1025	A1026	A1027	C1028	U1029	U1031	C1032	C1033	C1034	G1035	A1036	C1037	U1038	A1039	G1040	G1041	A1042	A1043	U1044	C1045	G1046	G1047	G1048	U1049	G1050	G1051	U1052	G1053																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
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U873	C874	G875	G876	G877	G878	G879	C880	A881	U882	C883	A884	G885	U886	A887	U888	U889	C890	A891	A892	U893	U894	G895	U896	C897	A898	G899	A900	G901	G902	U903	G904	A905	A906	A907	U908	U909	C910	U911	U912	G913	G914	A915	U916	U917	U918	A919	U920	U921	A922	G923	A924	G925	A926	C927	U928	A929	A930	C931	U932																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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G687	C688	C689	C690	C691	C692	C693	C694	C695	C696	C697	C698	C699	C700	C701	C702	C703	C704	C705	A706	A707	C708	C709	U710	U711	C712	A713	C714	U715	C716	C717	U718	U719	C720	U721	C722	C723	C724	U725	C726	C727	U728	U729	C730	C731	C732	A733	A734	C735	C736	A737	C738	C739	A740	A845	A846	U743	U744	U745	A746	C747	U748	U749																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
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• Molecule 2: 25S ribosomal RNA

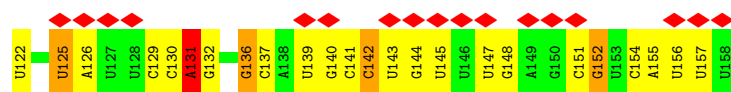


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G1131	C1069	A1002	G941	C818	C758	C696	G632	U571	G505	G445	C379	C315
A1132	A1003	A1003	U942	U819	U759	A697	C633	A572	G506	U446	U380	U316
A1133	U1070	A1004	U943	A820	G760	U698	C634	C573	U507	U447	U381	A317
G1134	U1071	G1005	C944	U821	A761	A699	G635	U574	U508	U448	U382	A318
A1135	C1072	A1006	C945	U822	U762	C700	G636	G575	U509	U449	G383	A319
A1136	U1073	A1007	C946	C823	G763	G701	C637	C576	G510	U450	G384	G320
C1137	U1074	U1007	U947	C824	U764	G702	C638	A577	G511	U451	U321	U322
U1138	A1075	C947	G948	U825	C765	U704	G703	G578	U512	U452	A387	A323
G1139	C949	A888	U826	U765	U766	U705	U640	G579	G513	U453	A388	A324
G1140	U1078	U889	U890	U829	U767	A706	U642	U581	C515	G454	A389	A325
A1141	A951	C890	A830	U830	C768	G708	U643	G582	A516	C	G590	U326
A1142	A952	U891	U831	U831	G769	U709	G644	G583	G517	C	G594	A327
A1143	G953	U892	U832	U832	G770	A710	A645	G584	G518	U	A395	U328
G1144	U954	C893	U833	U833	A771	U711	A646	A585	A519	C	A396	U329
G1145	U955	G894	U834	U834	U772	G712	A647	C586	U520	U	A397	A336
G1146	U956	A895	A835	U835	G773	U713	C648	G588	A521	G	A398	A337
G1147	C957	A896	A836	U836	G774	U714	C649	A589	A522	C	A399	A338
G1148	C958	U897	A837	U837	U775	G715	C650	G590	A523	U	G400	G337
G1149	C959	U898	C838	U838	U776	A716	G651	C591	C525	C	U401	A338
A1150	U960	U899	C839	U839	U777	G717	G652	A592	C526	C	A402	C339
A1151	C961	G900	C840	U841	U778	C718	A653	C593	A527	U	C403	C340
A1152	A962	G901	C841	U841	U779	G719	C654	U594	U528	U	G404	G341
G1153	G963	G902	C842	U842	G779	U719	C655	G595	A529	C	U405	A342
G1154	G964	U903	C843	U843	A780	A720	A656	C596	G	G	G406	U343
G1155	A965	A904	A844	U844	U782	G721	U660	G597	G	G	A407	A344
G1156	U966	U905	G845	U845	U783	U724	A660	A598	U536	G	A408	G345
A1157	A967	A906	A846	U846	A784	G725	G661	C599	A537	U	A409	C346
A1158	U968	G907	A847	U847	G785	G726	C662	G600	G538	U	U410	G347
A1159	C969	G908	A848	U848	A786	G727	C663	U601	G	A	U411	A348
G1160	A970	G909	U849	U849	G787	G728	A665	A602	C543	G	U412	A349
G1161	G971	G910	C849	U850	C788	G729	A666	G604	C544	G	U413	C350
A1162	G972	C911	U850	U850	G789	C730	C667	U605	U545	G	U414	A351
G1163	A973	G912	U851	U851	U790	C731	G668	C506	C546	A	U415	A352
A1164	G974	A913	U852	U852	U791	U731	C669	A607	G547	U	U416	U353
G1165	C975	A914	C853	U853	G792	G732	U670	A608	G548	C	A417	A354
G1166	U976	A915	C854	U854	C793	G733	C670	G609	G549	U	A418	A355
U1167	C977	G916	U855	U855	U794	C734	U671	G610	U550	U	G421	A356
U1168	G978	A917	C856	U856	G795	A735	A672	U611	A551	U	A422	G357
A1169	U979	C918	G857	U857	U796	A736	U673	U612	A552	U	A423	U358
A1170	A980	A920	A858	U858	G797	G737	G674	U613	A553	U	A424	G359
G1171	U981	A921	C859	U859	G798	G738	G675	G614	G554	U	G425	A361
U1172	C1043	A922	C860	U860	G799	G739	G676	C615	G555	U	G426	U362
G1173	A983	U922	C861	U861	G800	G740	A677	U616	U556	U	C427	G363
C1174	C1045	C923	U862	U862	A801	G741	G678	G617	A557	U	U428	A364
C1175	G1046	G924	C863	U863	C802	G742	U679	U618	U558	U	U429	A365
C1176	A1047	A925	C864	U864	G803	C743	U681	A621	U559	U	U430	A366
G1177	U986	A926	G865	U865	C804	A744	U682	A622	A560	U	U431	A367
A1178	U987	C927	U866	U866	C805	G745	U683	G685	G560	U	U432	G368
A1179	U988	U928	U867	U867	G806	A746	U684	U620	C561	U	U492	A369
A1180	U1050	C929	U868	U868	C807	C747	U685	U621	C562	U	G437	U370
U1181	U1051	C930	U869	U869	U810	U748	U689	U622	U563	U	G438	A372
A1182	U1052	A931	U870	U870	U811	C749	A690	G623	U564	U	A438	A373
C1183	U1053	U930	U871	U871	G812	G750	A691	U624	G565	U	C439	A374
A1184	A1054	C931	U872	U872	G813	U751	A692	U625	G566	U	U440	A375
C1185	U1055	U932	U873	U873	U814	C753	A693	U626	G567	U	U441	G376
G1186	U1056	G933	U874	U874	U815	A755	C894	U627	A569	U	G442	A377
C1187	A1057	A934	U875	U875	G816	U756						
G1188	U1058	U935	U876	U876	U817							
C1189	A997	U936	U877	U877	U818							
U1190	G1069	G937	U878	U878	U819							
A1191	U1128	U938	U879	U879	A816							
	A1062	U939										
	G1063											
	A1064											
	A1065											
	G1066											
	U1067											



A2747	A2748	U2681	G2620	G2556	A2494	U2434	A2372	G2311	G2248	A2183	G2121	U2059	C
G2749	U2682	C2682	G2621	A2557	C2495	G2435	A2373	A2312	G2249	U2184	G2122	A2060	U
U2750	U2683	C2496	G2622	U2558	C2496	U2436	C2374	U2313	G2250	G2185	G2123	G2061	U
G2751	C2684	C2497	G2623	U2559	U2497	G2437	G2375	U2314	G2251	U2186	G2124	G2062	G
U2752	G2685	U2498	G2624	C2560	U2498	A2438	G2376	G2315	G2252	A2125	A2125	U2063	U
G2753	A2686	U2499	G2625	A2561	U2499	A2439	C2377	G2316	G2253	U2127	U2126	C2064	G
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G2755	U2688	G2563	G2627	G2563	U2501	A2441	U2379	U2318	A2255	U2129	C2128	U2066	G
A2756	A2689	U2502	A2628	U2564	U2502	G2442	U2380	U2319	A2256	U2130	U2129	C2066	G
G2757	G2690	G2503	U2629	G2564	A2443	A2443	U2381	A2320	U2257	U2131	U2130	C2067	C
U2758	A2691	U2504	U2630	C2565	G2444	G2444	G2382	A2321	U2258	A2132	A2131	U2068	U
C2759	C2692	U2505	U2631	U2566	U2445	A2445	A2384	G2322	G2259	C2132	U2132	U2069	G
U2760	C2693	U2506	U2632	C2567	U2446	U2446	A2386	C2323	G2261	U2133	U2133	G2070	U
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G2772	G2706	A2519	U2645	G2585	A2458	A2458	G2400	U2337	U2272	A2145	A2145	G2082	G
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U2779	U2719	G2528	U2653	G2592	U2465	U2465	C2407	U2345	A2279	A2152	A2152	U2089	U
A2780	A2720	A2529	U2654	A2593	G2466	G2466	U2408	A2346	U2280	U2153	U2153	U2090	G
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		A2560	U2689	U2626	U2499	U2499	U2440	U2379	U2313	U2186	U2186	U2118	U
		U2561	U2690	U2627	U2500	U2500	U2441	U2380	U2314	U2187	U2187	U2119	C
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		G2586	U2710	U2647	U2520	U2520	U2461	U2400	U2334	U2207	U2207		
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		A2591	U2715	U2652	U2525	U2525	U2466	U2405	U2339	U2212	U2212		
		G2592	U2716	U2653	U2526	U2526	U2467	U2406	U2340	U2213	U2213		
		A2593	U2717	U2654	U2527	U2527	U2468	U2407	U2341	U2214	U2214		
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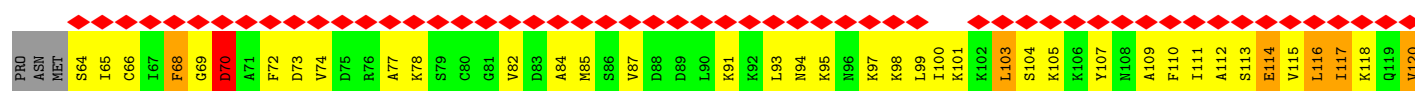
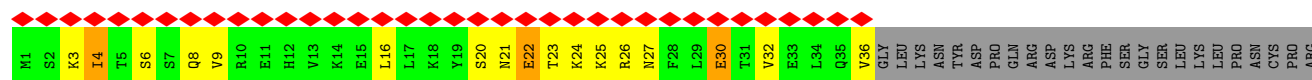
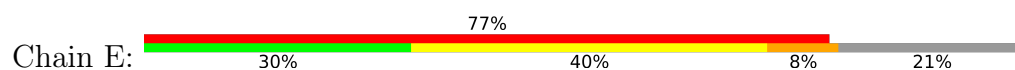




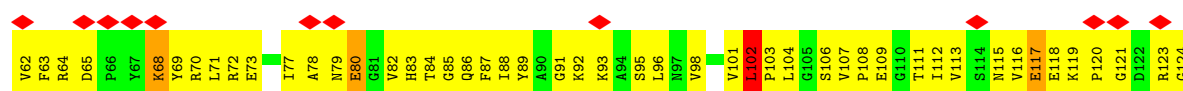
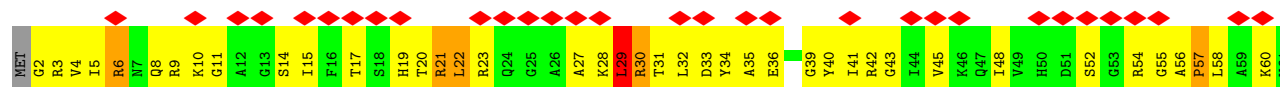
• Molecule 4: 5S ribosomal RNA

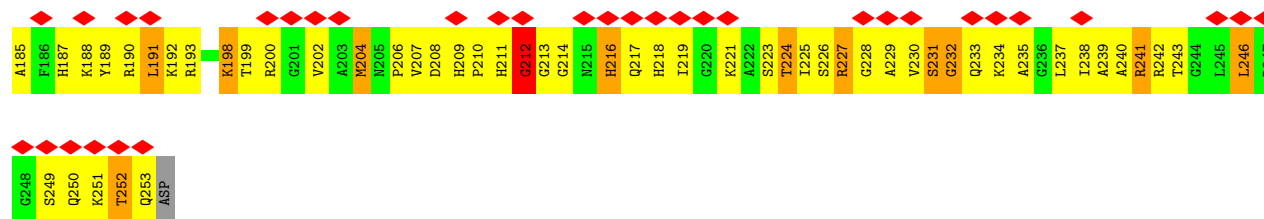


• Molecule 5: uL1 (yeast L1)

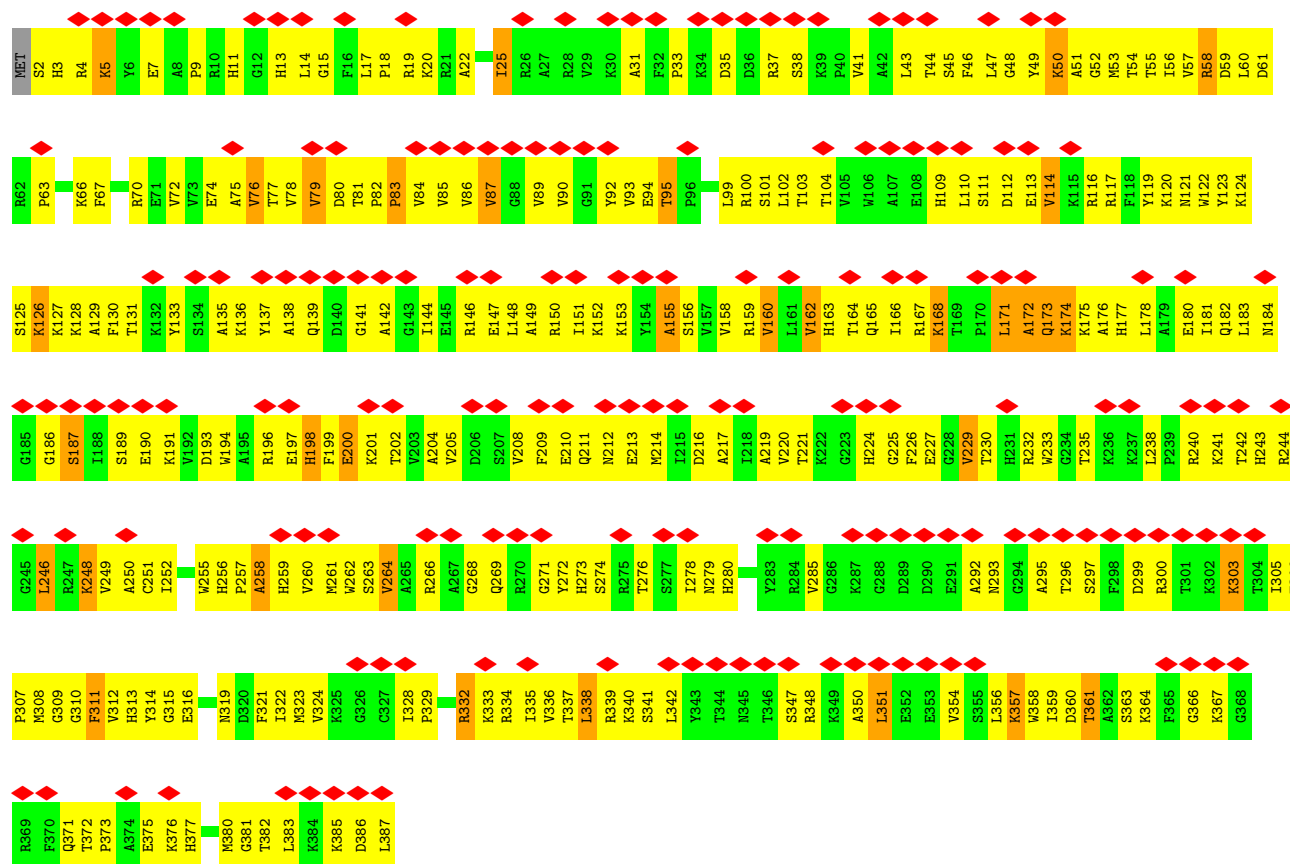


• Molecule 6: uL2 (yeast L2)

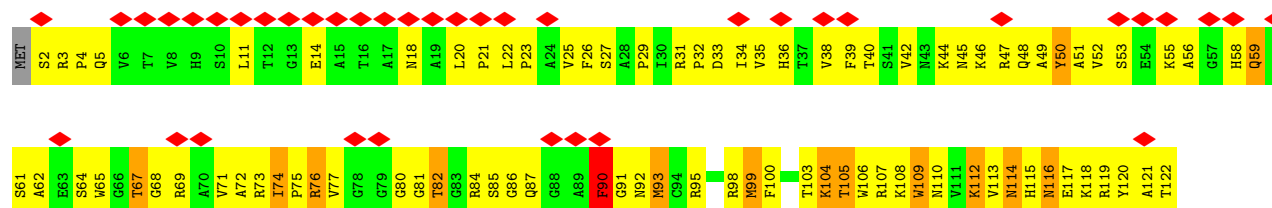


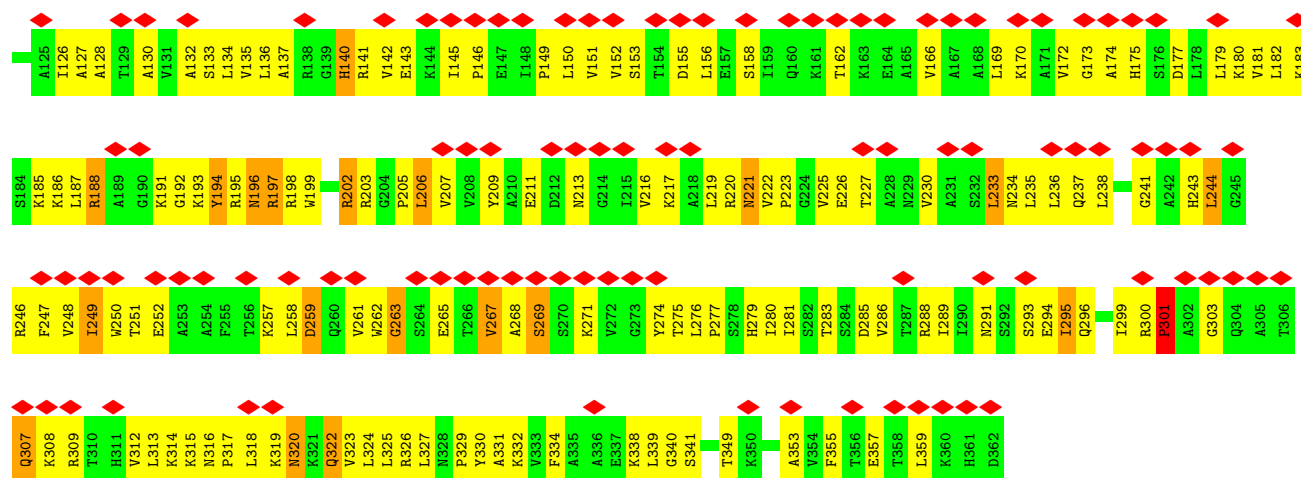


• Molecule 7: uL3 (yeast L3)

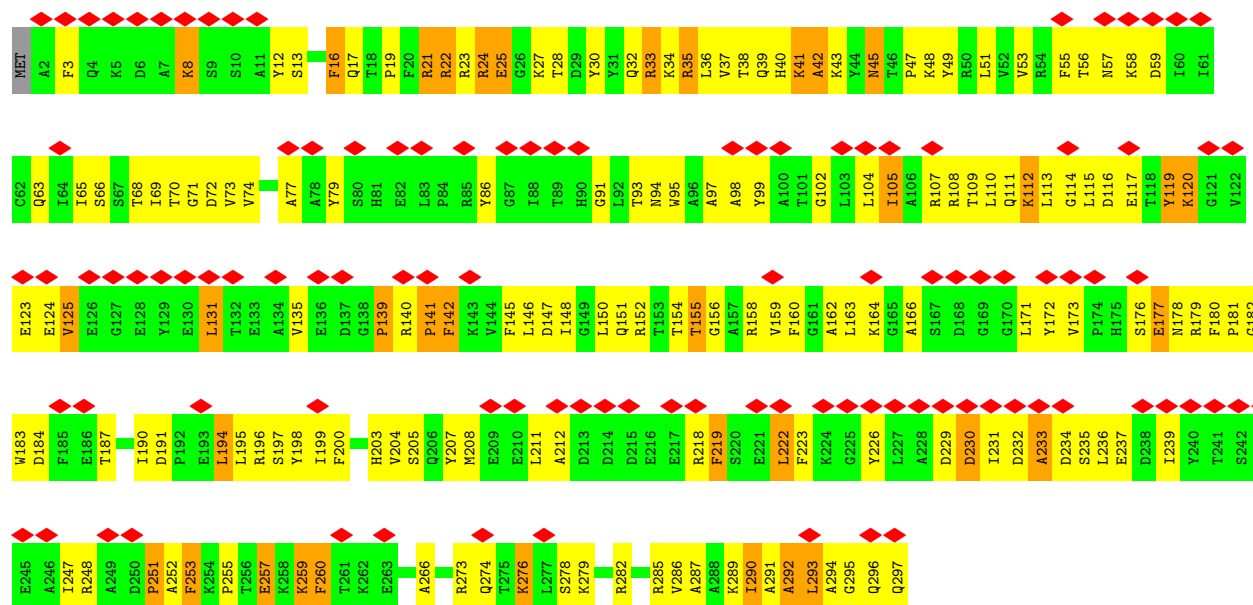


• Molecule 8: uL4 (yeast L4)

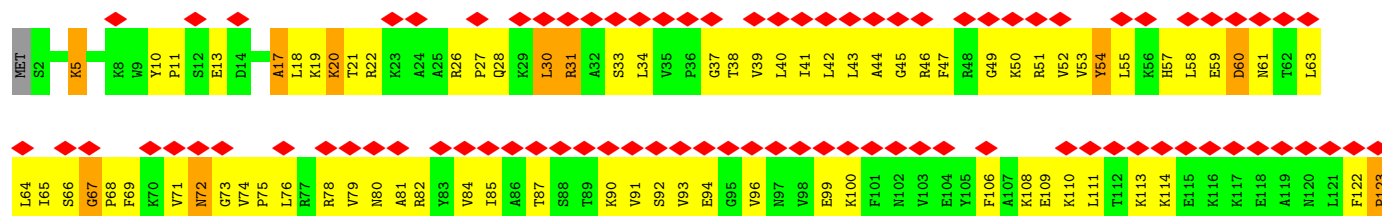


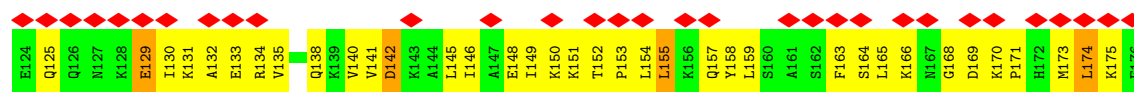


• Molecule 9: uL18 (yeast L5)

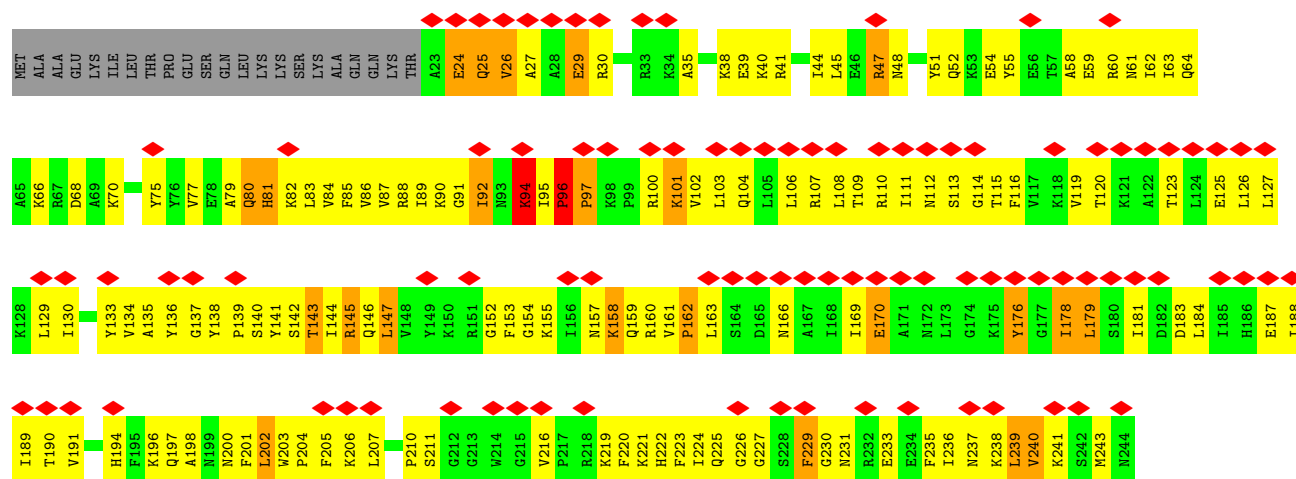


• Molecule 10: eL6 (yeast L6)

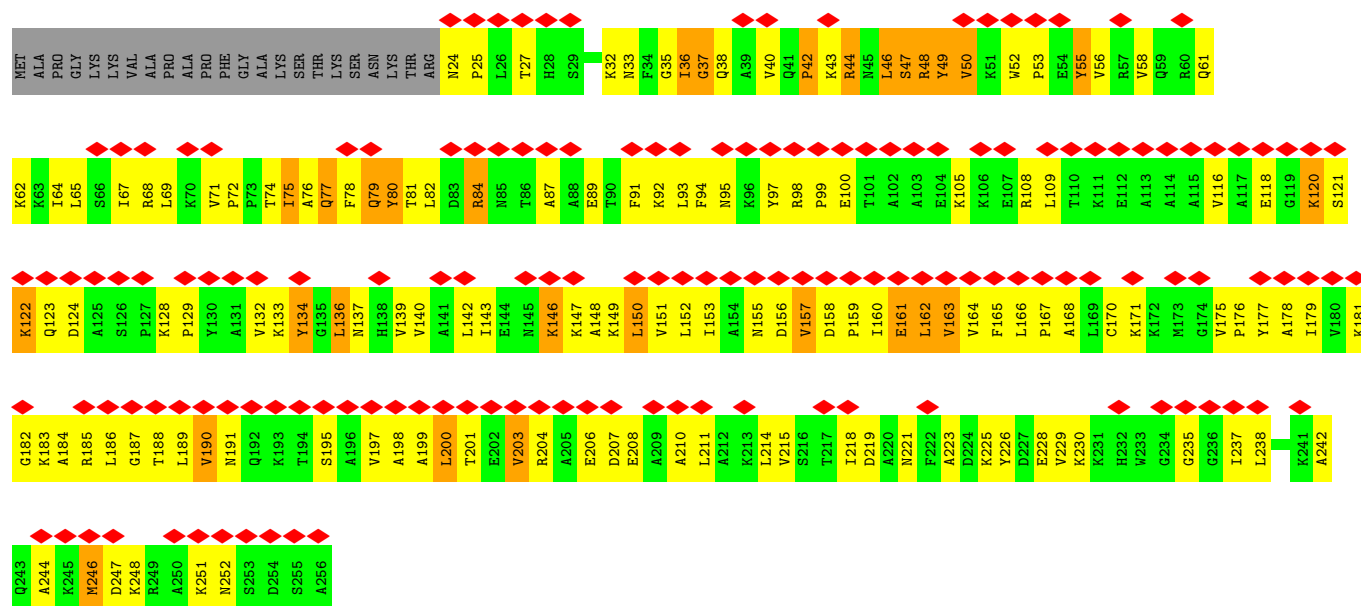




• Molecule 11: uL30 (yeast L7)

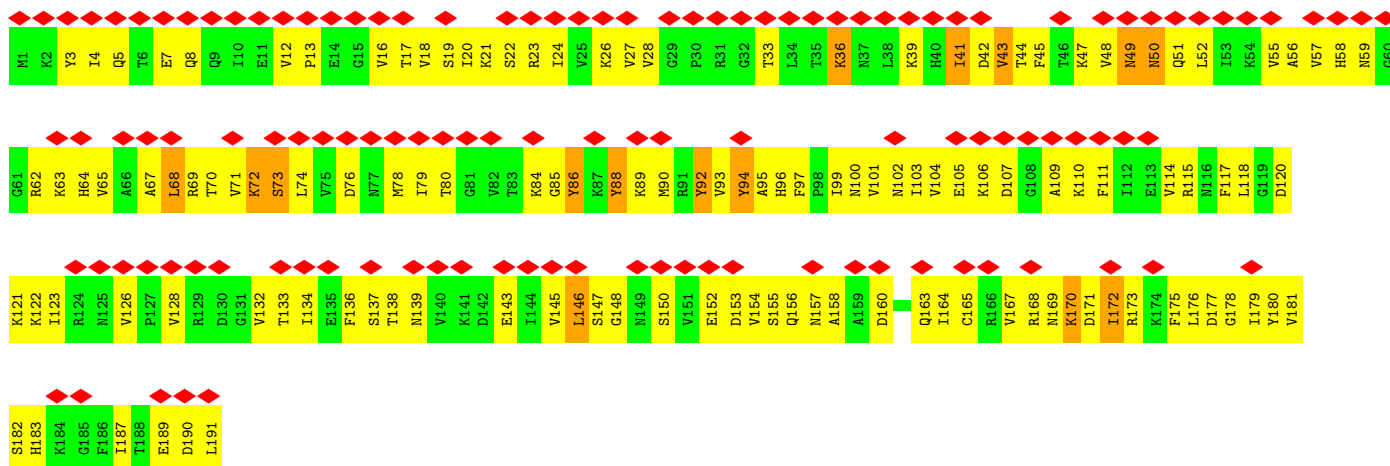


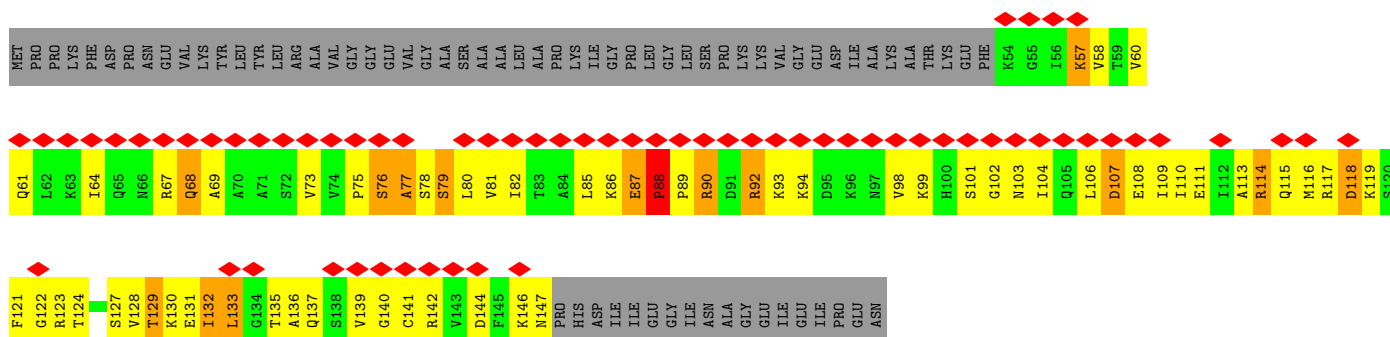
• Molecule 12: eL8 (yeast L8)



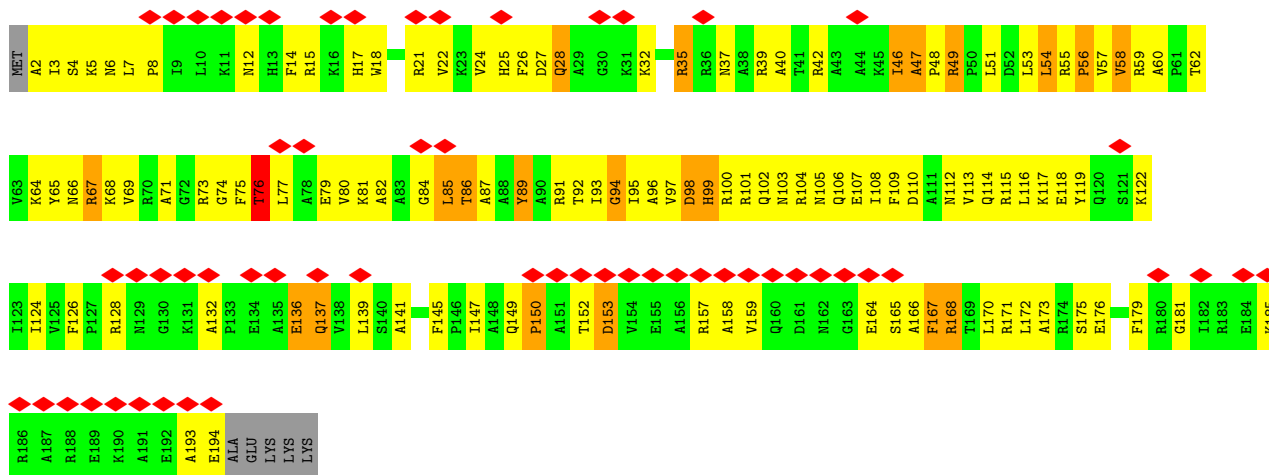
• Molecule 13: uL6 (yeast L9)



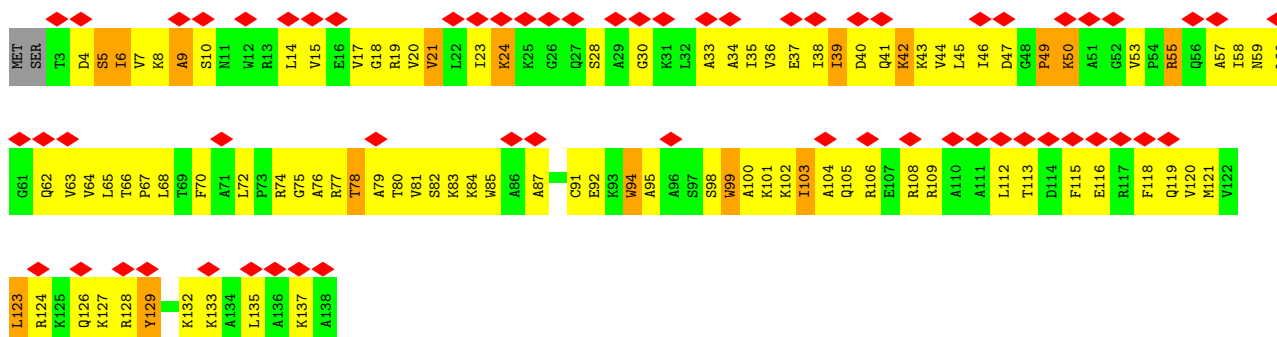




• Molecule 17: eL13 (yeast L13)

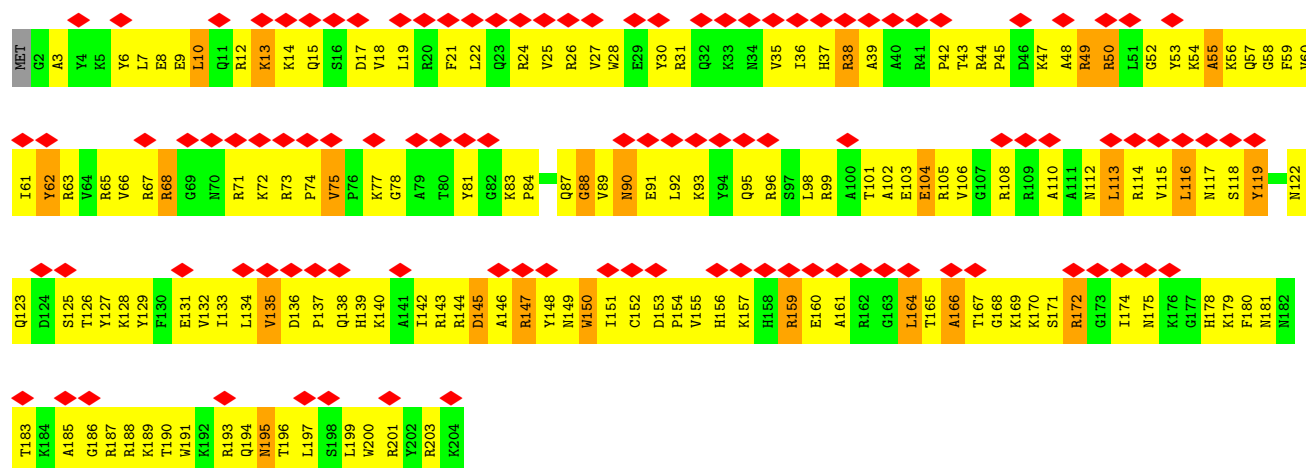


• Molecule 18: eL14 (yeast L14)

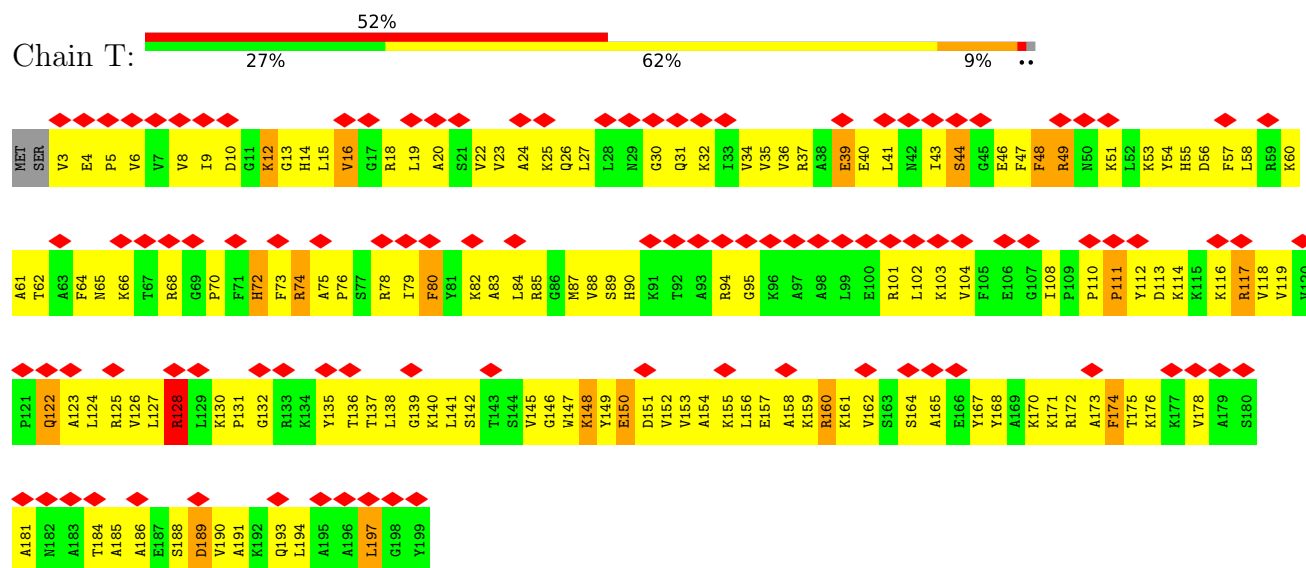


• Molecule 19: eL15 (yeast L15)

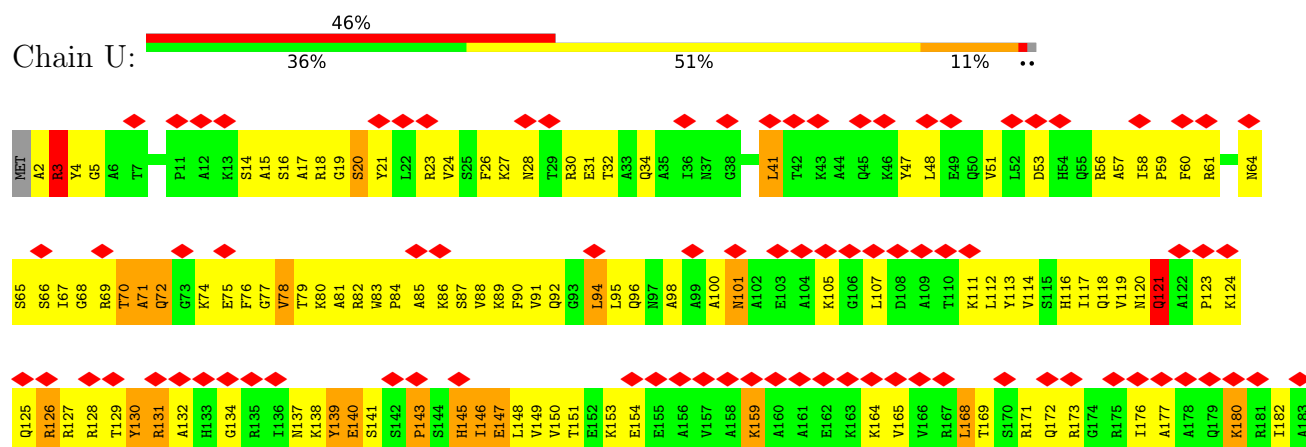




• Molecule 20: uL13 (yeast L16)

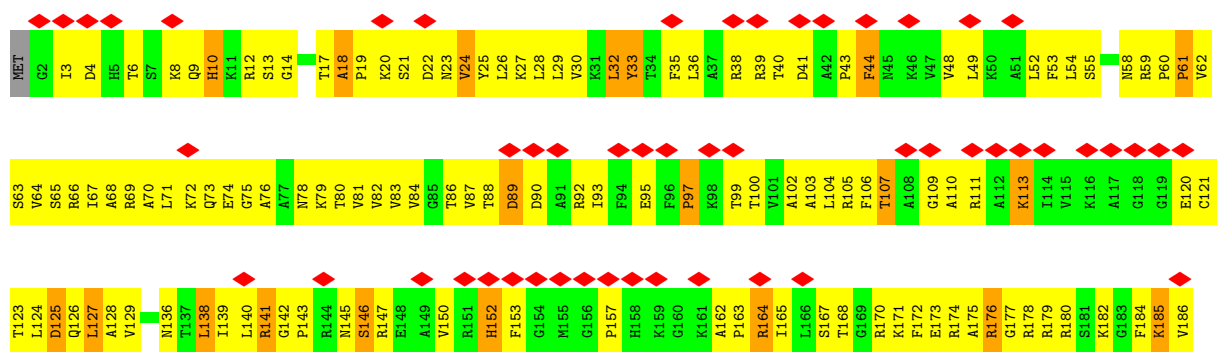


• Molecule 21: uL22 (yeast L17)




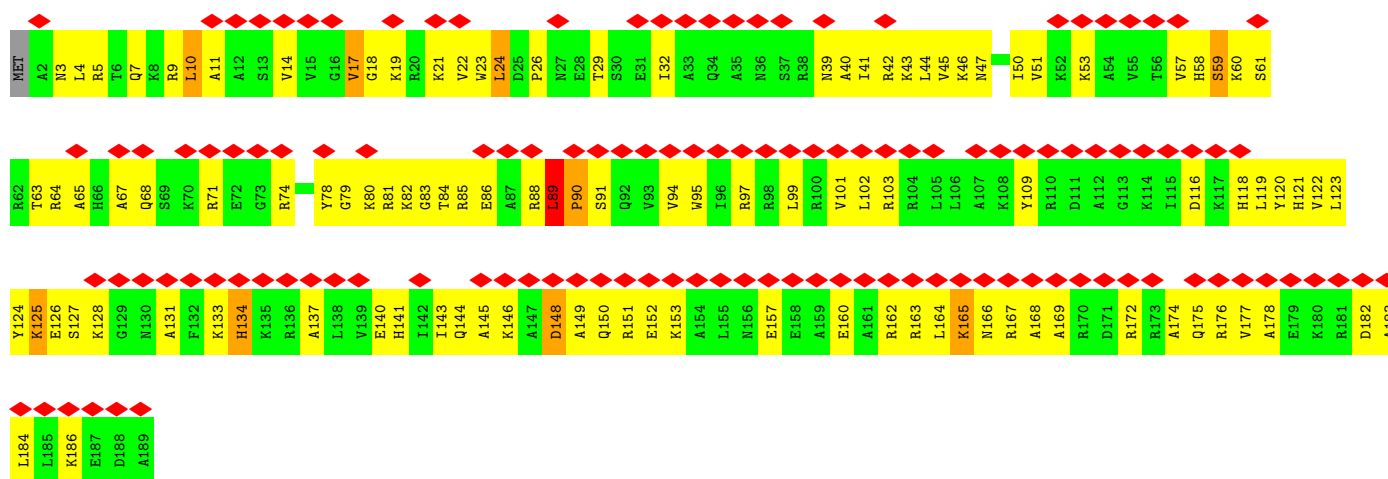
• Molecule 22: eL18 (yeast L18)

Chain V: 



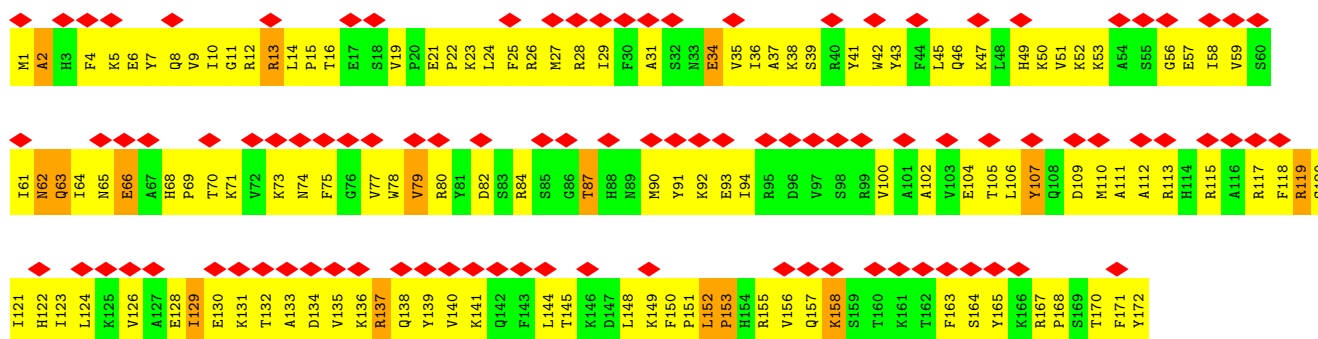
• Molecule 23: eL19 (yeast L19)

Chain W: 



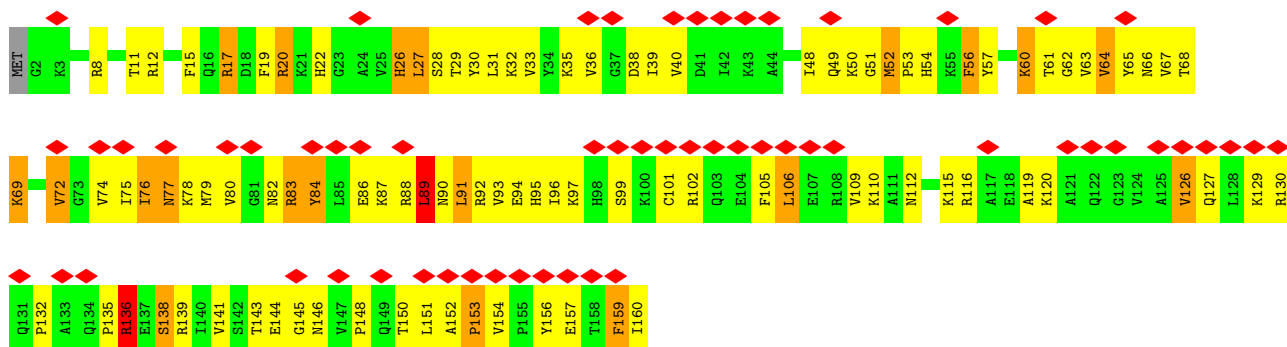
• Molecule 24: eL20 (yeast L20)

Chain X: 

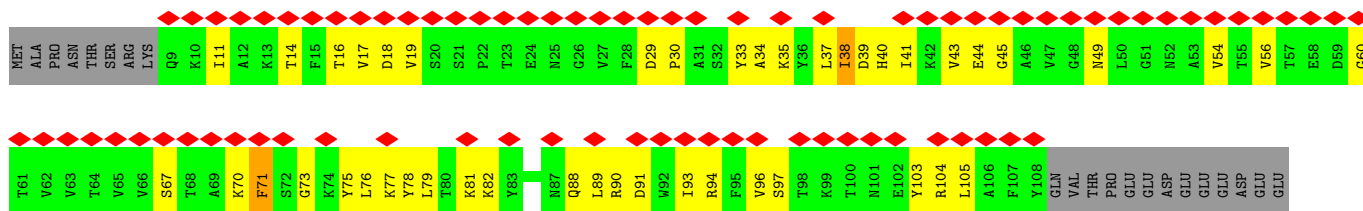


• Molecule 25: eL21 (yeast L21)

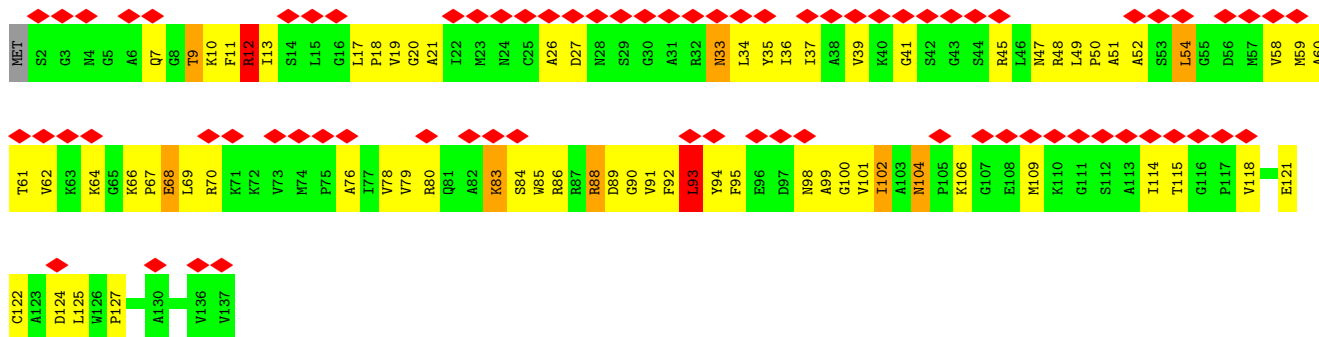
Chain Y: 



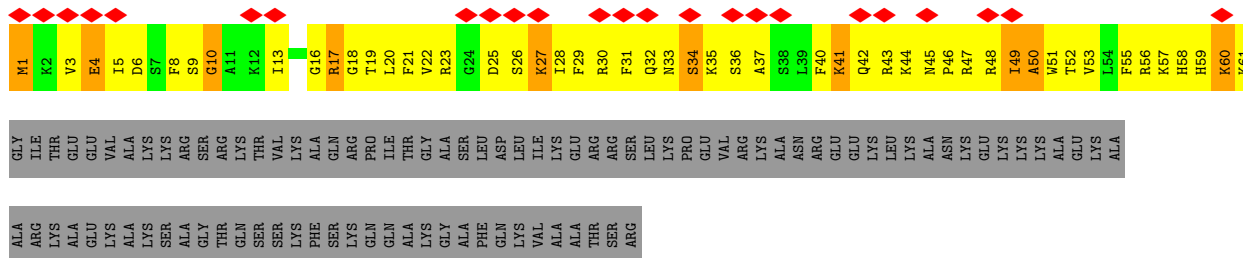
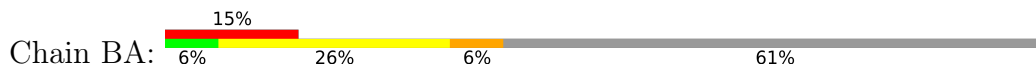
• Molecule 26: eL22 (yeast L22)



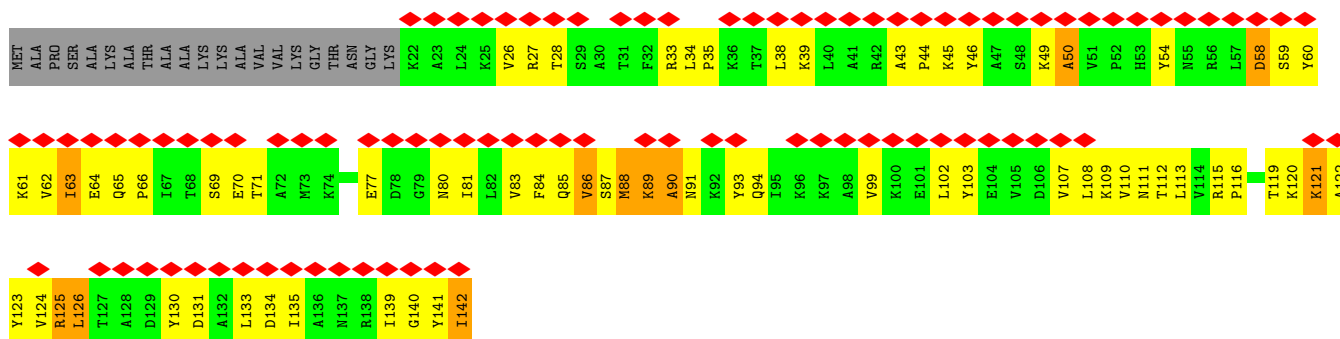
• Molecule 27: uL14 (yeast L23)



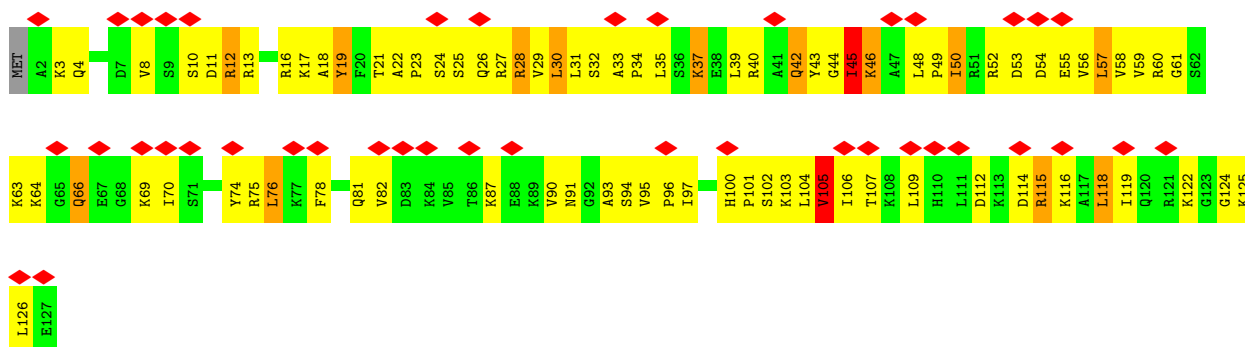
• Molecule 28: eL24 (yeast L24)



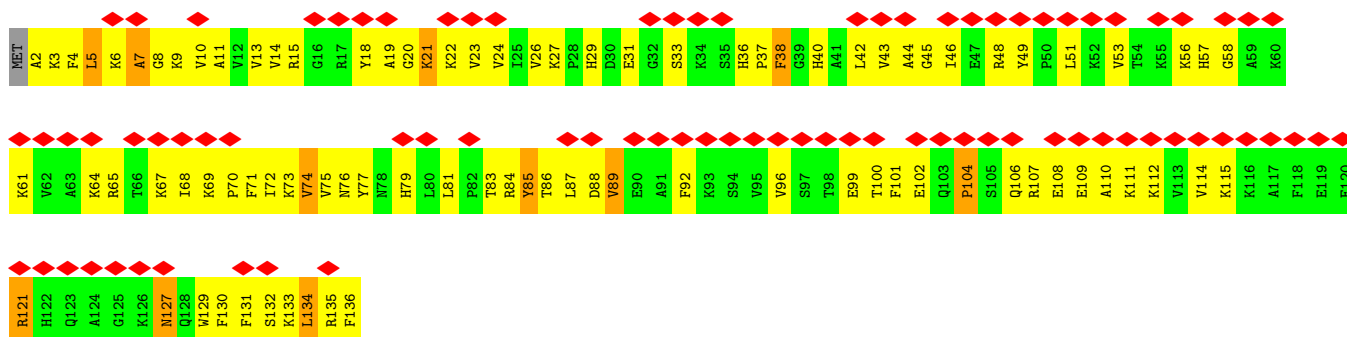
• Molecule 29: uL23 (yeast L25)



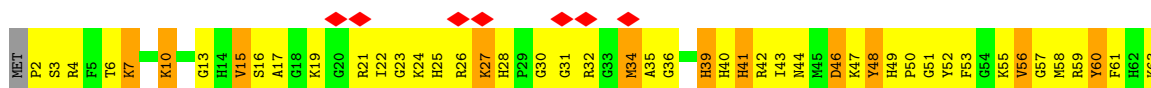
• Molecule 30: uL24 (yeast L26)

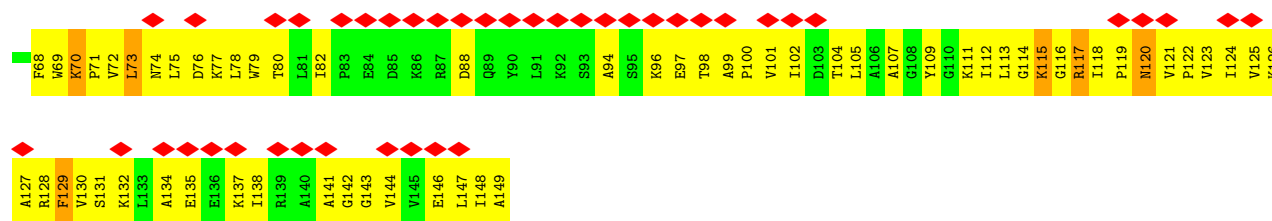


• Molecule 31: eL27 (yeast L27)

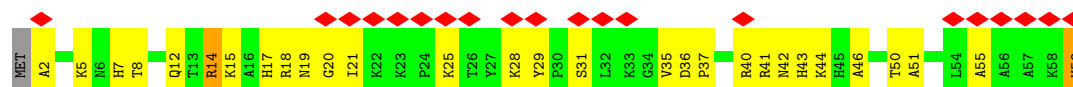


• Molecule 32: uL15 (yeast L28)

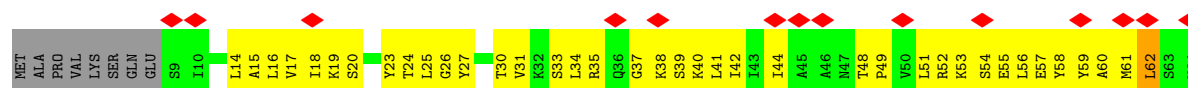




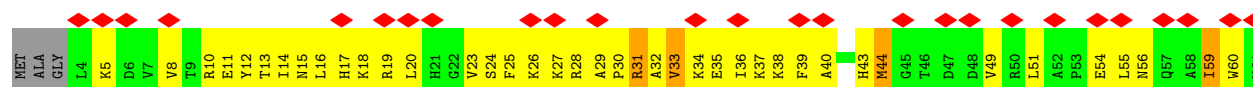
• Molecule 33: eL29 (yeast L29)



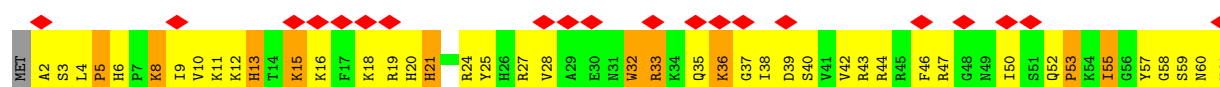
• Molecule 34: eL30 (yeast L30)



• Molecule 35: eL31 (yeast L31)

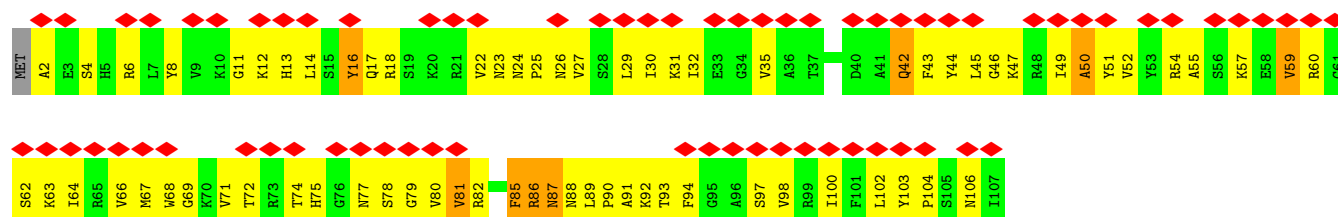


• Molecule 36: eL32 (yeast L32)

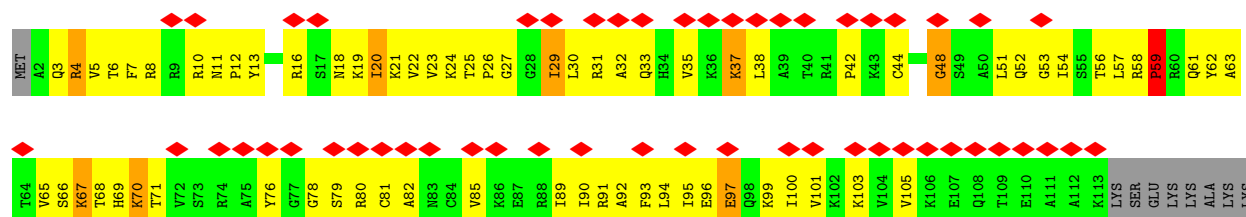




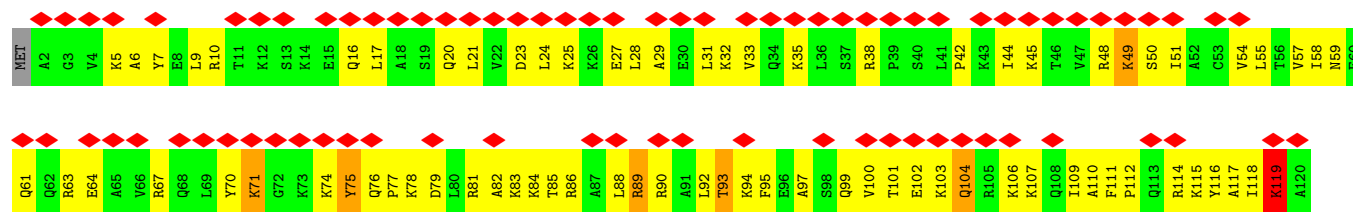
• Molecule 37: eL33 (yeast L33)



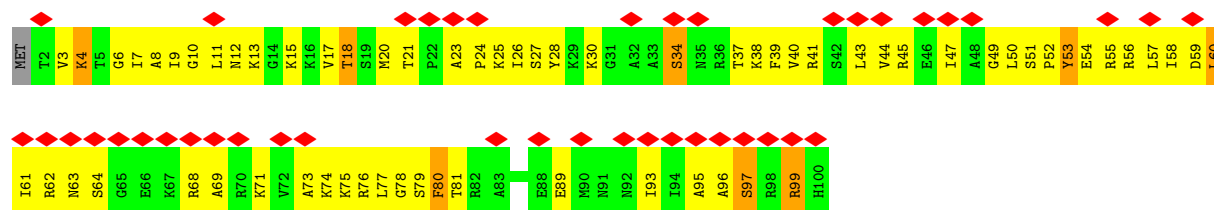
• Molecule 38: eL34 (yeast L34)



• Molecule 39: uL29 (yeast L35)

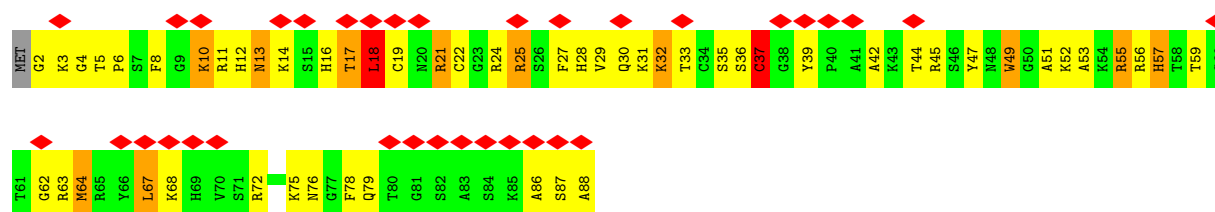


• Molecule 40: eL36 (yeast L36)



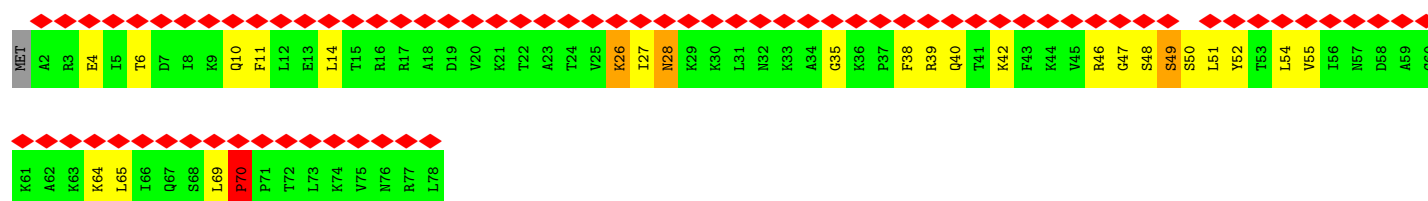
• Molecule 41: eL37 (yeast L37)

Chain OA: 




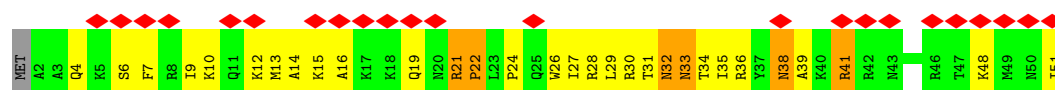
- Molecule 42: eL38 (yeast L38)

Chain PA: 



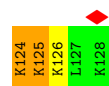
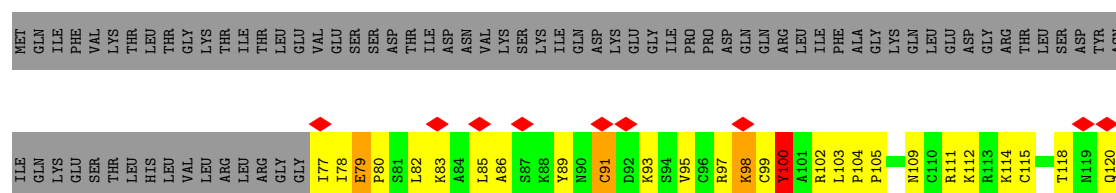
- Molecule 43: eL39 (yeast L39)

Chain QA: 



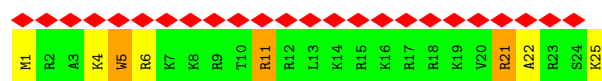
- Molecule 44: eL40 (yeast L40)

Chain RA: 

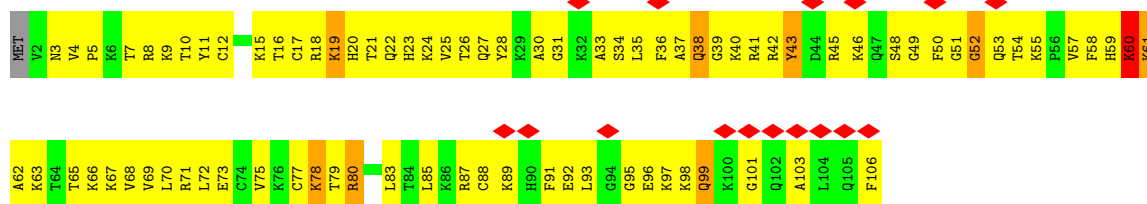


- Molecule 45: eL41 (yeast L41)

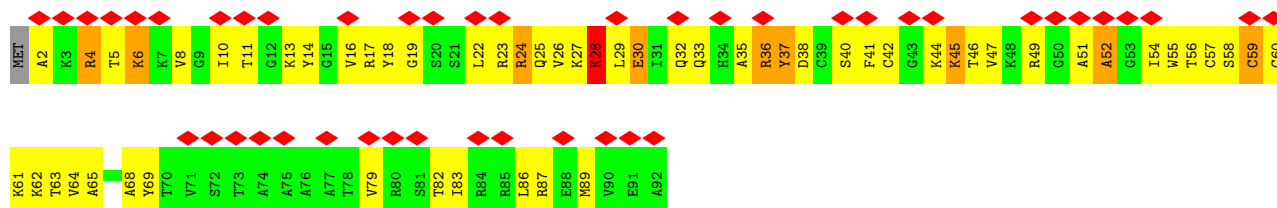
Chain SA: 



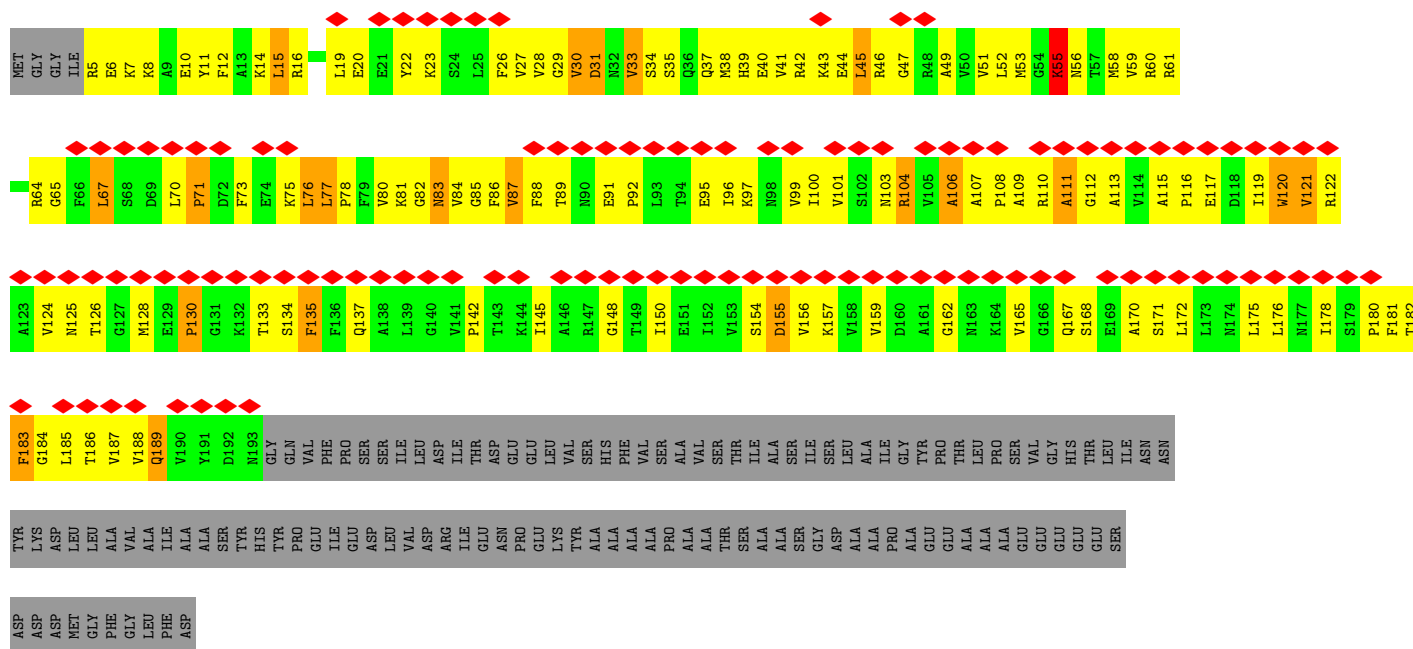
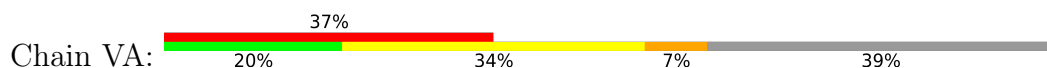
- Molecule 46: eL42 (yeast L42)



• Molecule 47: eL43 (yeast L43)



• Molecule 48: uL10 (yeast P0)

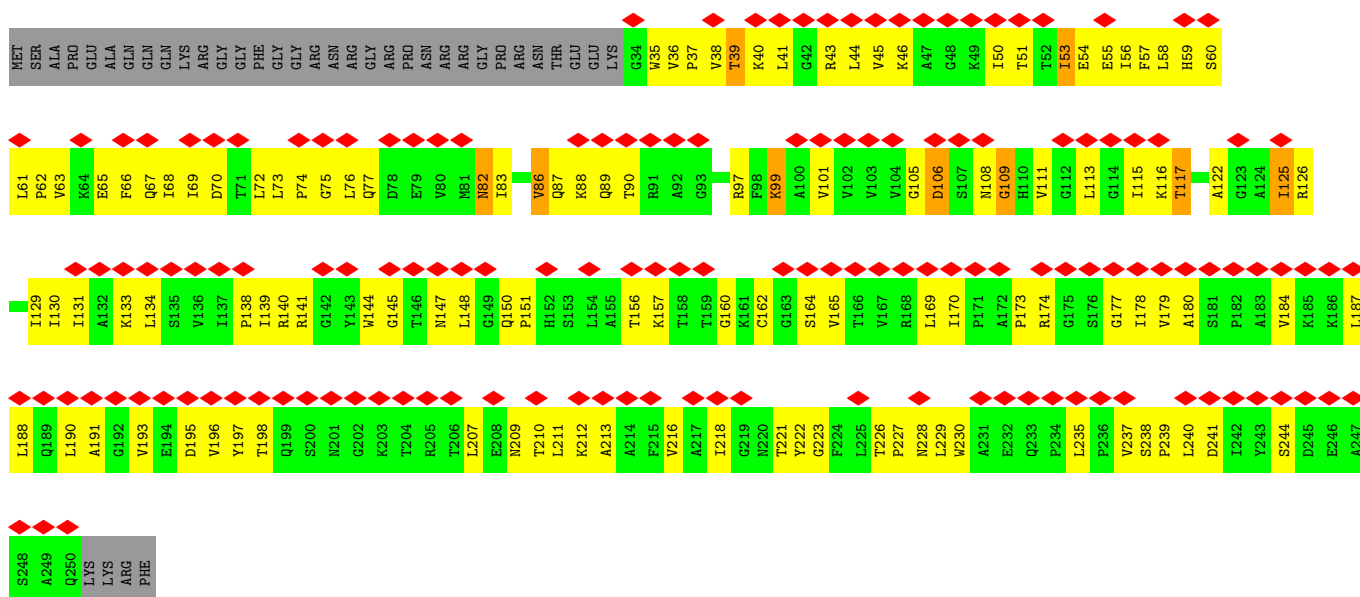


• Molecule 49: RACK1 (yeast Asc1)

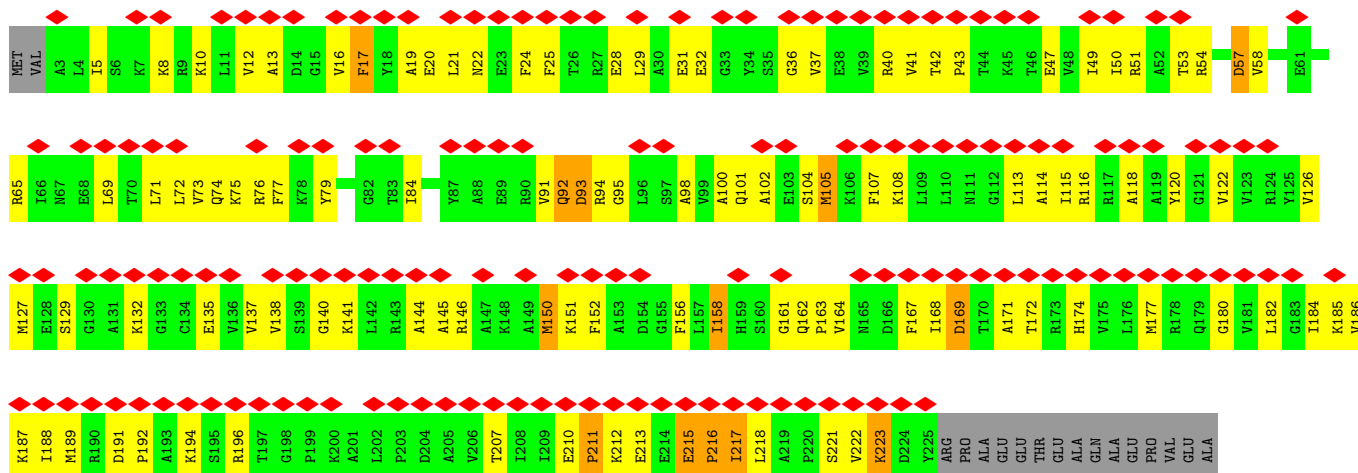




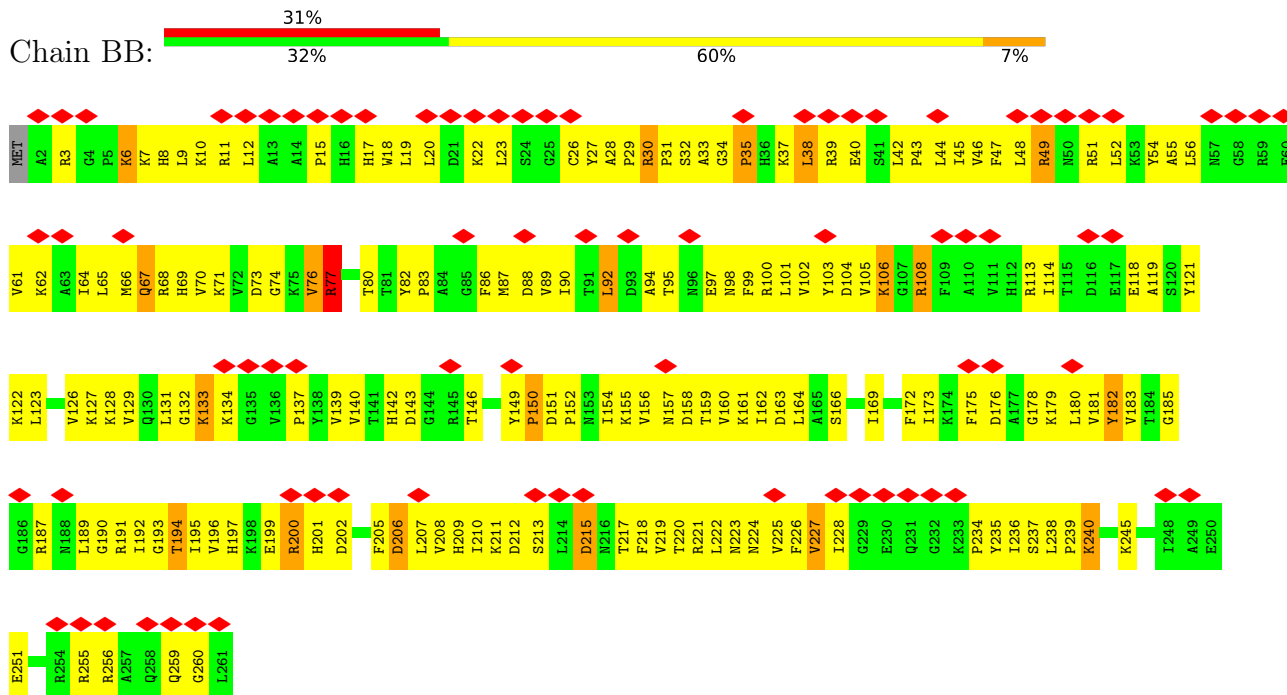
- Molecule 52: uS5 (yeast S2)



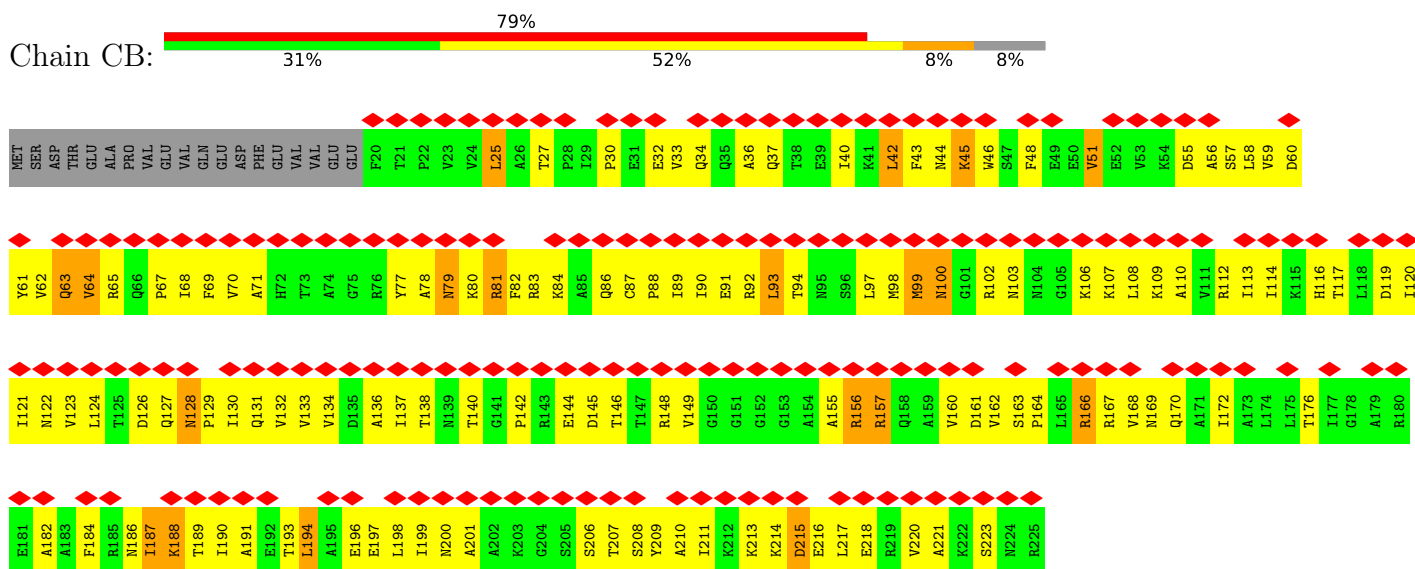
- Molecule 53: uS3 (yeast S3)



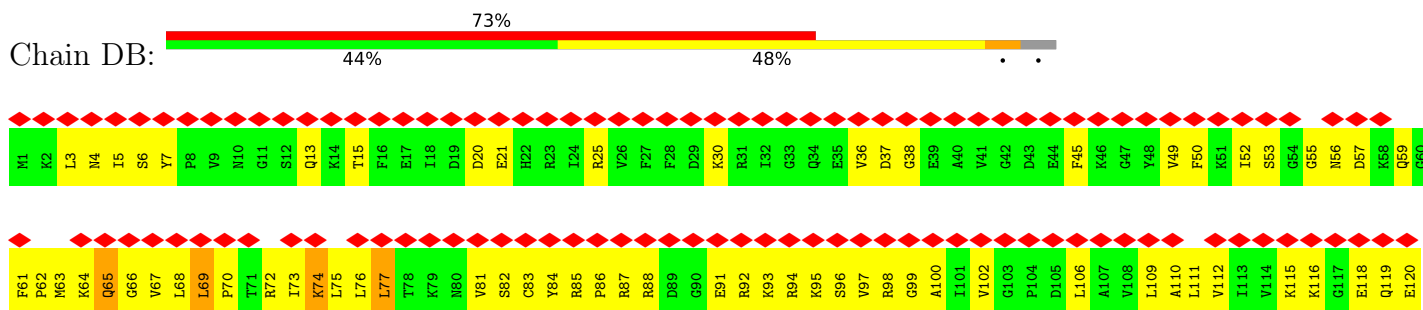
- Molecule 54: eS4 (yeast S4)

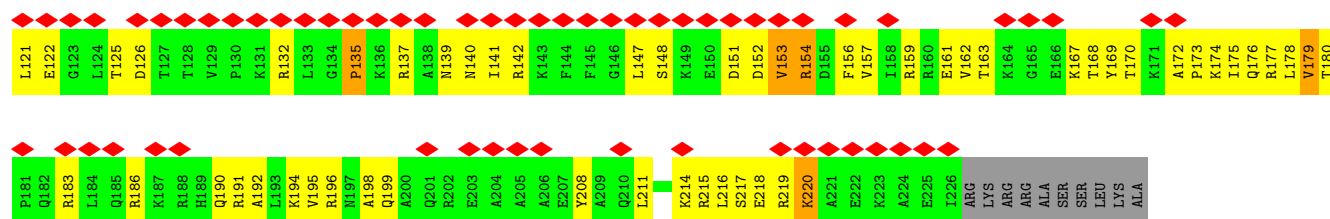


- Molecule 55: uS7 (yeast S5)

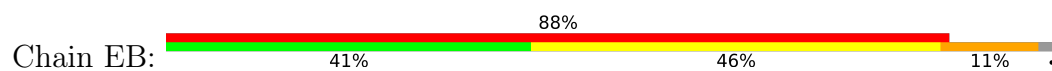


- Molecule 56: eS6 (yeast S6)

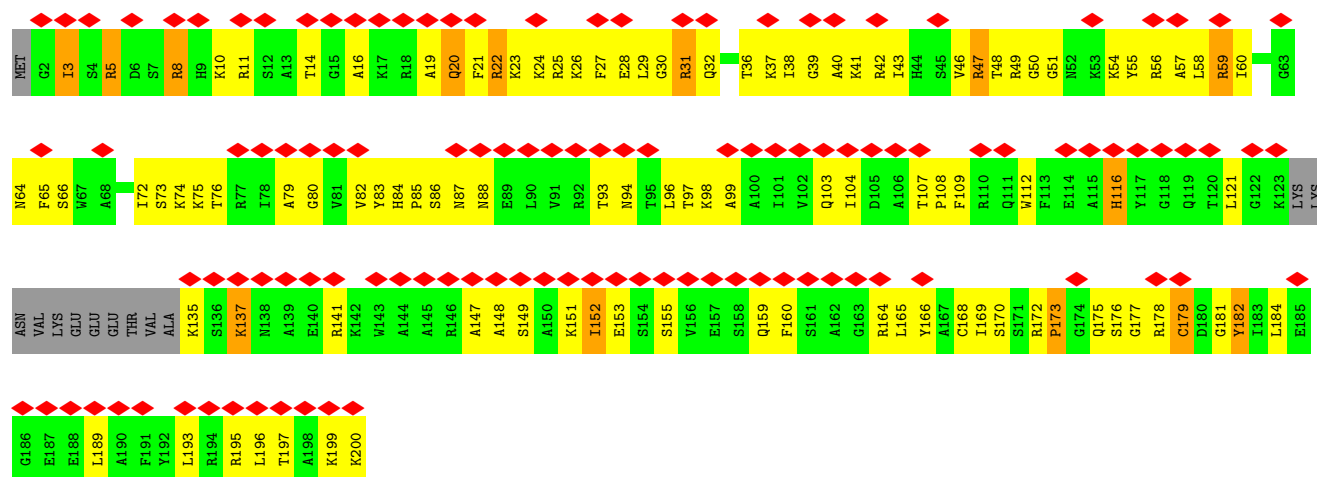




• Molecule 57: eS7 (yeast S7)

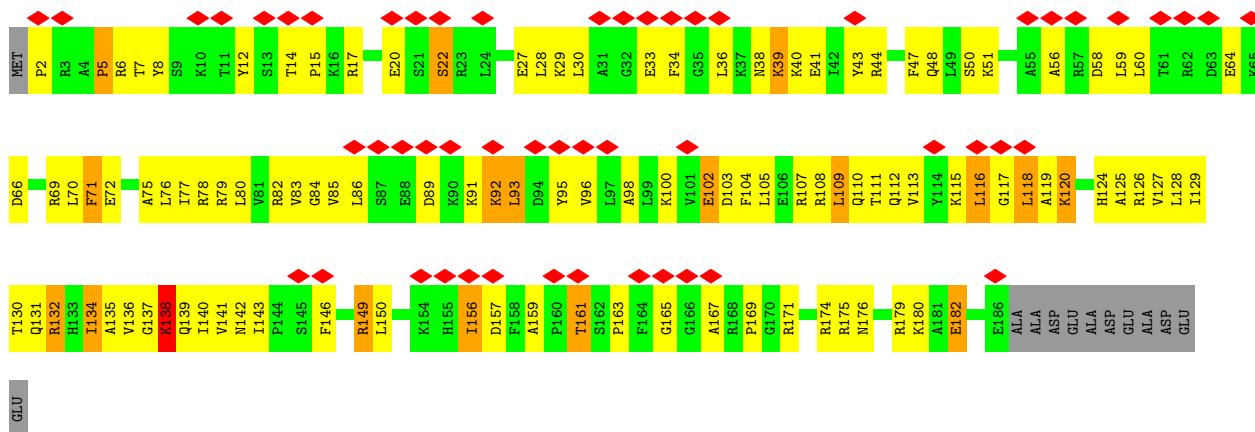


• Molecule 58: eS8 (yeast S8)

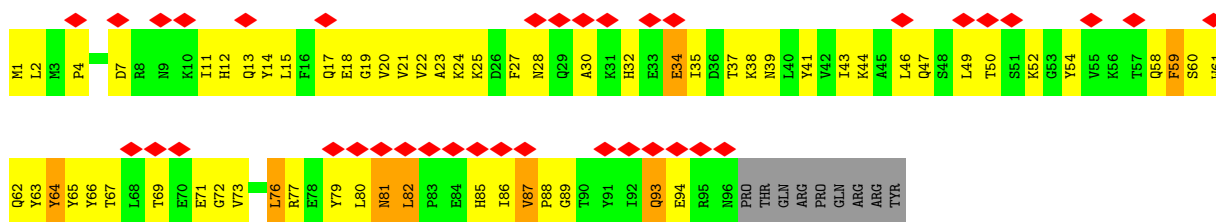


• Molecule 59: uS4 (yeast S9)

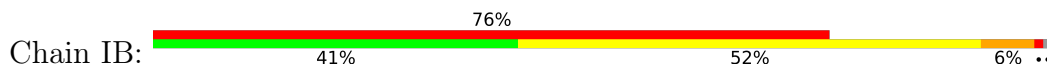




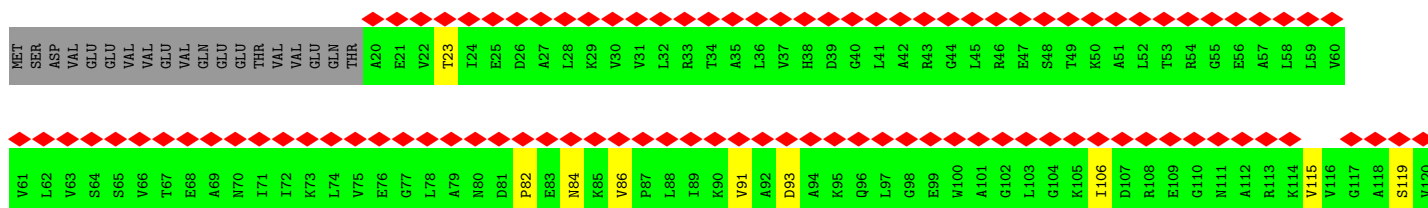
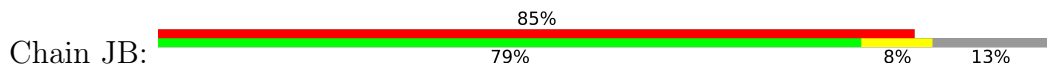
- Molecule 60: eS10 (yeast S10)




- Molecule 61: uS17 (yeast S11)

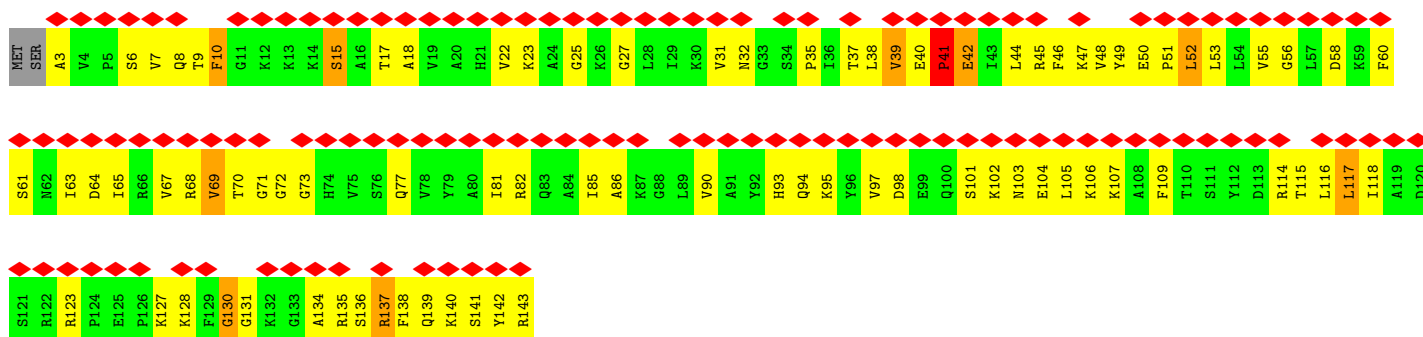


- Molecule 62: eS12 (yeast S12)




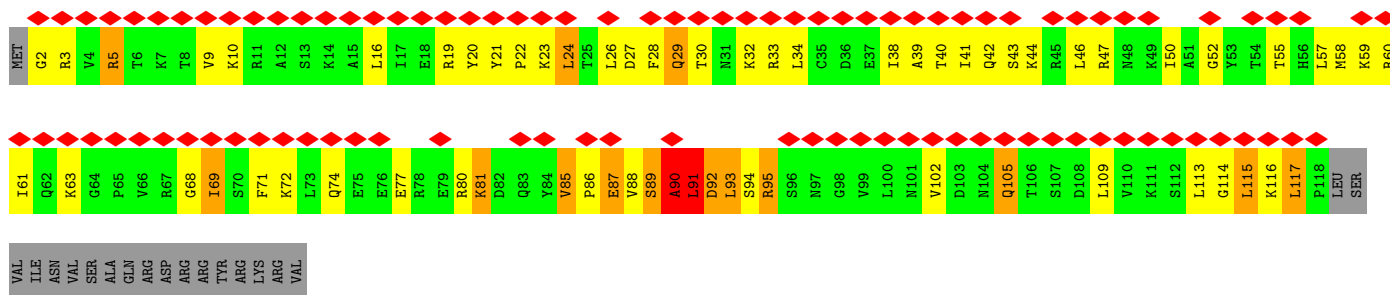


Chain NB: 



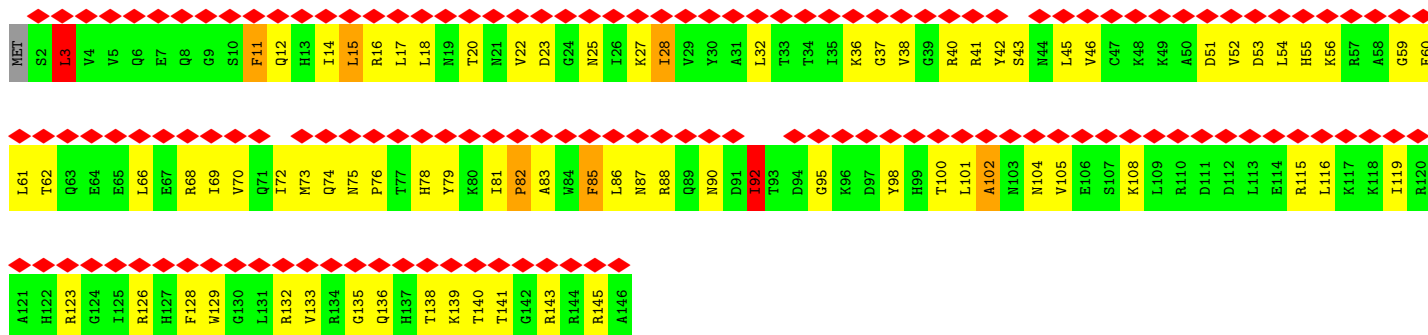
• Molecule 67: eS17 (yeast S17)

Chain OB: 




• Molecule 68: uS13 (yeast S18)

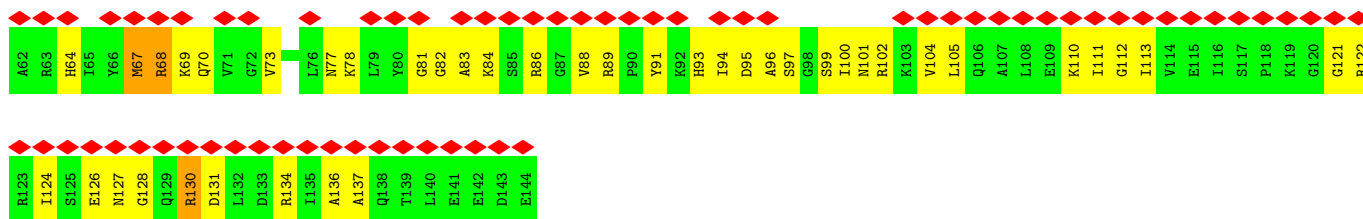
Chain PB: 



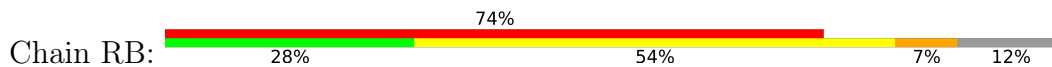
• Molecule 69: eS19 (yeast S19)

Chain QB: 

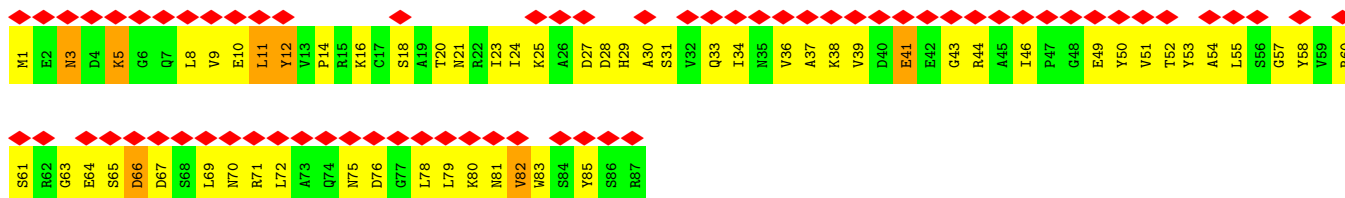
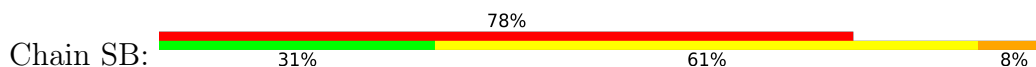




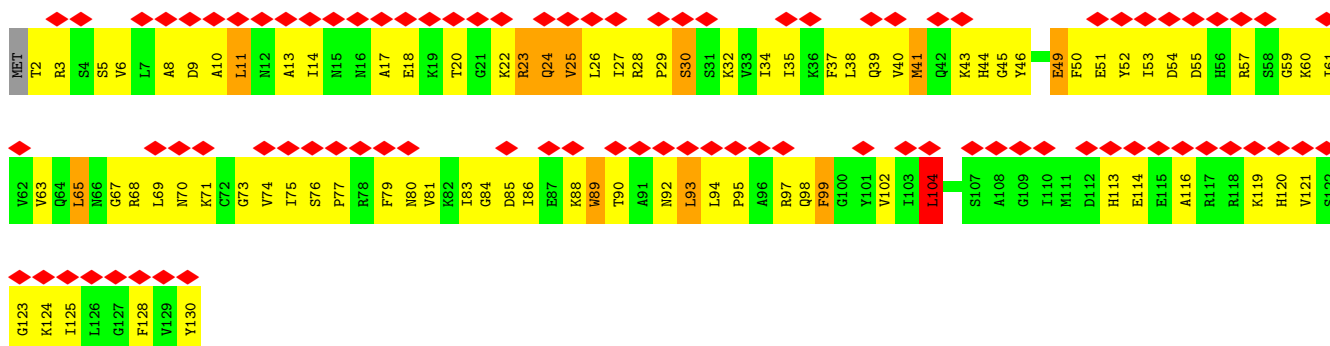
• Molecule 70: uS10 (yeast S20)



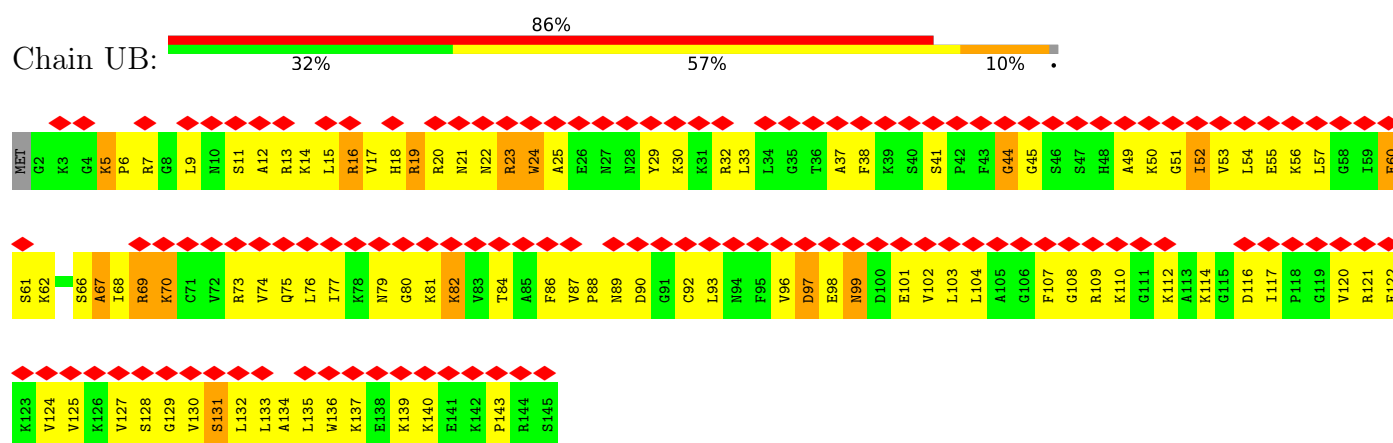
• Molecule 71: eS21 (yeast S21)



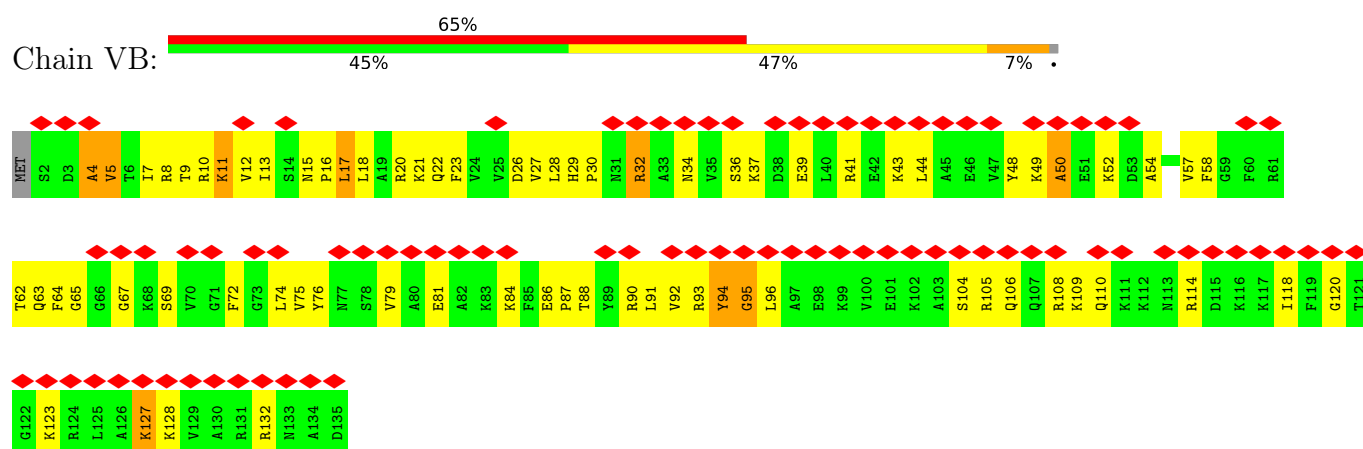
• Molecule 72: uS8 (yeast S22)



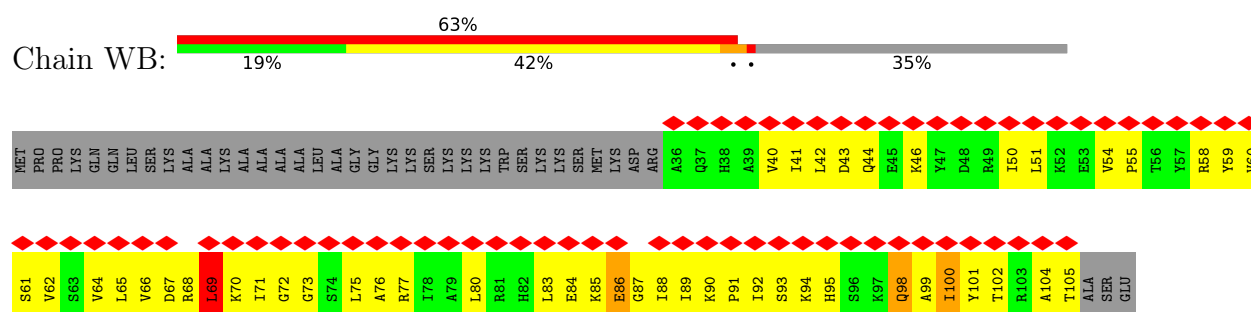
• Molecule 73: uS12 (yeast S23)



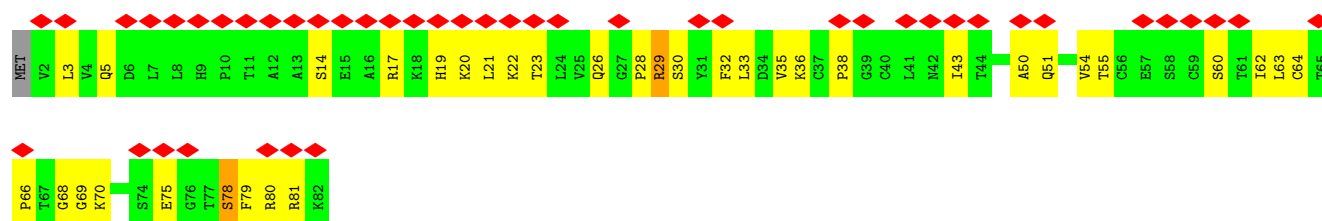
• Molecule 74: eS24 (yeast S24)



• Molecule 75: eS25 (yeast S25)

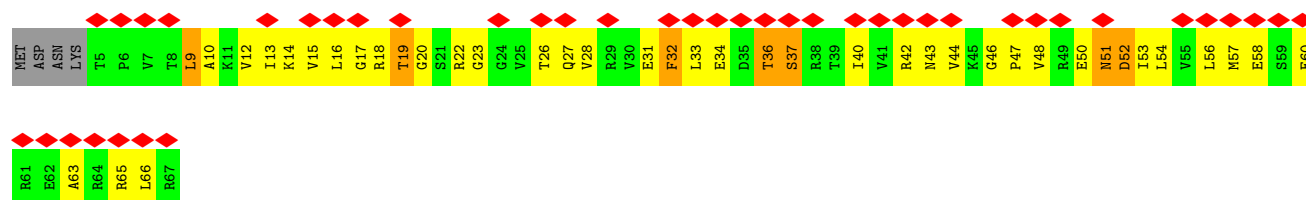


Chain YB: 




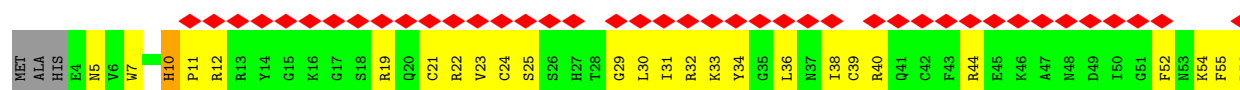
• Molecule 78: eS28 (yeast S28)

Chain ZB: 



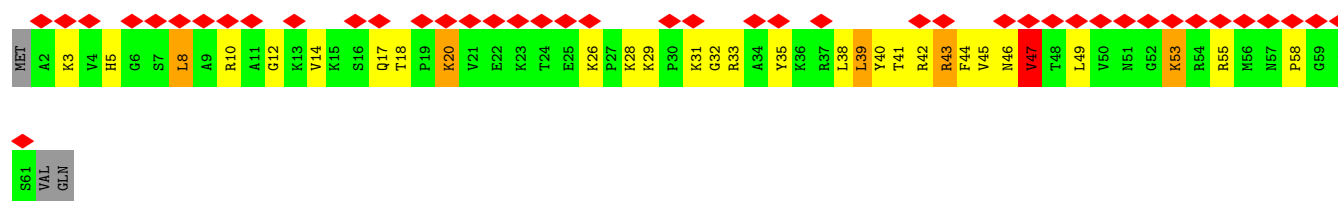
• Molecule 79: uS14 (yeast S29)

Chain AC: 




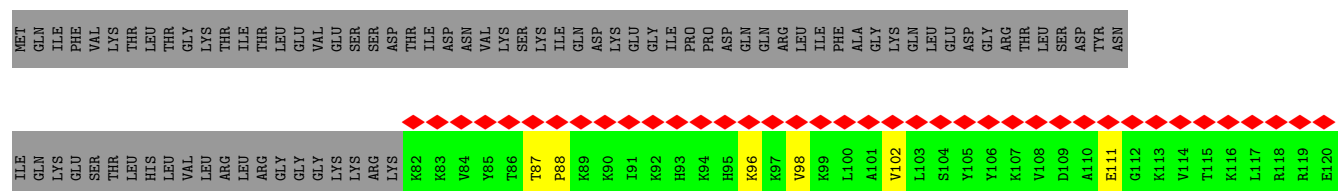
• Molecule 80: eS30 (yeast S30)

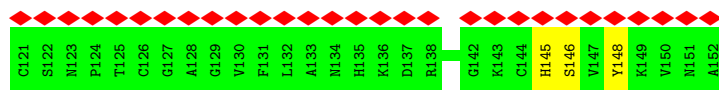
Chain BC: 



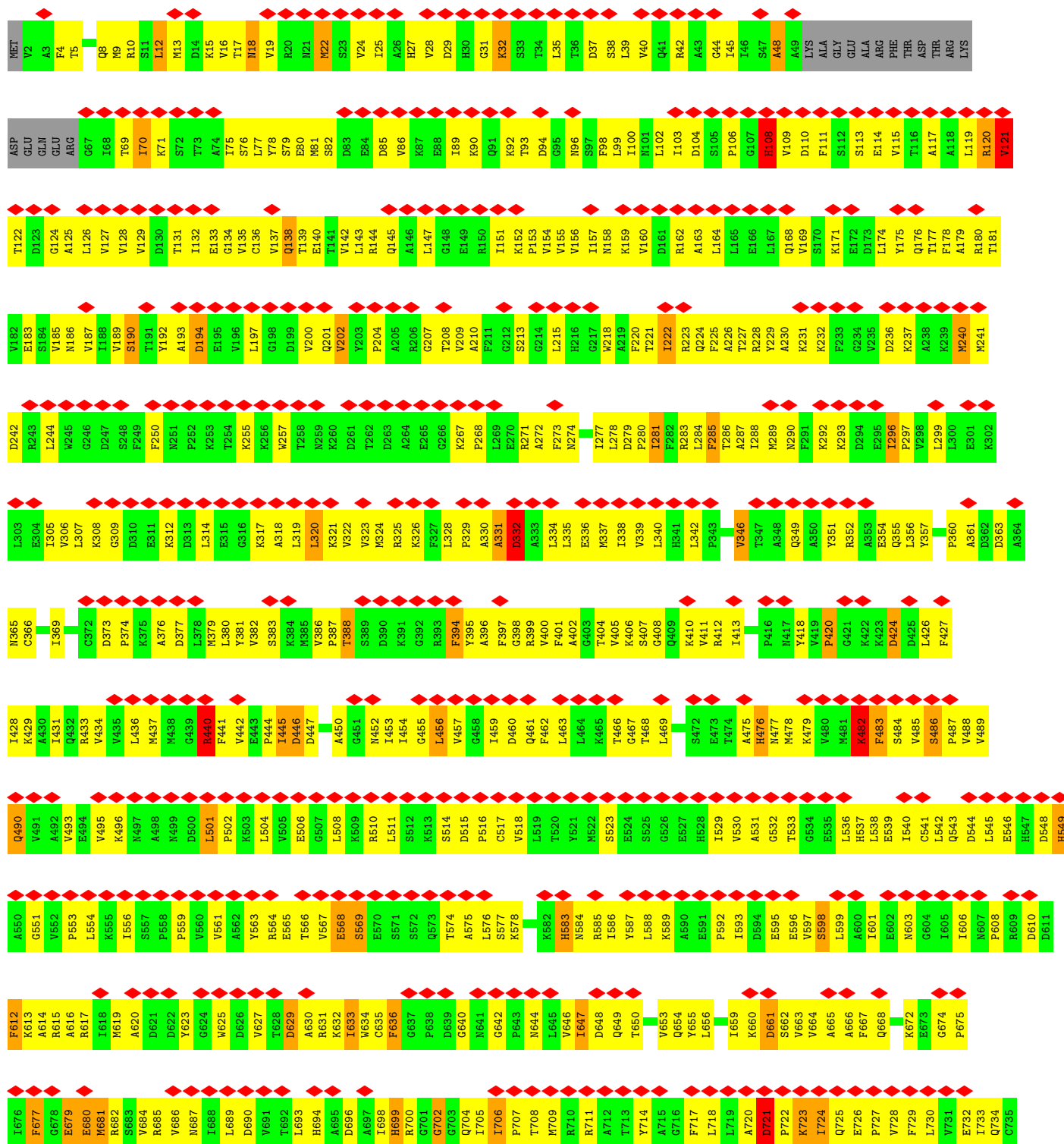
• Molecule 81: eS31 (yeast S31)

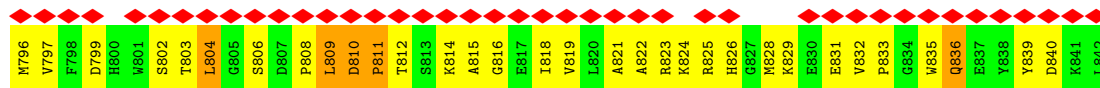
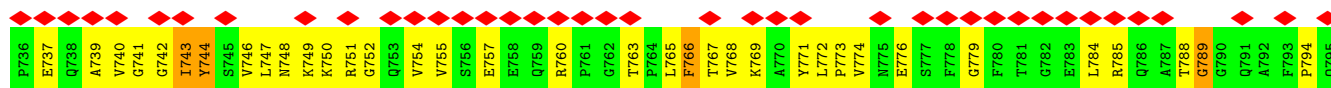
Chain CC: 



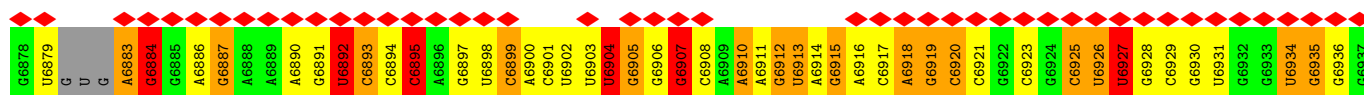
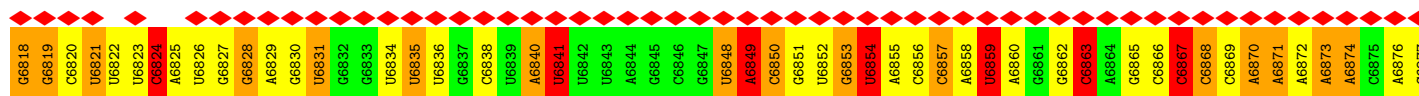
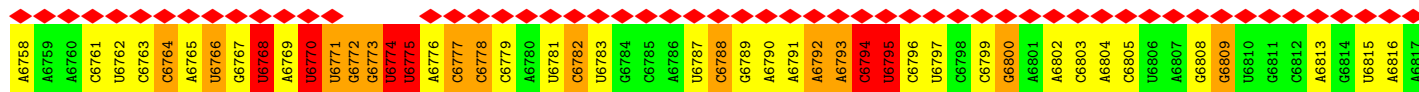
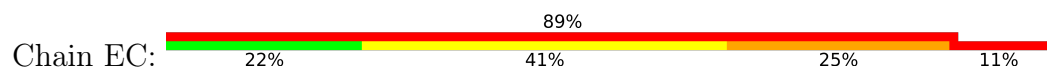


• Molecule 82: yeast eEF2





• Molecule 83: IRES



## 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 ( $e^-/\text{\AA}^2$ )	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	0.055	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: 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	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(°)	Ideal(°)
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(°)	Ideal(°)
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 [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul

statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
86	SO1	DC	903	-	35,39,39	2.82	20 (57%)	39,64,64	2.03	8 (20%)
84	GDP	DC	901	85	24,30,30	1.93	5 (20%)	30,47,47	1.74	6 (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
86	SO1	DC	903	-	-	4/21/104/104	0/7/5/5
84	GDP	DC	901	85	-	3/12/32/32	0/3/3/3

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(°)	Ideal(°)
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:

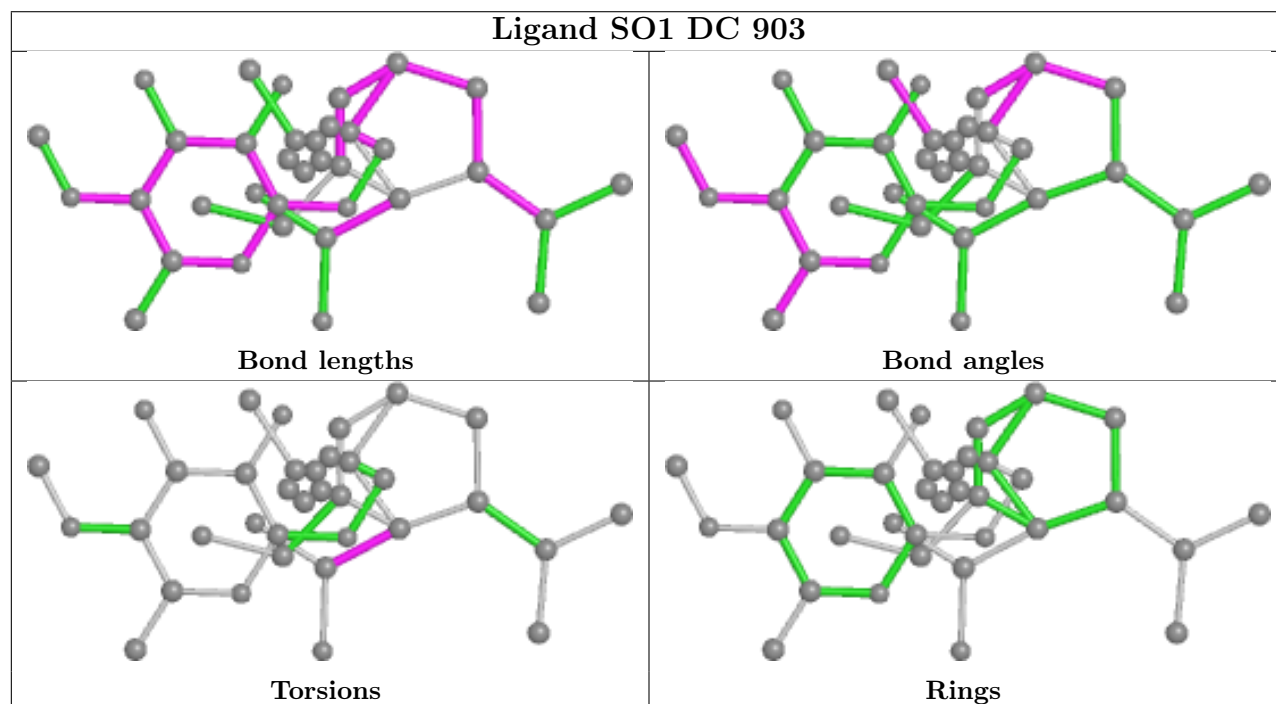
Mol	Chain	Res	Type	Atoms
84	DC	901	GDP	O4'-C4'-C5'-O5'
84	DC	901	GDP	C3'-C4'-C5'-O5'
86	DC	903	SO1	C2-C1-C5-O14
86	DC	903	SO1	C2-C1-C5-O15
86	DC	903	SO1	C3-C1-C5-O15

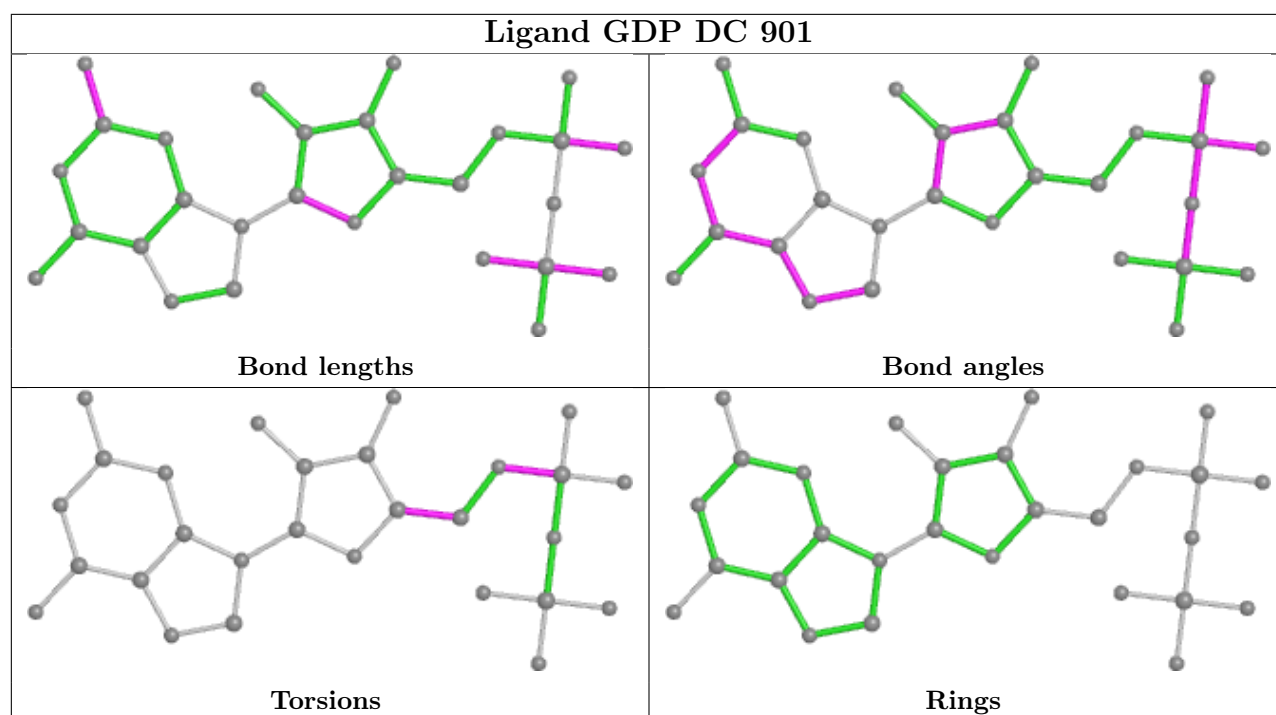
There are no ring outliers.

2 monomers are involved in 4 short contacts:

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

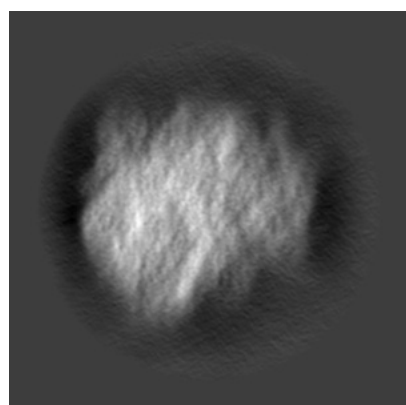
## 6 Map visualisation [i](#)

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

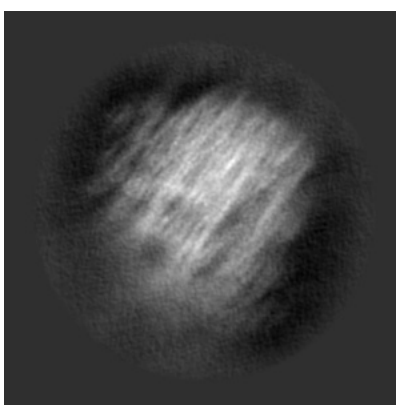
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

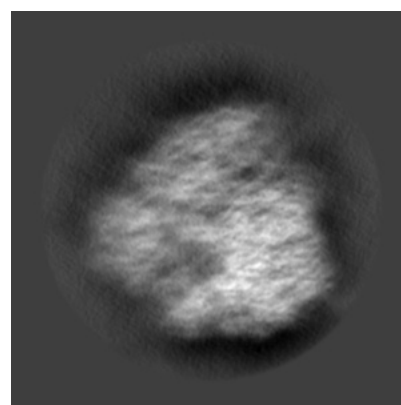
#### 6.1.1 Primary map



X



Y

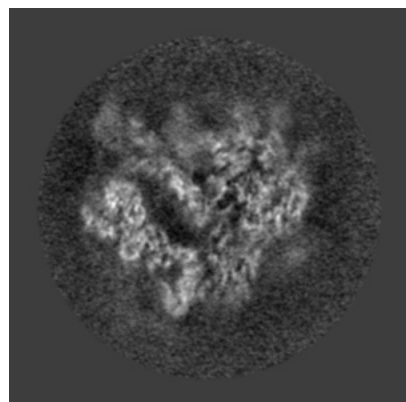


Z

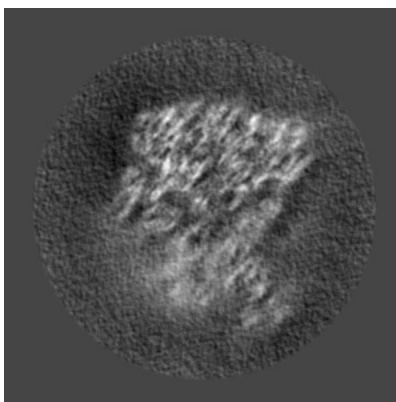
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

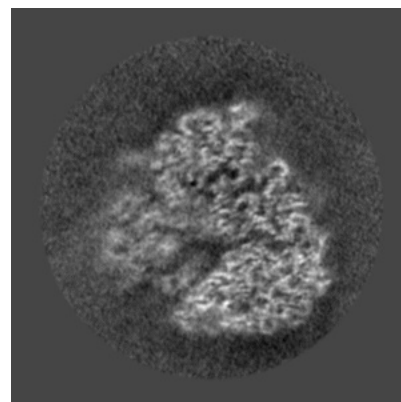
#### 6.2.1 Primary map



X Index: 256



Y Index: 256

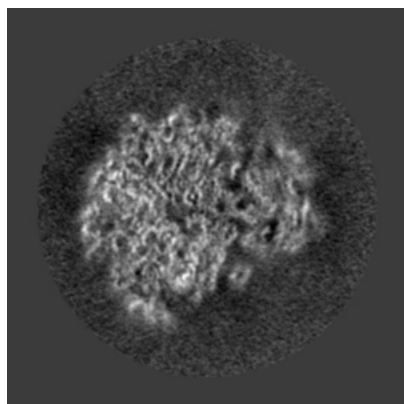


Z Index: 256

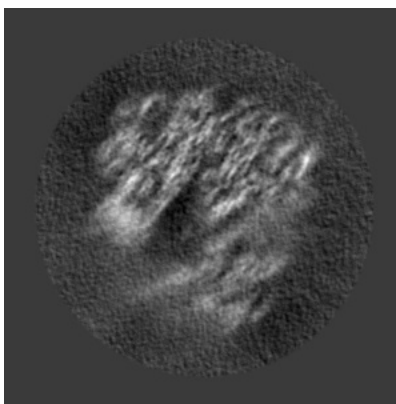
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

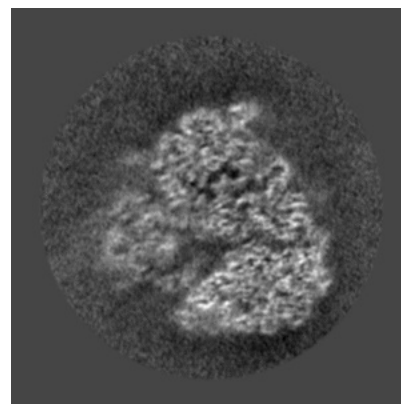
### 6.3.1 Primary map



X Index: 287



Y Index: 221

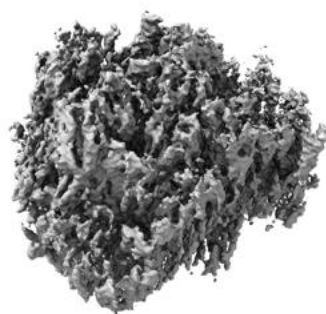


Z Index: 258

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

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 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.

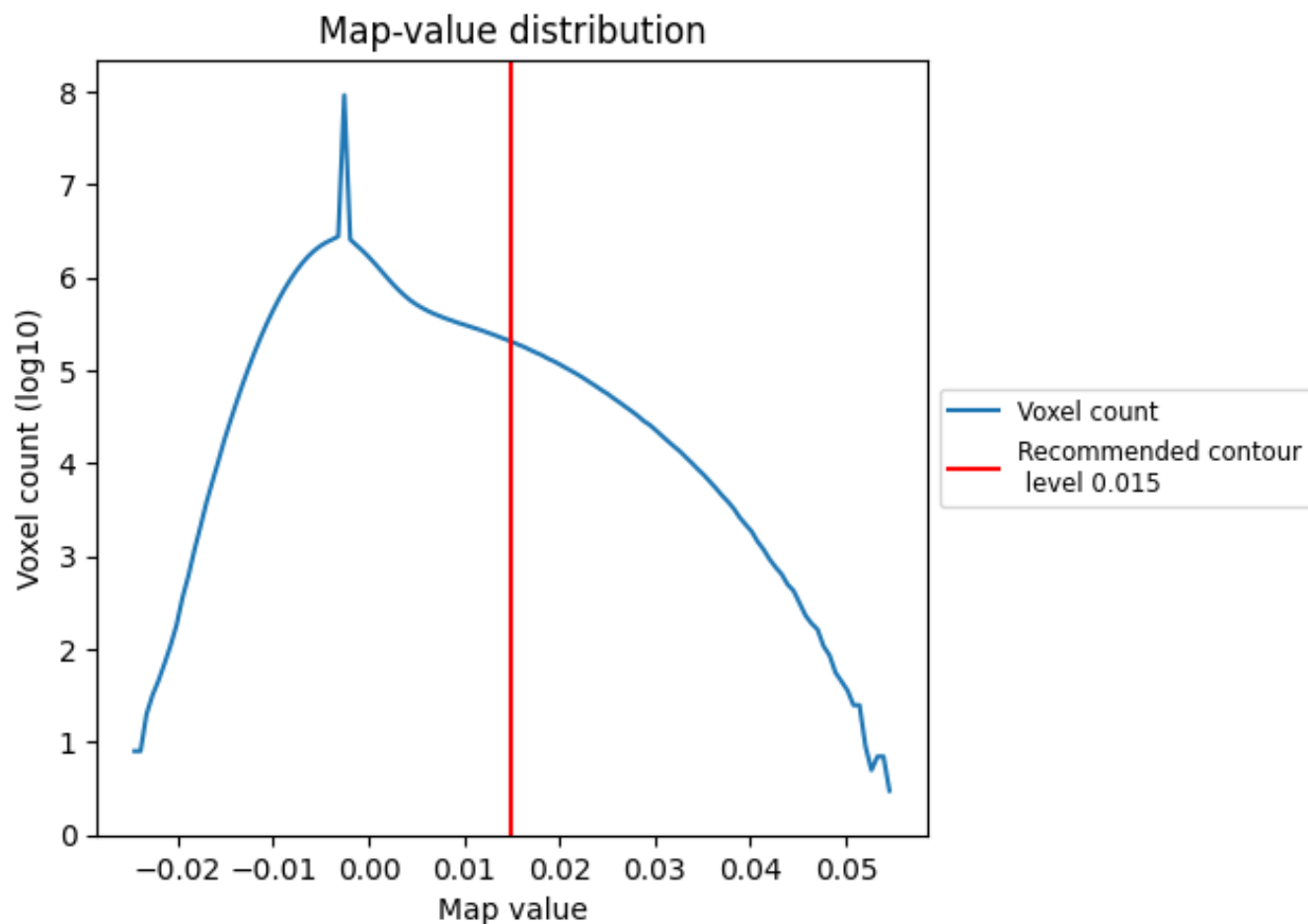
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

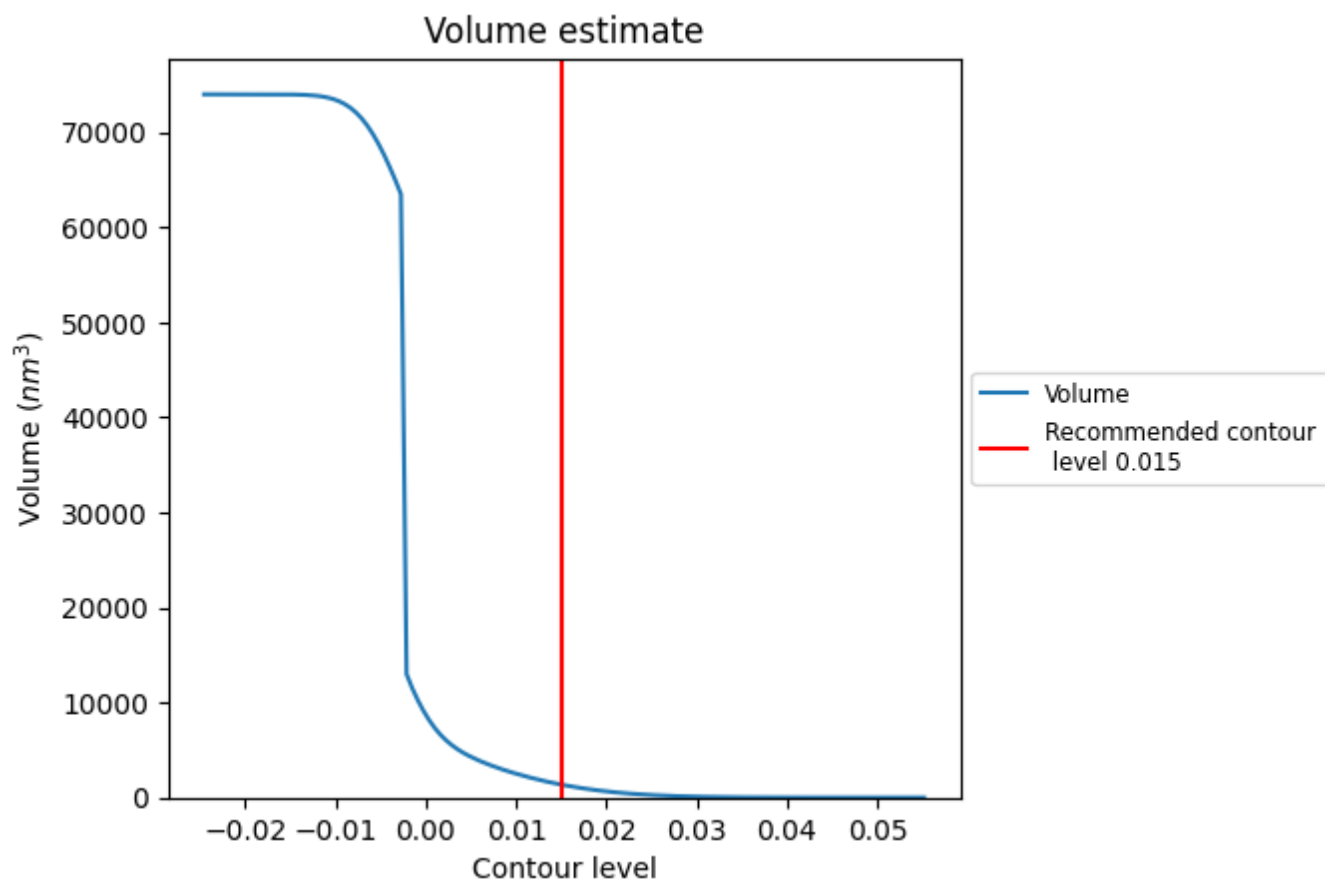
This section contains the results of statistical analysis of the map.

### 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.

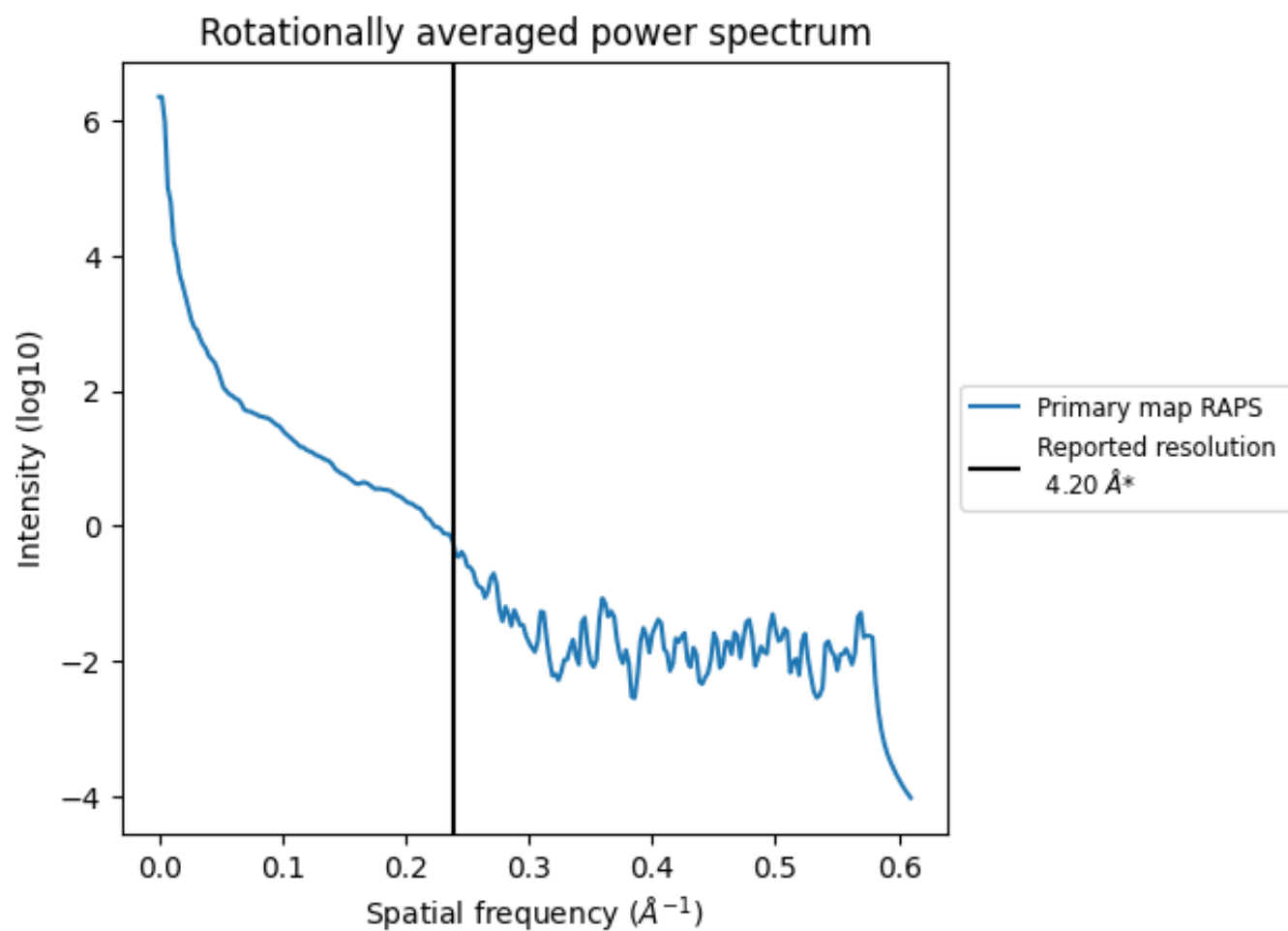
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1368 nm<sup>3</sup>; 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 ⓘ



\*Reported resolution corresponds to spatial frequency of 0.238 Å<sup>-1</sup>

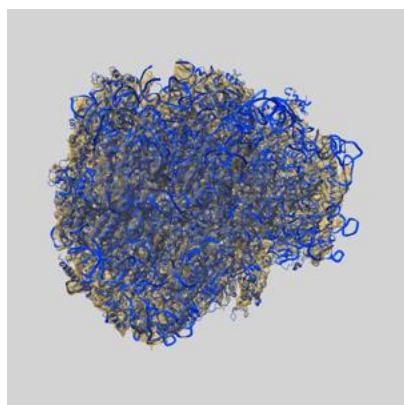
## 8 Fourier-Shell correlation

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

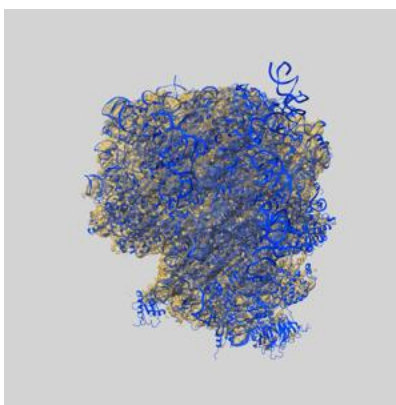
## 9 Map-model fit [i](#)

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

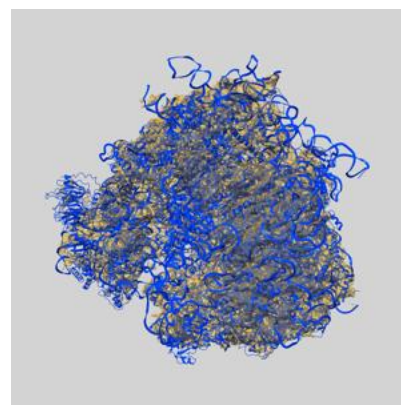
### 9.1 Map-model overlay [i](#)



X



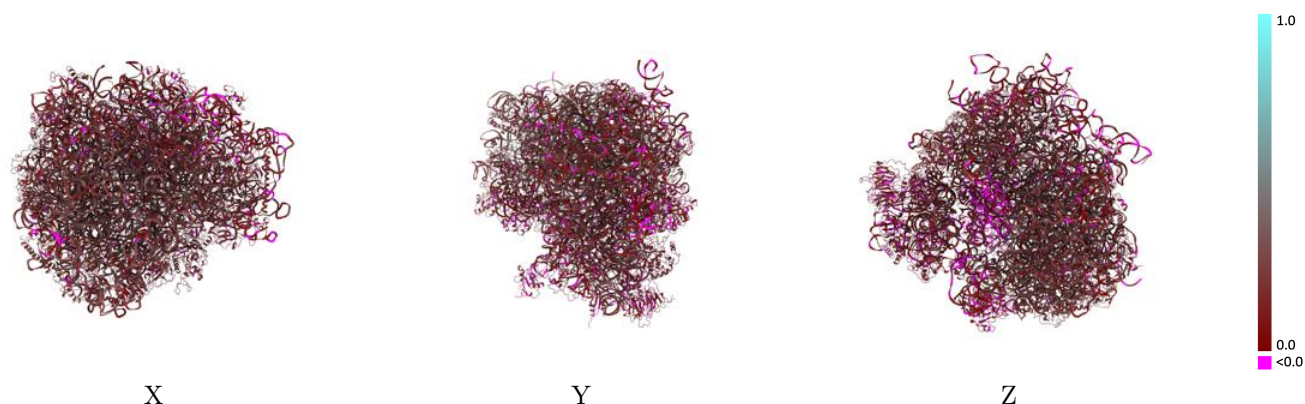
Y



Z

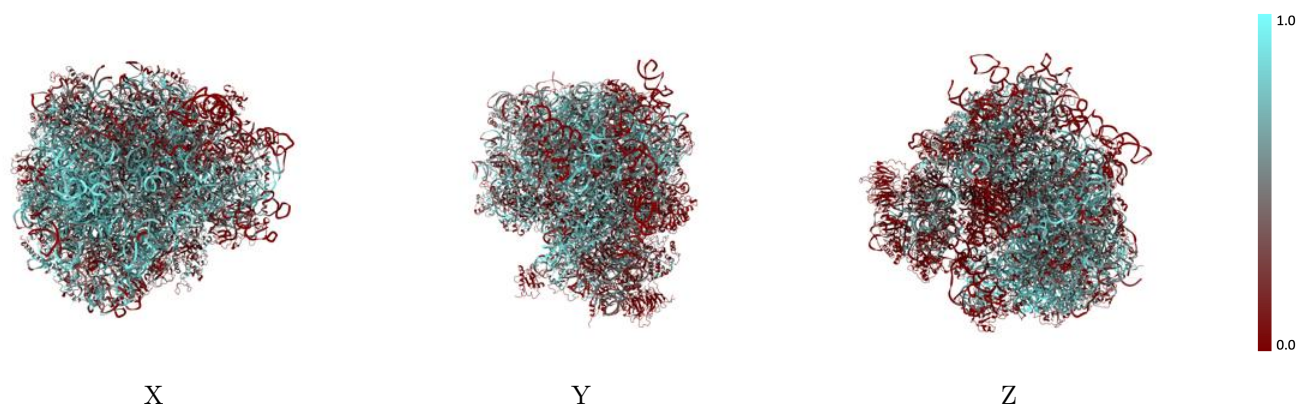
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



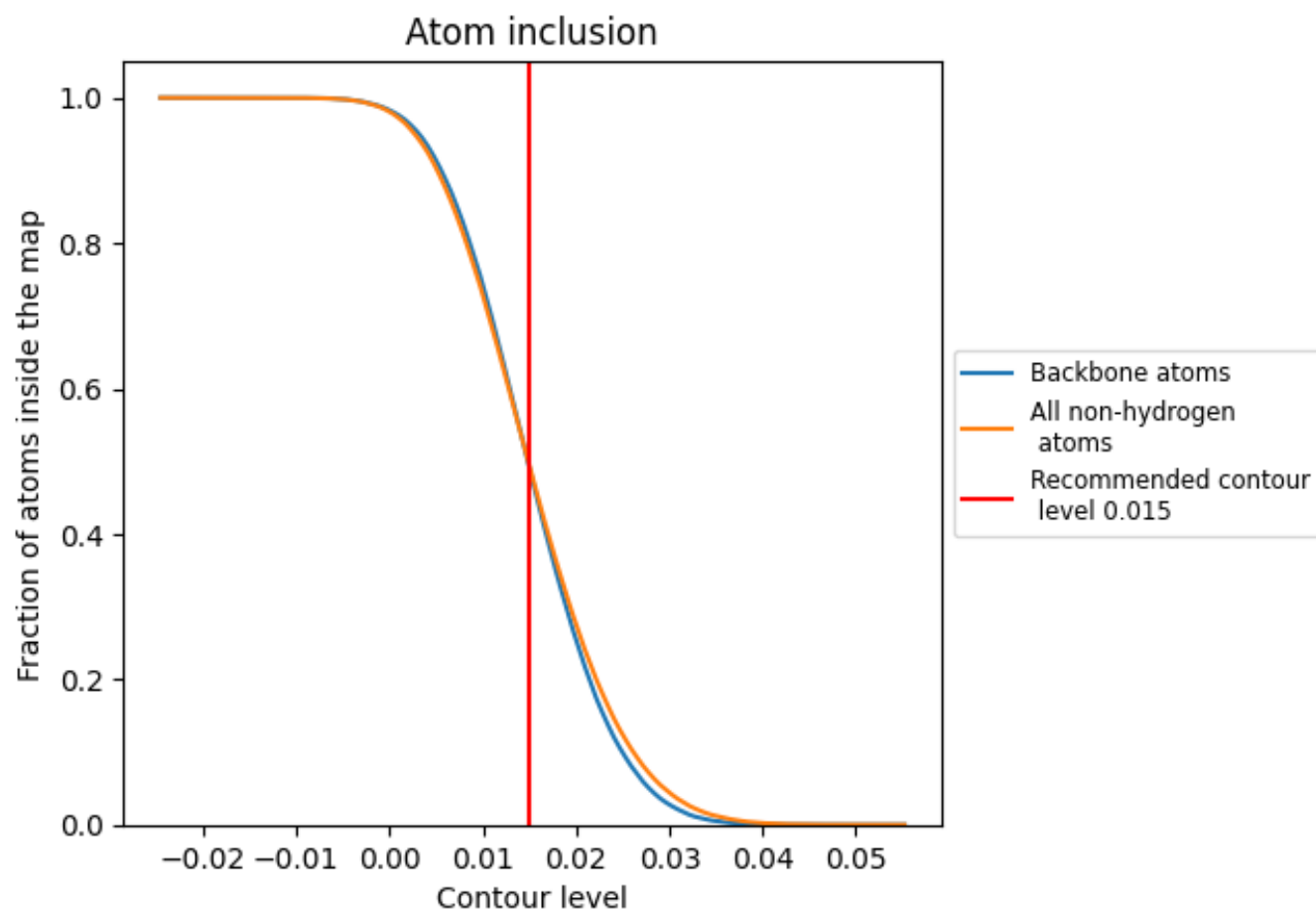
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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	0.4936	0.2100
A	0.4886	0.1870
AA	0.3888	0.2650
AB	0.2652	0.1660
AC	0.2635	0.1450
B	0.6929	0.2430
BA	0.5091	0.2440
BB	0.5816	0.2120
BC	0.2549	0.1610
C	0.6222	0.2320
CA	0.1996	0.2000
CB	0.1552	0.1440
CC	0.0317	0.0500
D	0.8628	0.2350
DA	0.5636	0.2180
DB	0.2034	0.1920
DC	0.3236	0.1850
E	0.0291	0.1090
EA	0.3060	0.1650
EB	0.0785	0.1560
EC	0.0998	0.0830
F	0.4865	0.2290
FA	0.5792	0.2680
FB	0.3702	0.1920
G	0.4468	0.2570
GA	0.5717	0.2360
GB	0.5617	0.1960
H	0.5190	0.2580
HA	0.6101	0.2070
HB	0.4863	0.1050
I	0.5651	0.1950
IA	0.4444	0.2540
IB	0.2372	0.1940
J	0.2931	0.2270
JA	0.6187	0.2830

















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Chain	Atom inclusion	Q-score
JB	 0.0181	 0.0670
K	 0.4349	 0.2330
KA	 0.2968	 0.2550
KB	 0.2794	 0.1800
L	 0.2934	 0.1840
LA	 0.4542	 0.2080
LB	 0.0079	 0.0460
M	 0.3219	 0.2300
MA	 0.2903	 0.2020
MB	 0.1542	 0.1380
N	 0.5279	 0.2150
NA	 0.5188	 0.2510
NB	 0.1231	 0.1430
O	 0.4567	 0.1960
OA	 0.4970	 0.2240
OB	 0.1350	 0.1630
P	 0.2849	 0.1070
PA	 0.0167	 0.1330
PB	 0.0528	 0.1280
Q	 0.6106	 0.2470
QA	 0.4639	 0.2600
QB	 0.1442	 0.1430
R	 0.4985	 0.2340
RA	 0.6658	 0.2650
RB	 0.1522	 0.1520
S	 0.4274	 0.2240
SA	 0.0235	 0.0800
SB	 0.2135	 0.2110
T	 0.4000	 0.2400
TA	 0.7624	 0.2350
TB	 0.2743	 0.2240
U	 0.4689	 0.2450
UA	 0.4284	 0.2330
UB	 0.1635	 0.2150
V	 0.5595	 0.2570
VA	 0.3580	 0.1540
VB	 0.2889	 0.1760
W	 0.3158	 0.2080
WA	 0.0395	 0.1300
WB	 0.0457	 0.1330
X	 0.3870	 0.2450
XA	 0.2231	 0.2070

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Chain	Atom inclusion	Q-score
XB	 0.0206	 0.0390
Y	 0.5294	 0.2540
YA	 0.0035	 0.0120
YB	 0.3654	 0.2160
Z	 0.2289	 0.1930
ZA	 0.3091	 0.2340
ZB	 0.2929	 0.2090