



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 12:55 PM UTC

PDB ID : 5JUP / pdb_00005jup
EMDB ID : EMD-6644
Title : Saccharomyces cerevisiae 80S ribosome bound with elongation factor eEF2-GDP-sordarin and Taura Syndrome Virus IRES, Structure II (mid-rotated 40S subunit)
Authors : Abeyrathne, P.; Koh, C.S.; Grant, T.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2016-05-10
Resolution : 3.50 Å (reported)

This is a wwPDB EM 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:

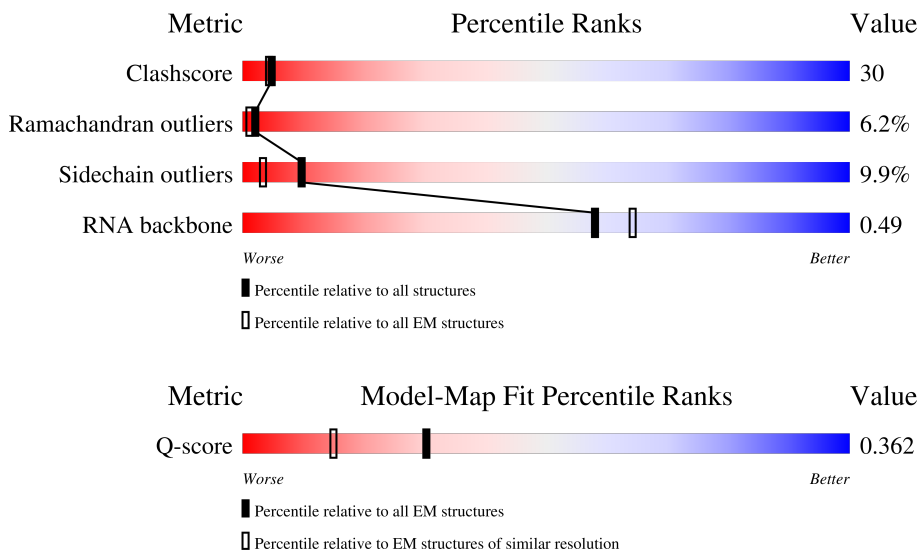
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	15087 (2.80 - 3.80)

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	
2	B	3396	
3	C	158	

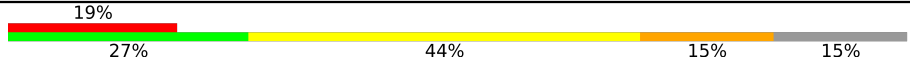
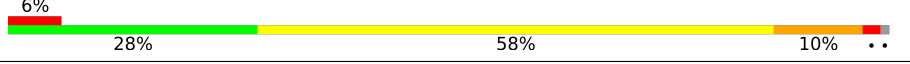
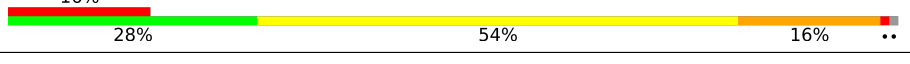
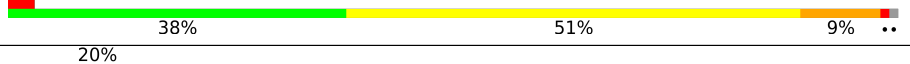

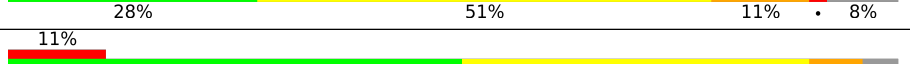

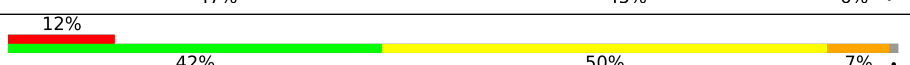
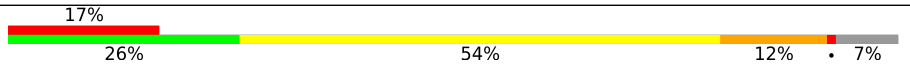


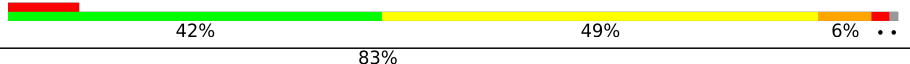

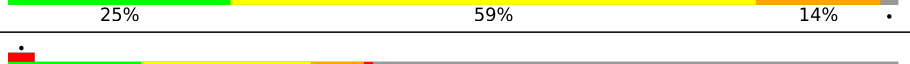
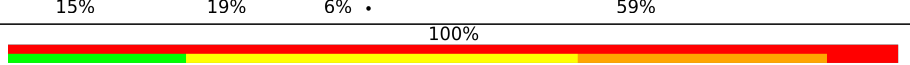

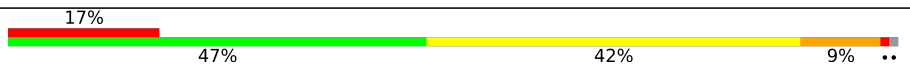

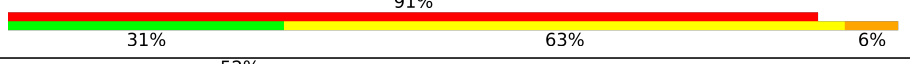
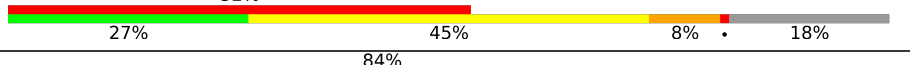

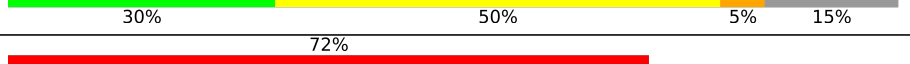



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Mol	Chain	Length	Quality of chain
4	D	121	23% 70% 7%
5	E	217	5% 34% 30% 10% 21%
6	F	254	12% 33% 56% 9%
7	G	387	7% 43% 48% 9%
8	H	362	38% 46% 15%
9	I	297	12% 37% 53% 9%
10	J	176	14% 47% 41% 11%
11	K	244	5% 34% 48% 8% 9%
12	L	256	17% 30% 45% 16% 9%
13	M	191	12% 40% 52% 5%
14	N	221	18% 39% 45% 11% 5%
15	O	174	11% 39% 45% 12%
16	P	165	52% 15% 30% 8% 43%
17	Q	199	12% 39% 46% 12%
18	R	138	9% 38% 46% 14%
19	S	204	7% 32% 54% 12%
20	T	199	7% 47% 46% 5%
21	U	184	9% 51% 38% 11%
22	V	186	40% 53% 6%
23	W	189	30% 40% 48% 11%
24	X	172	11% 34% 48% 17%
25	Y	160	9% 38% 48% 12%
26	Z	121	17% 35% 46% 17%
27	AA	137	17% 42% 46% 11%
28	BA	155	6% 15% 20% 5% 61%

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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	<p>59%</p> <p>48%</p> <p>39%</p> <p>5%</p> <p>5%</p>
80	BC	63	<p>51%</p> <p>40%</p> <p>44%</p> <p>10%</p> <p>5%</p>
81	CC	152	<p>47%</p> <p>38%</p> <p>8%</p> <p>53%</p>
82	DC	842	<p>43%</p> <p>24%</p> <p>47%</p> <p>23%</p> <p>2%</p>
83	EC	201	<p>92%</p> <p>25%</p> <p>38%</p> <p>28%</p> <p>6%</p>

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 212656 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
56	DB	226	1820	1142	350	325	3	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

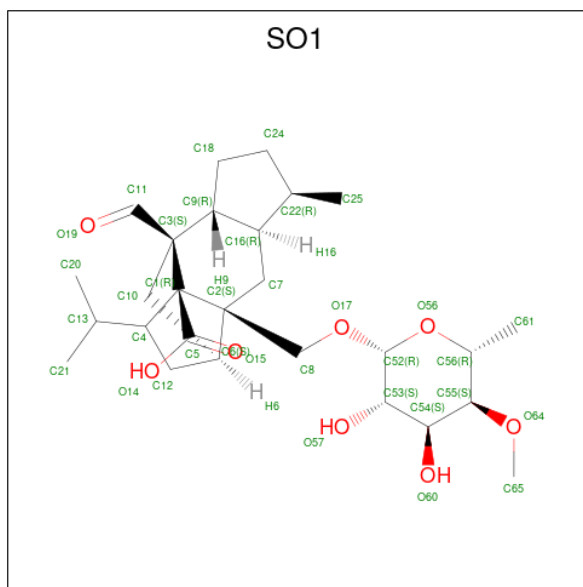
- Molecule 82 is a protein called yeast eEF2.

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

- Molecule 83 is a RNA chain called IRES.

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

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

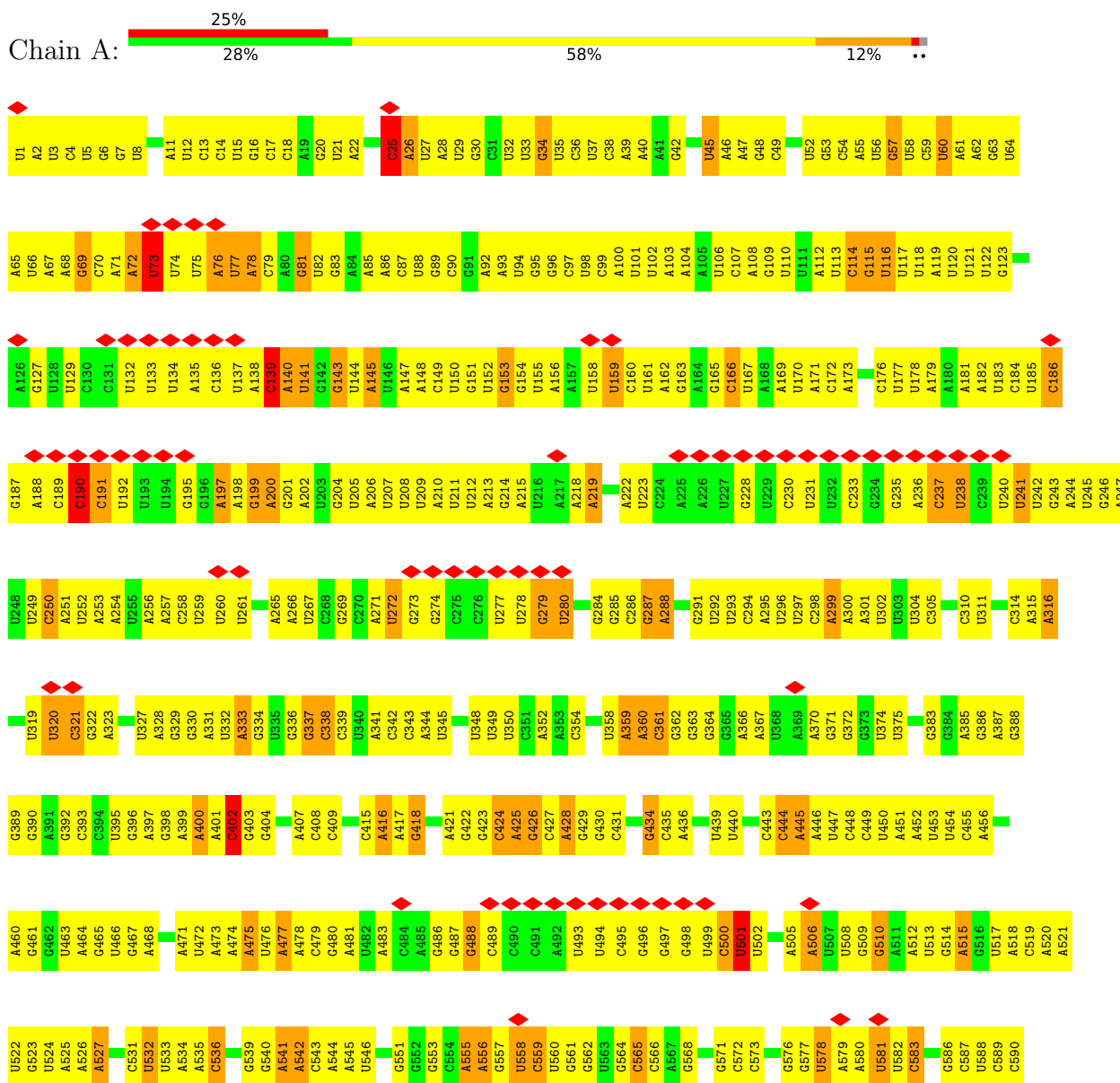


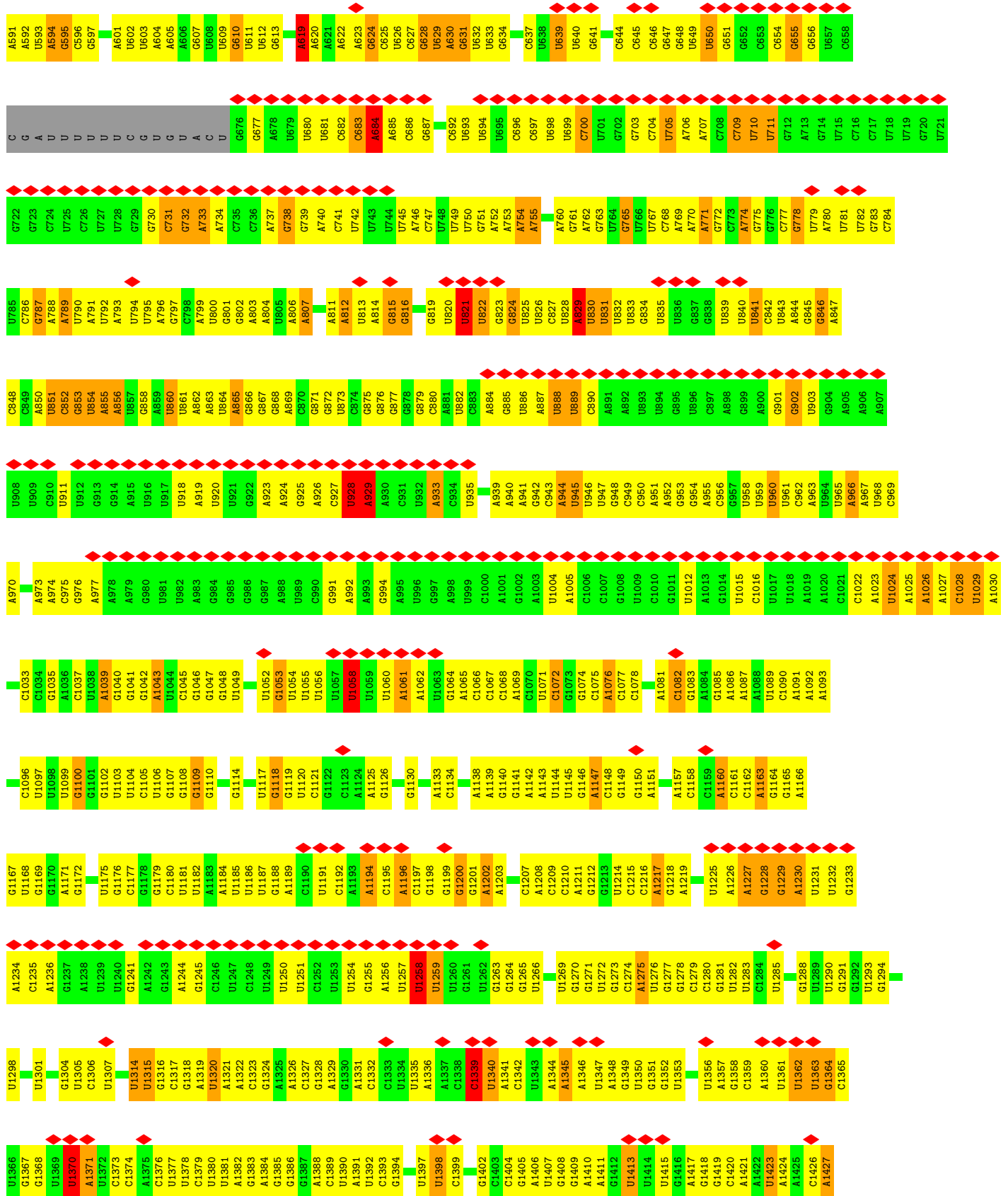
Mol	Chain	Residues	Atoms			AltConf
86	DC	1	Total	C	O	0
			35	27	8	

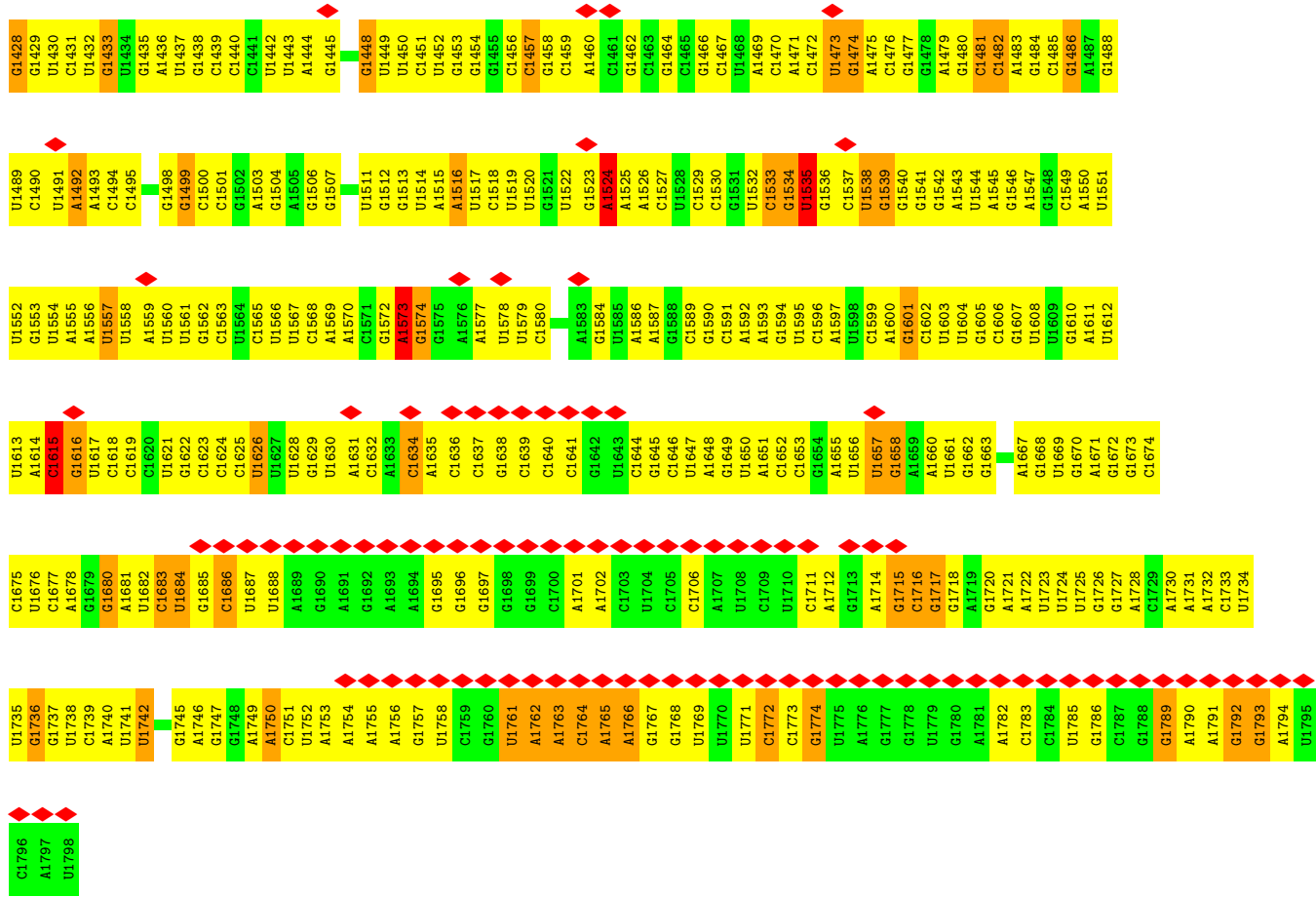
3 Residue-property plots

These plots are drawn for all protein, RNA, 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.

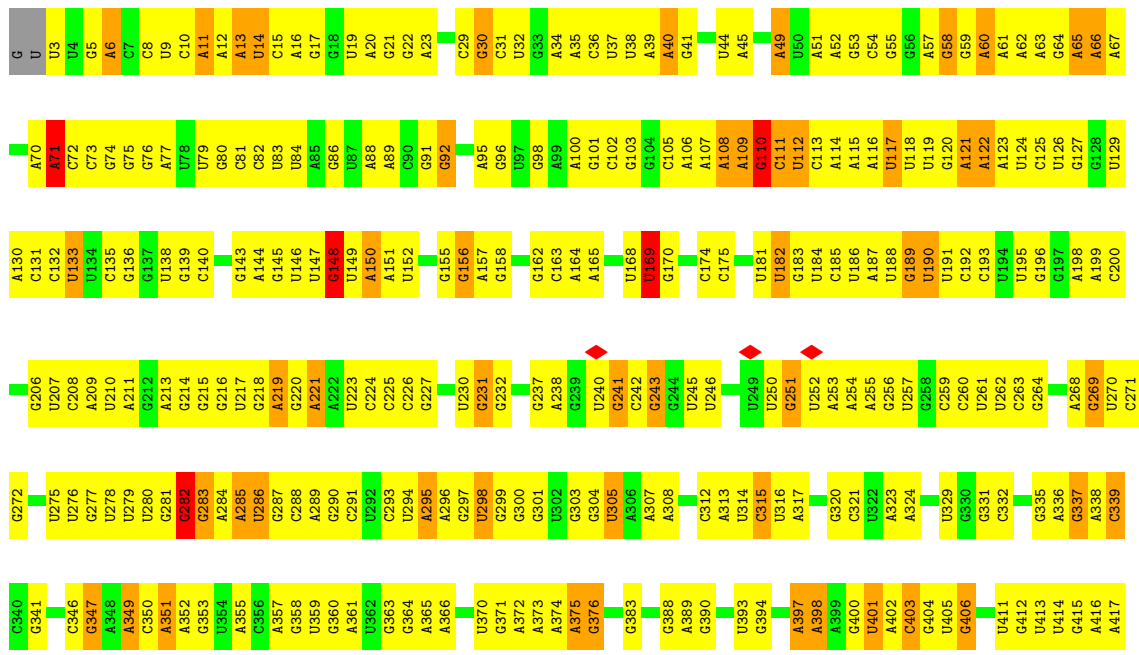
• Molecule 1: 18S ribosomal RNA

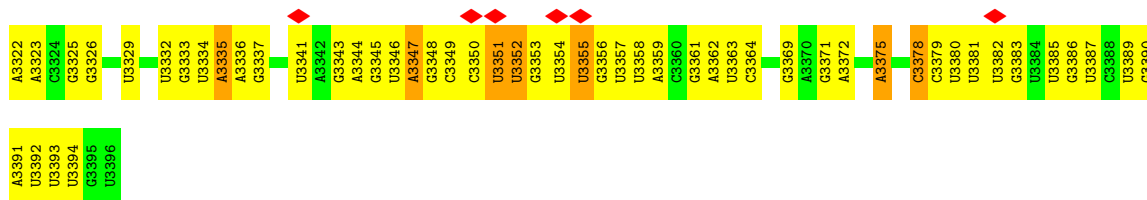






• Molecule 2: 25S ribosomal RNA

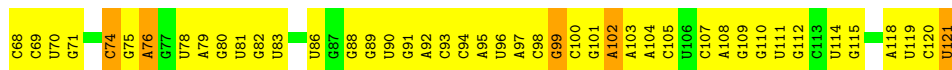




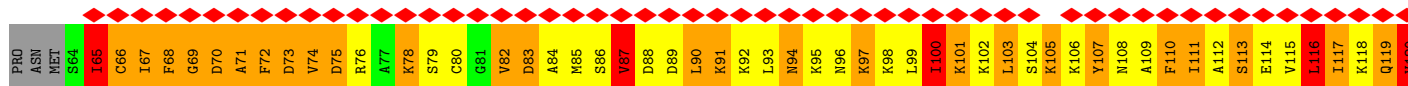
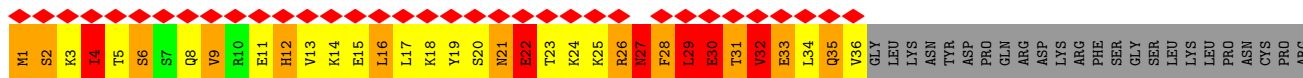
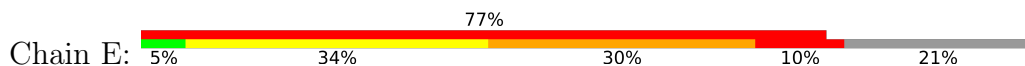
• Molecule 3: 5.8S ribosomal RNA



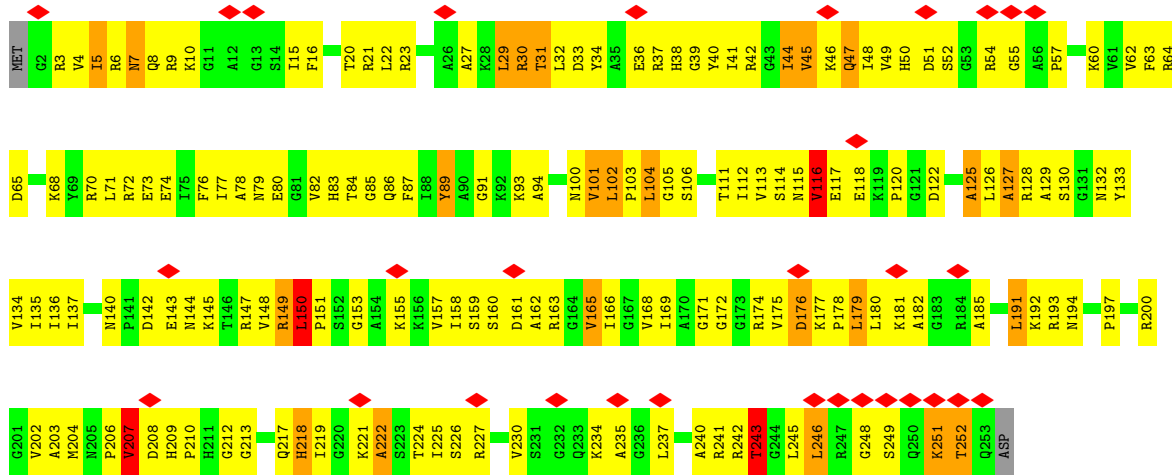
• Molecule 4: 5S ribosomal RNA



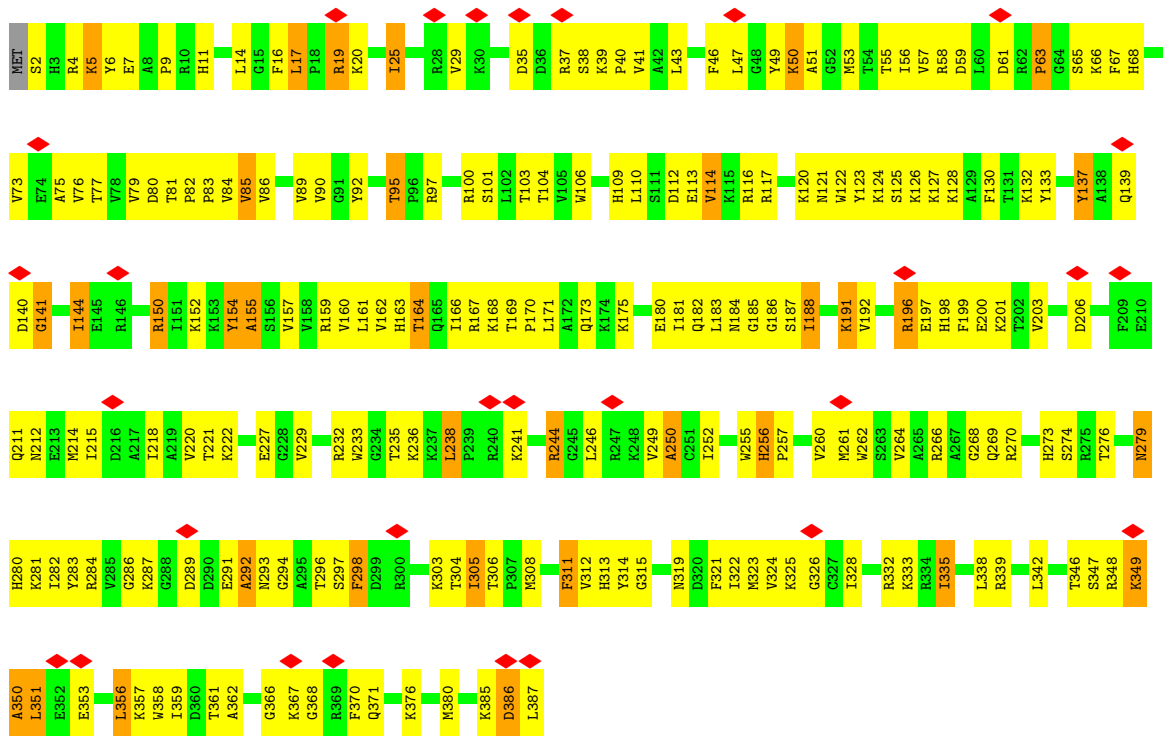
• Molecule 5: uL1 (yeast L1)



• Molecule 6: uL2 (yeast L2)

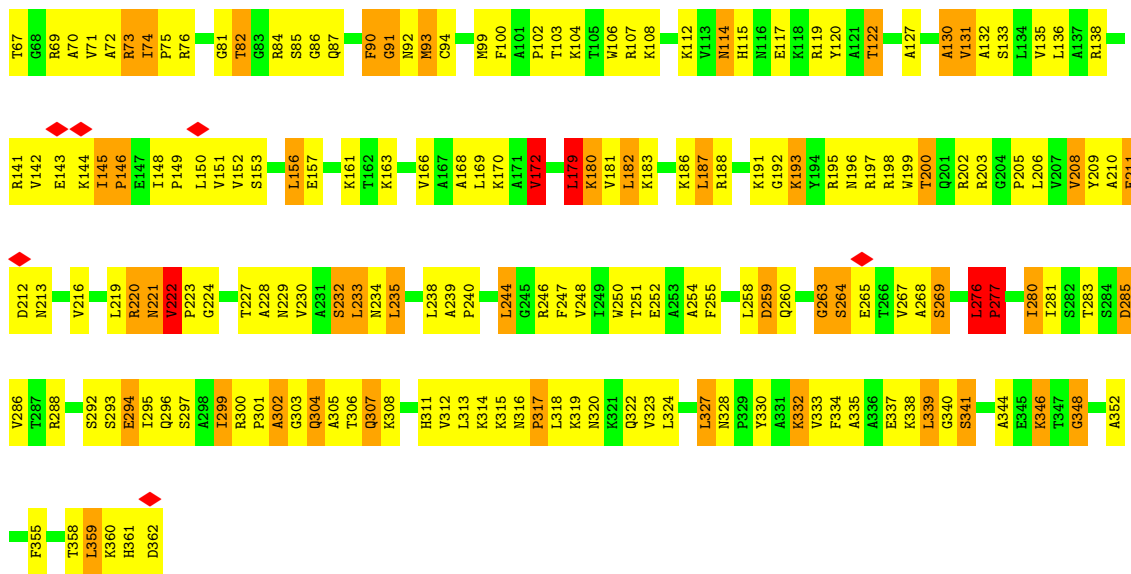


• Molecule 7: uL3 (yeast L3)

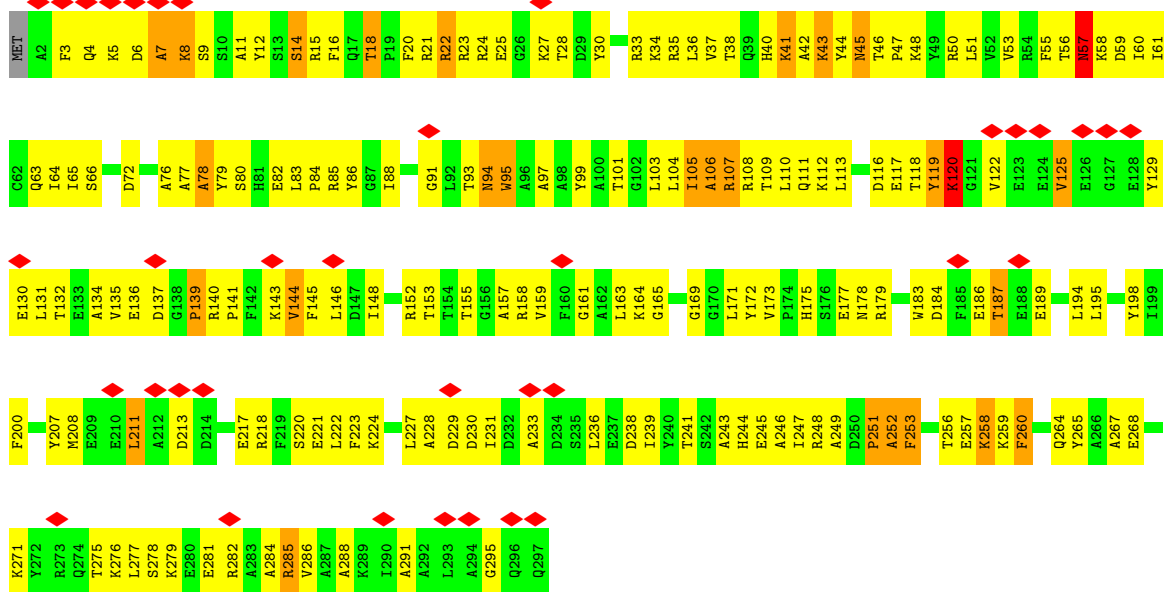
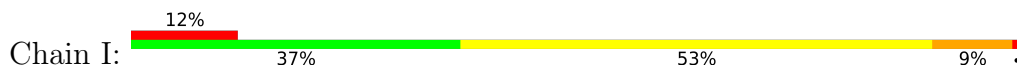


• Molecule 8: uL4 (yeast L4)

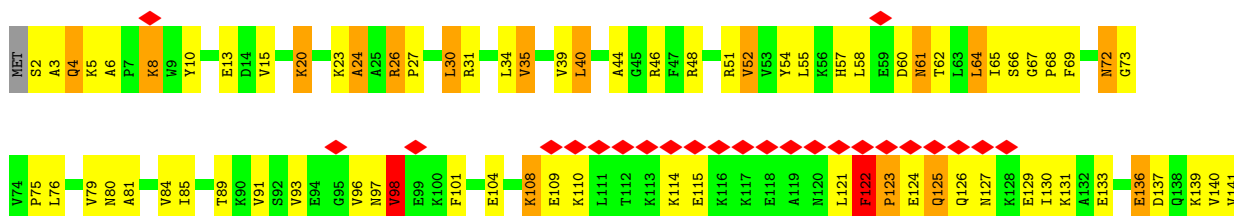


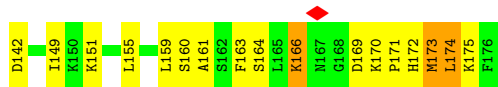


• Molecule 9: uL18 (yeast L5)

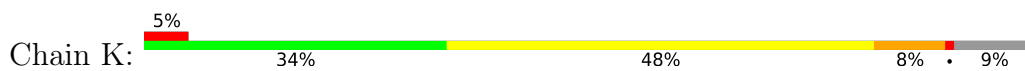


• Molecule 10: eL6 (yeast L6)

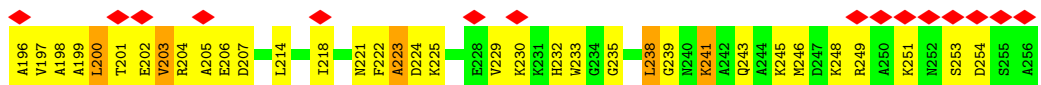
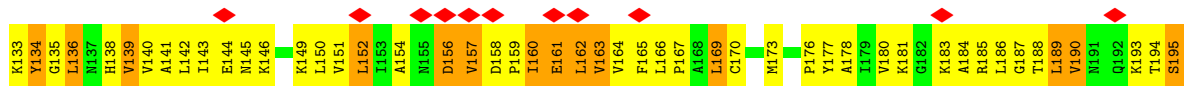
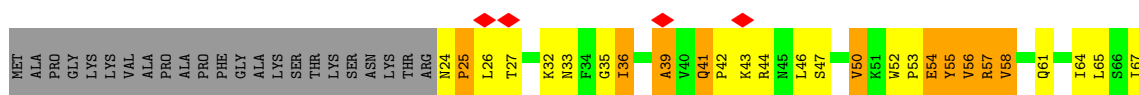




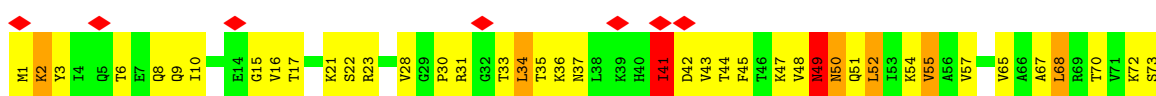
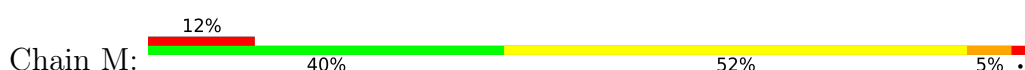
• Molecule 11: uL30 (yeast L7)

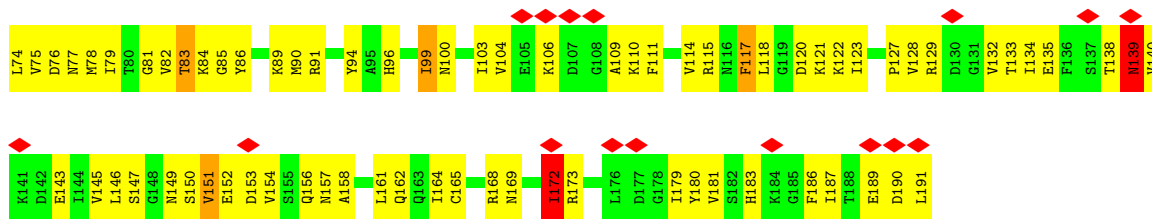


• Molecule 12: eL8 (yeast L8)

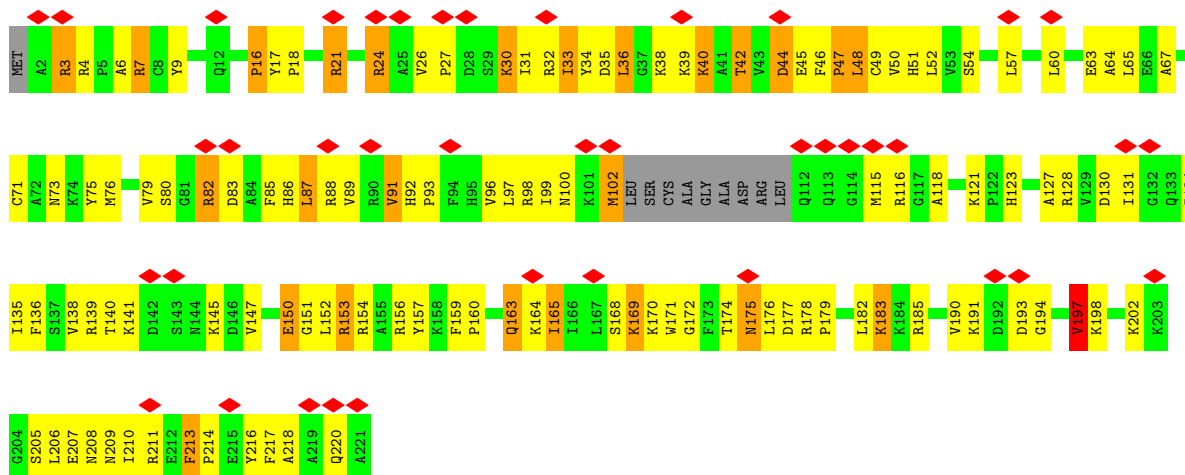


• Molecule 13: uL6 (yeast L9)

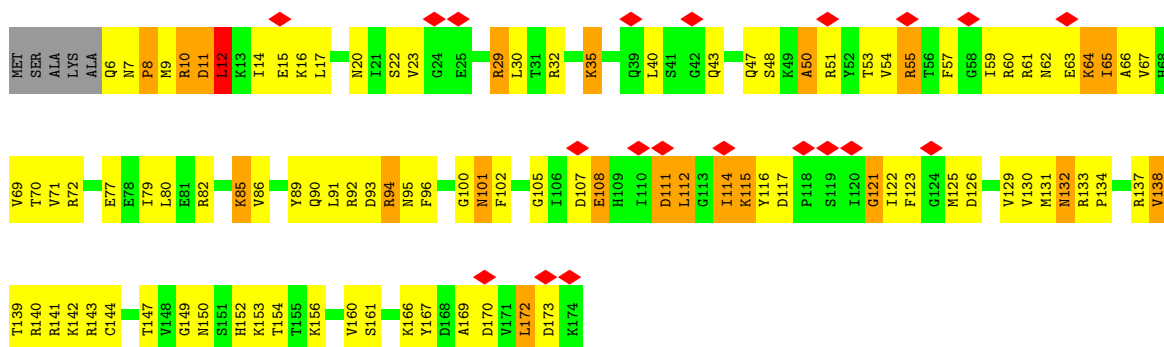




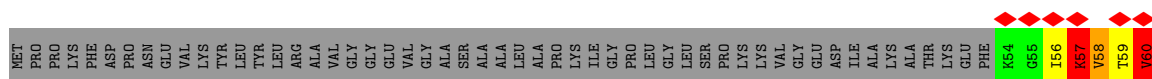
• Molecule 14: uL16 (yeast L10)

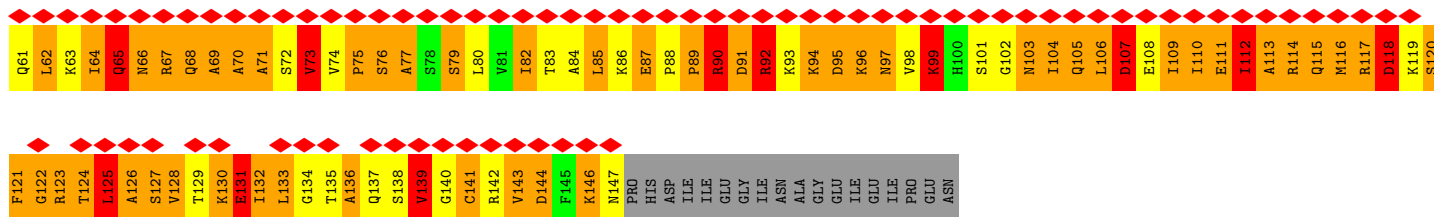


• Molecule 15: uL5 (yeast L11)

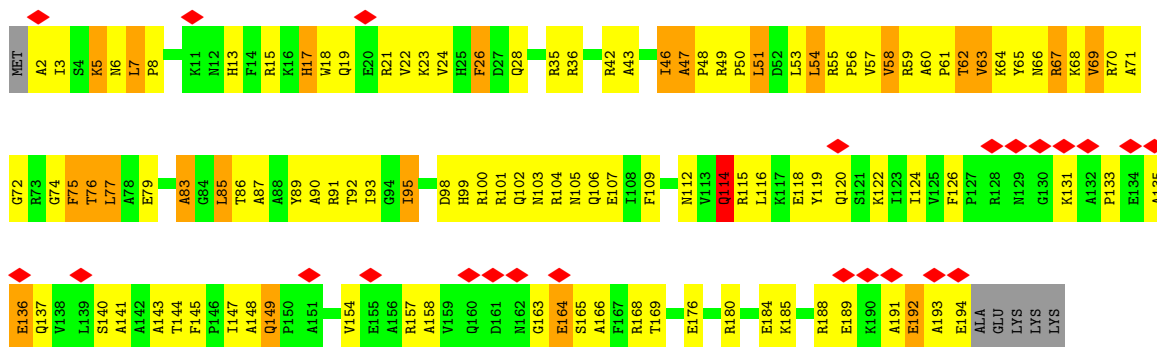


• Molecule 16: uL11 (yeast L12)

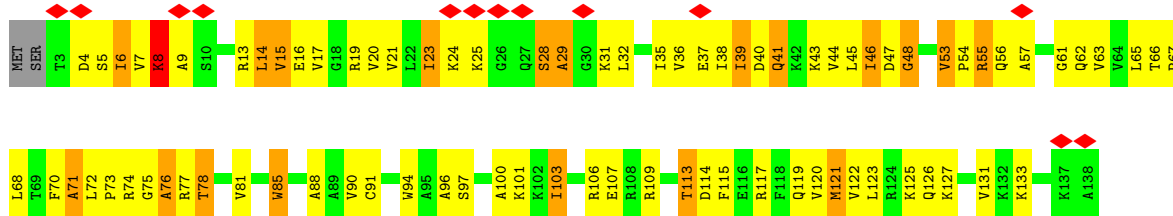




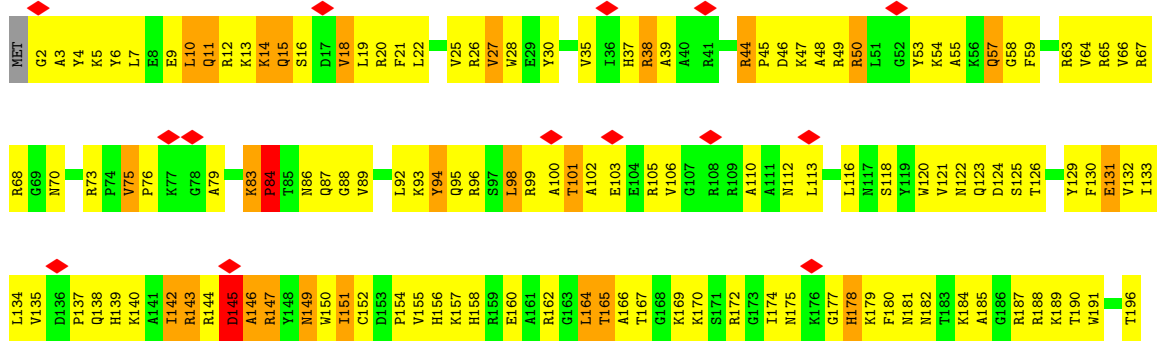
• Molecule 17: eL13 (yeast L13)

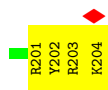


• Molecule 18: eL14 (yeast L14)

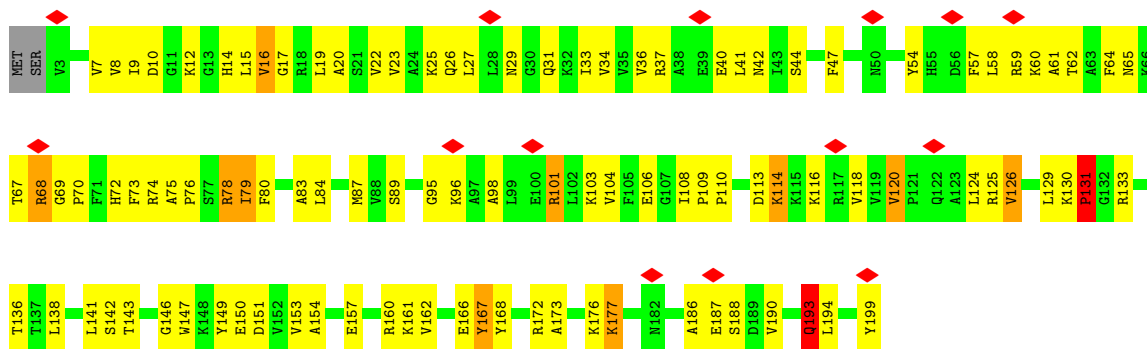


• Molecule 19: eL15 (yeast L15)

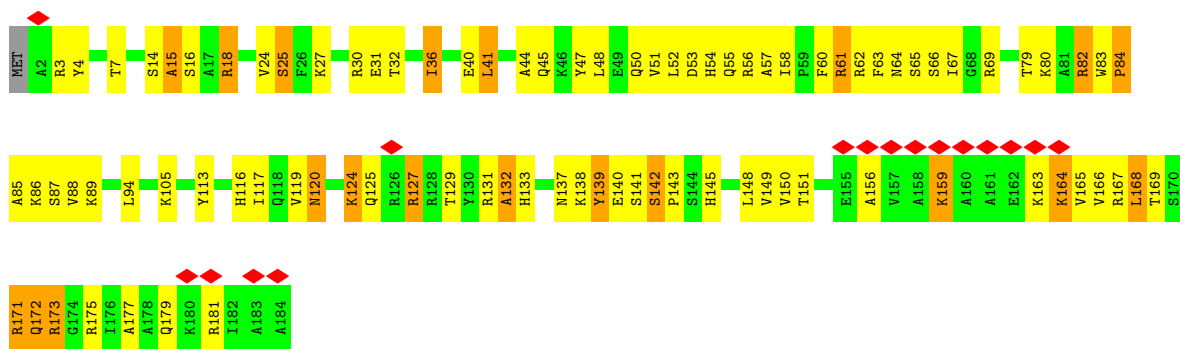




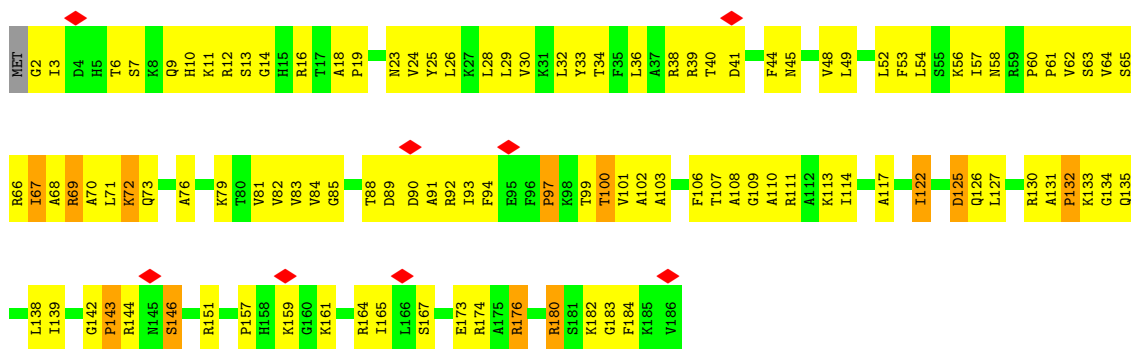
• Molecule 20: uL13 (yeast L16)



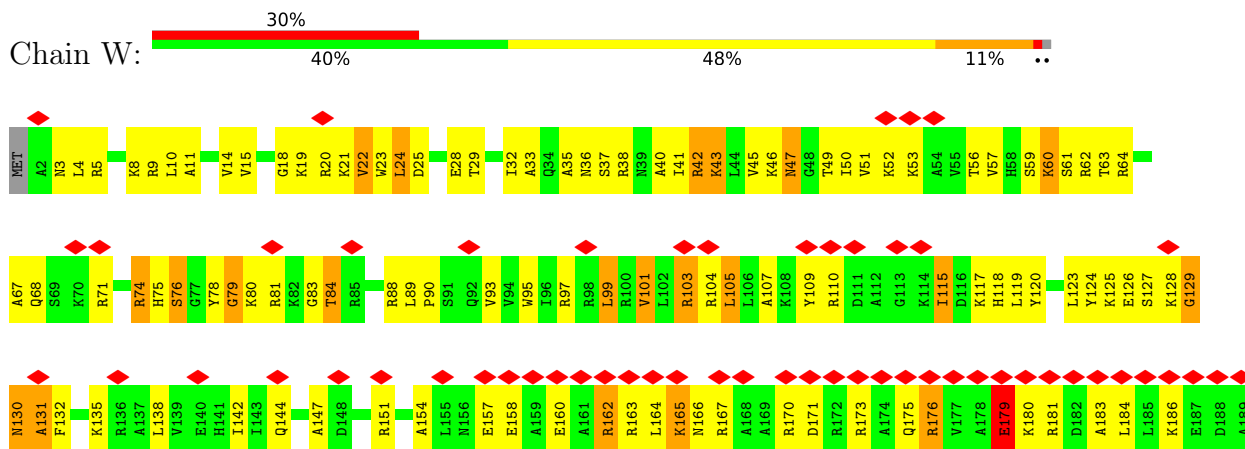
• Molecule 21: uL22 (yeast L17)



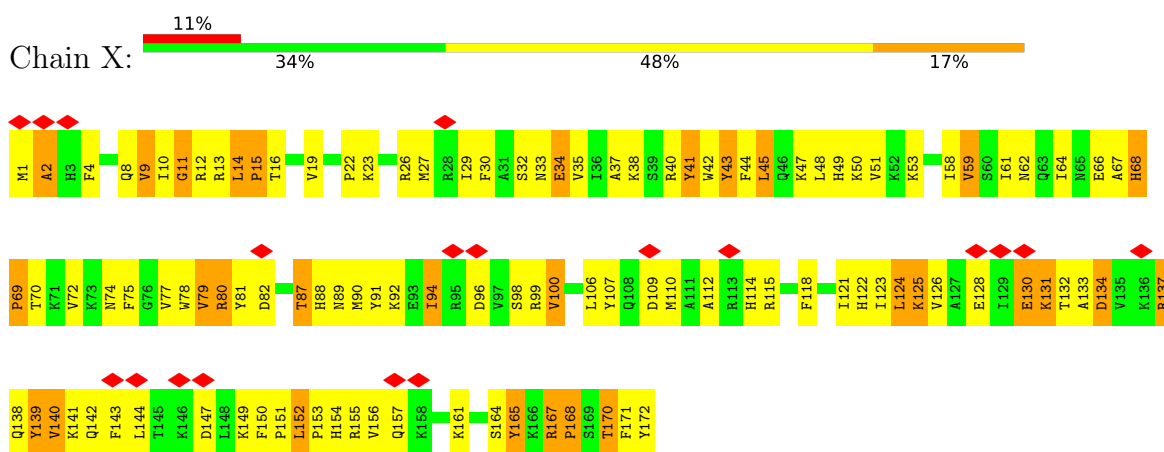
• Molecule 22: eL18 (yeast L18)



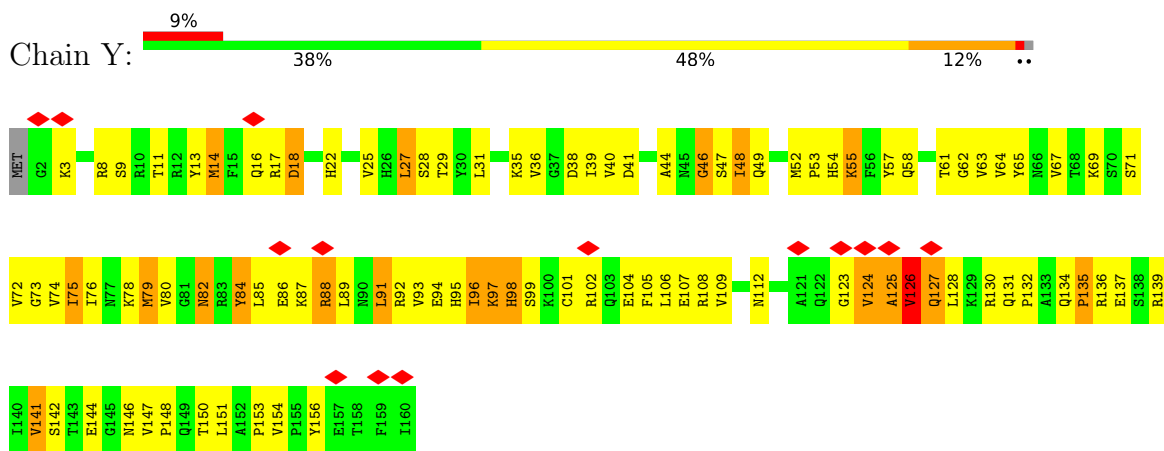
• Molecule 23: eL19 (yeast L19)



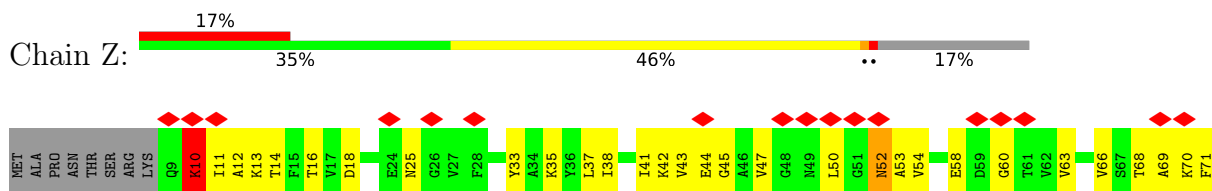
• Molecule 24: eL20 (yeast L20)

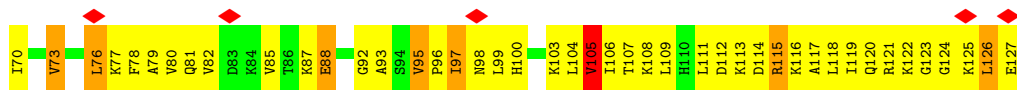


• Molecule 25: eL21 (yeast L21)

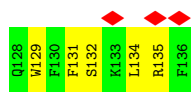
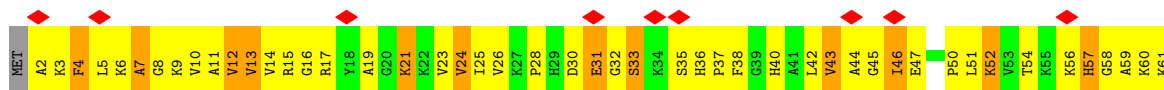


• Molecule 26: eL22 (yeast L22)

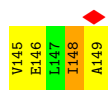
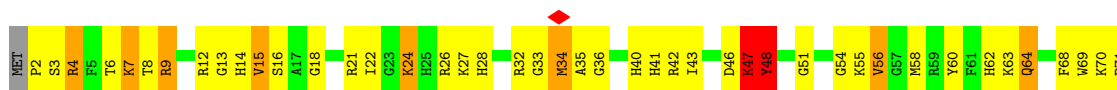




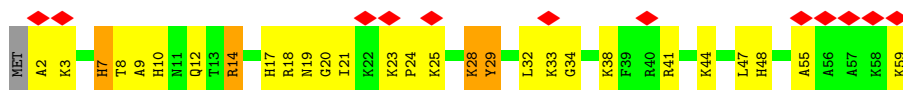
• Molecule 31: eL27 (yeast L27)



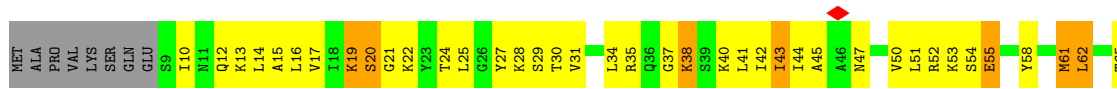
• Molecule 32: uL15 (yeast L28)



• Molecule 33: eL29 (yeast L29)

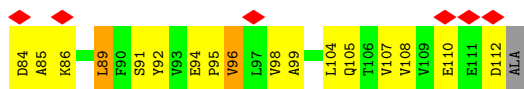
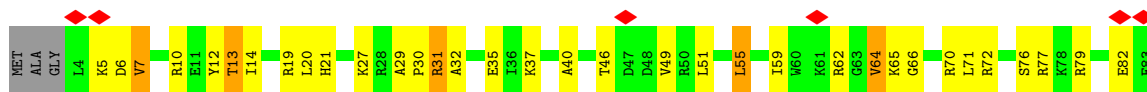


• Molecule 34: eL30 (yeast L30)

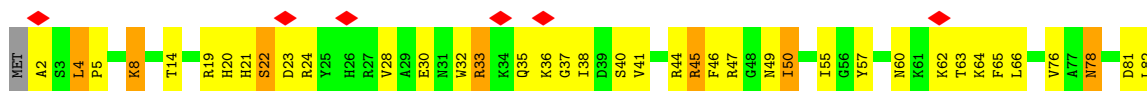




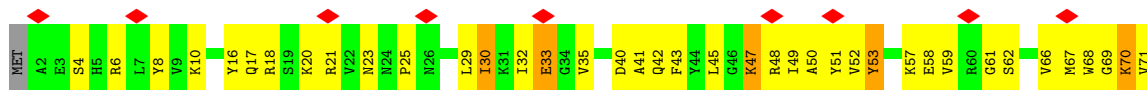
• Molecule 35: eL31 (yeast L31)



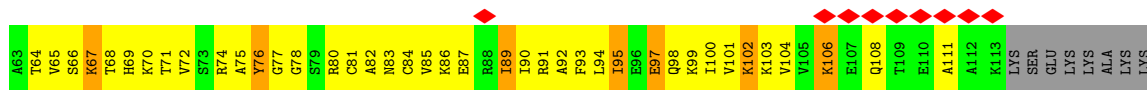
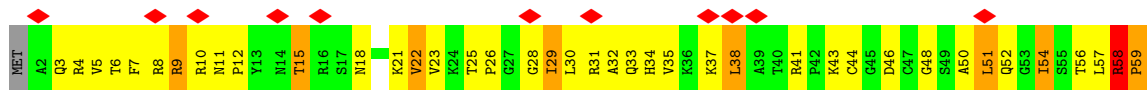
• Molecule 36: eL32 (yeast L32)



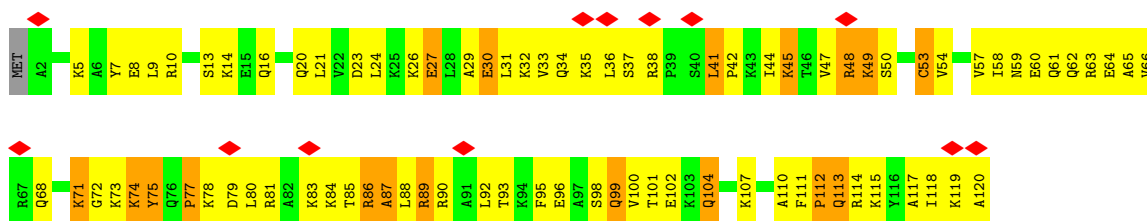
• Molecule 37: eL33 (yeast L33)



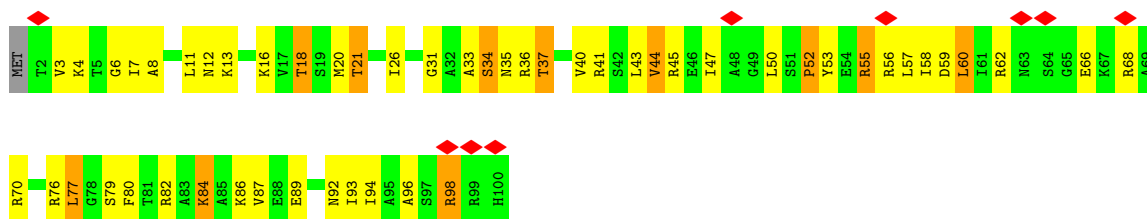
• Molecule 38: eL34 (yeast L34)



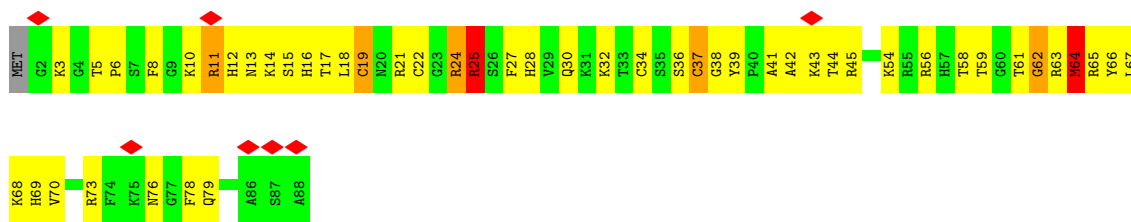
• Molecule 39: uL29 (yeast L35)



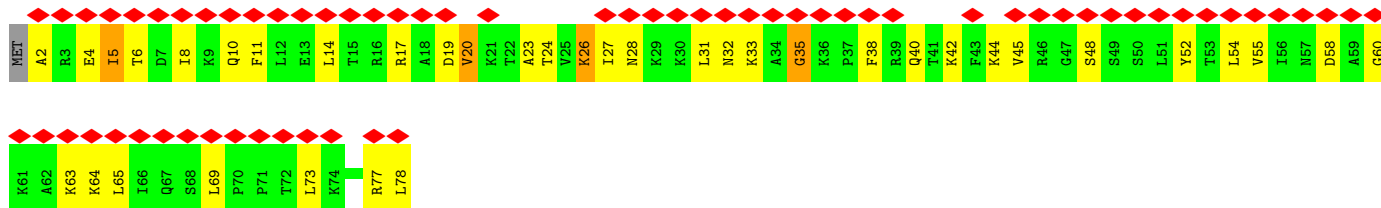
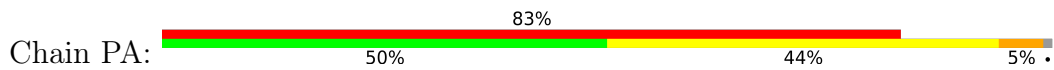
• Molecule 40: eL36 (yeast L36)



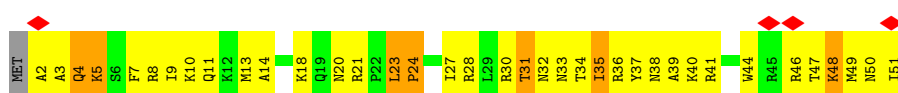
• Molecule 41: eL37 (yeast L37)



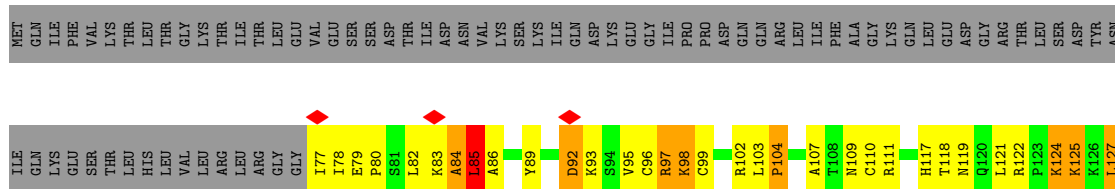
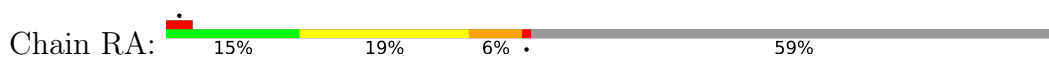
• Molecule 42: eL38 (yeast L38)



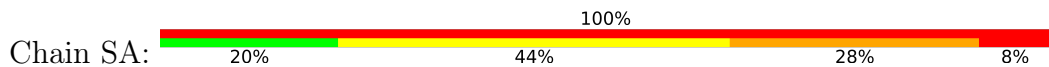
• Molecule 43: eL39 (yeast L39)



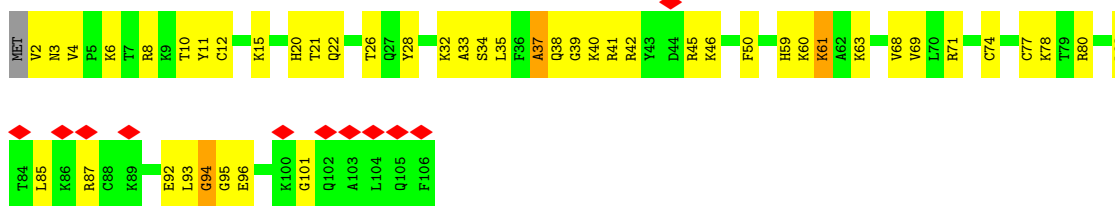
• Molecule 44: eL40 (yeast L40)



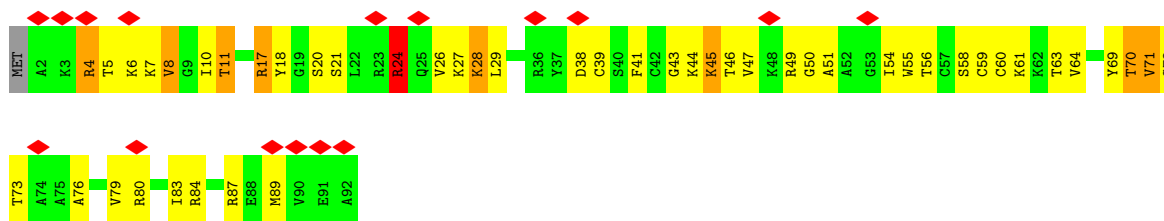
• Molecule 45: eL41 (yeast L41)



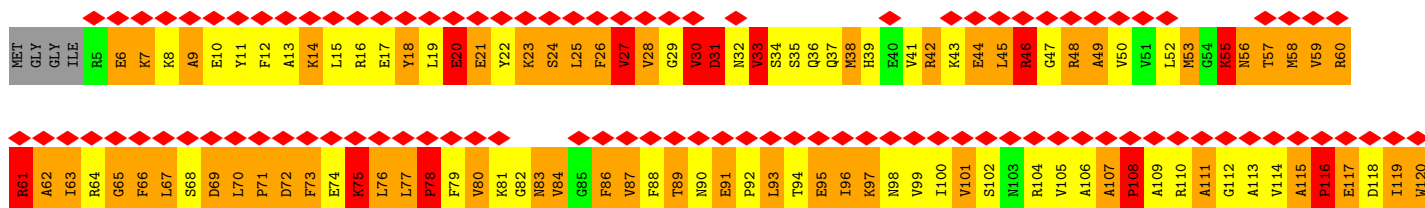
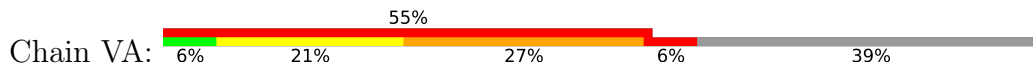
• Molecule 46: eL42 (yeast L42)

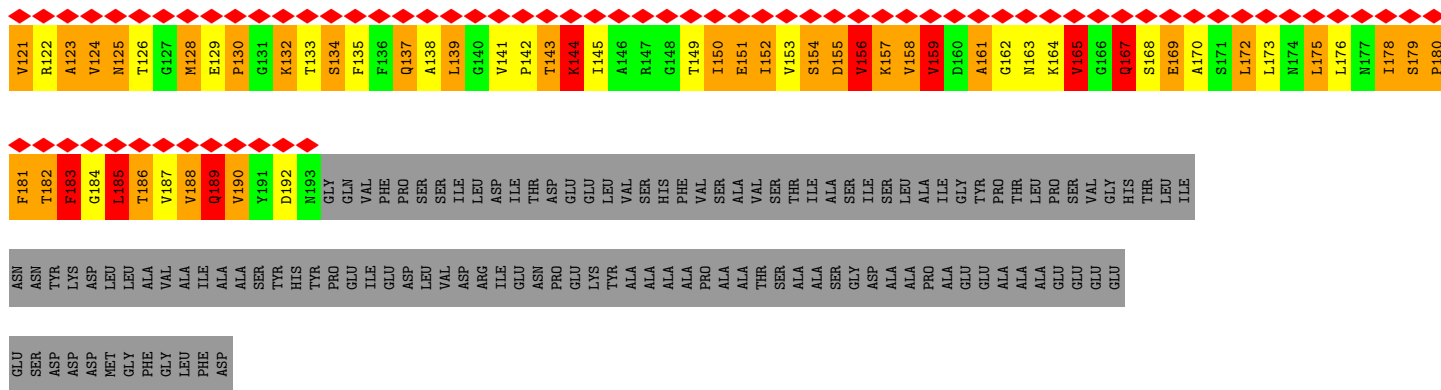


• Molecule 47: eL43 (yeast L43)

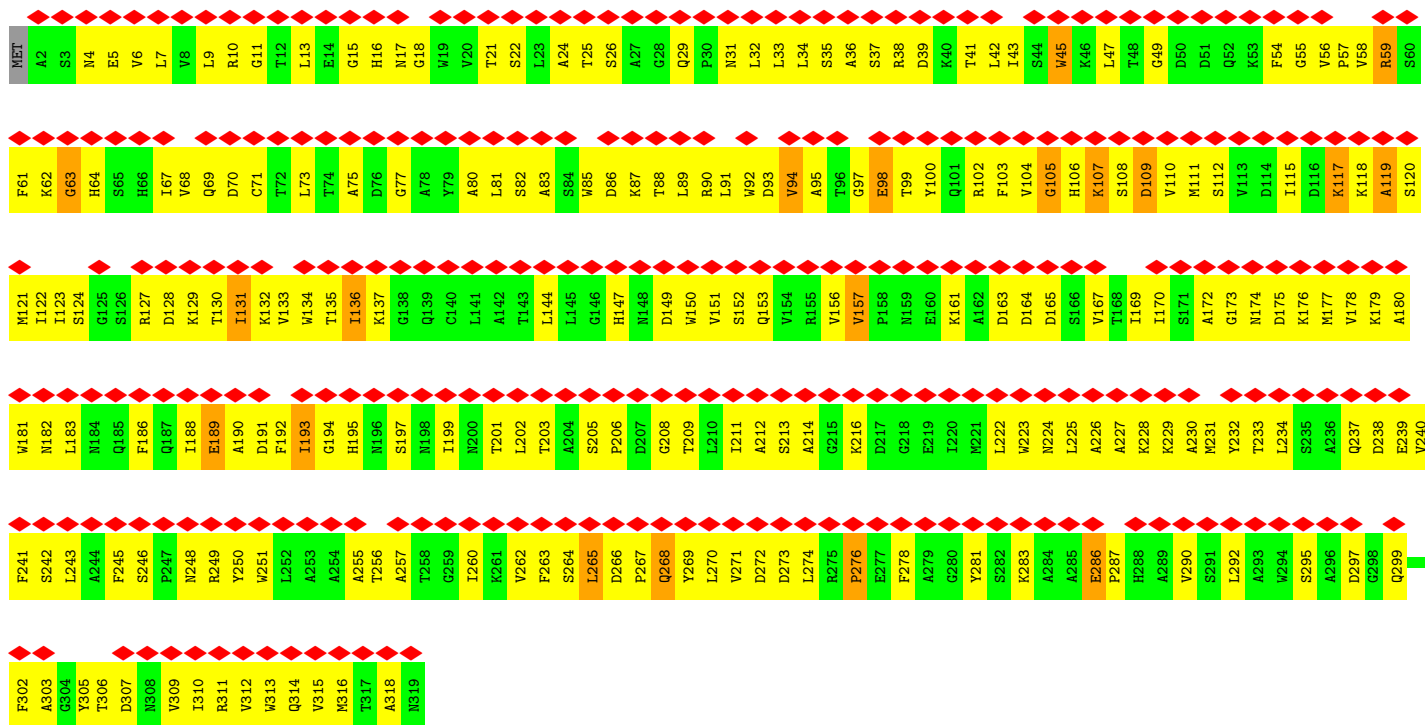


• Molecule 48: uL10 (yeast P0)

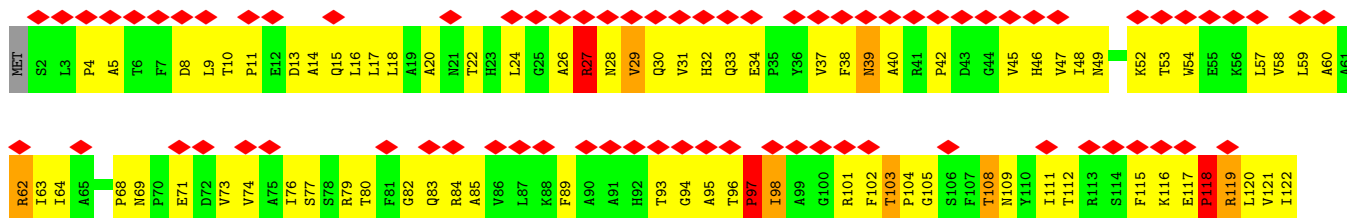


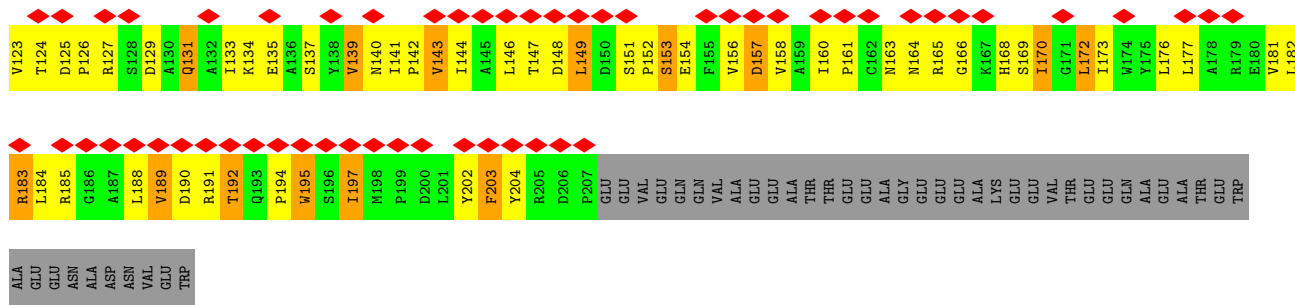


• Molecule 49: RACK1 (yeast Asc1)

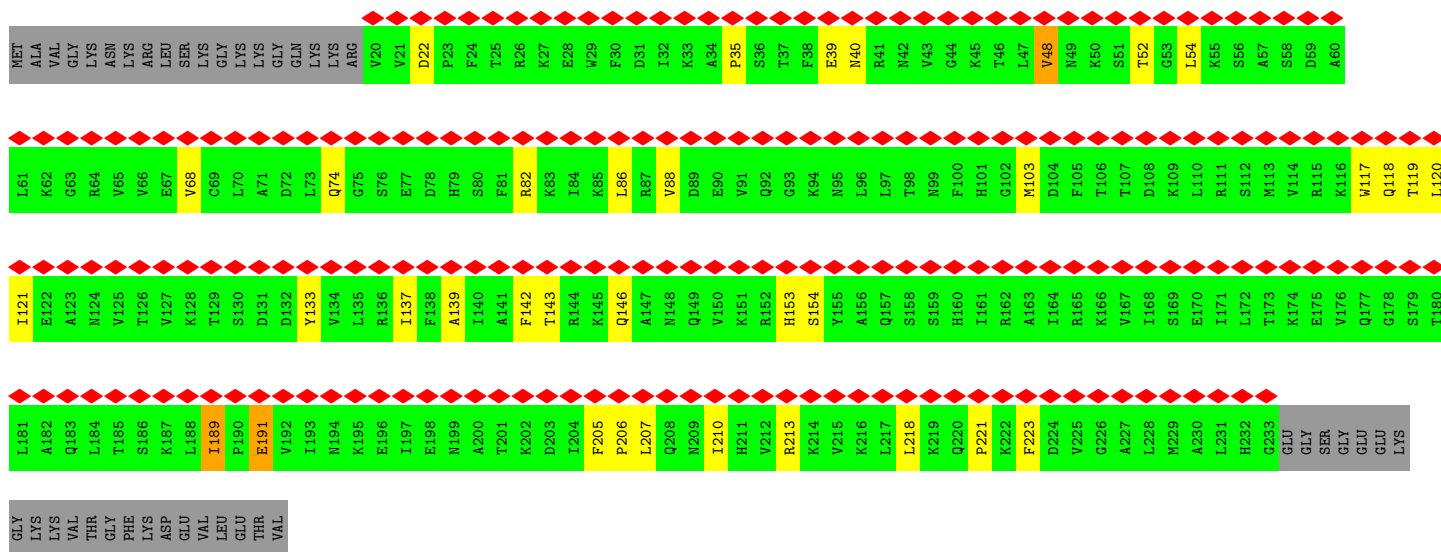
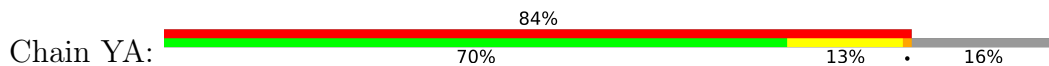


• Molecule 50: uS2 (yeast S0)

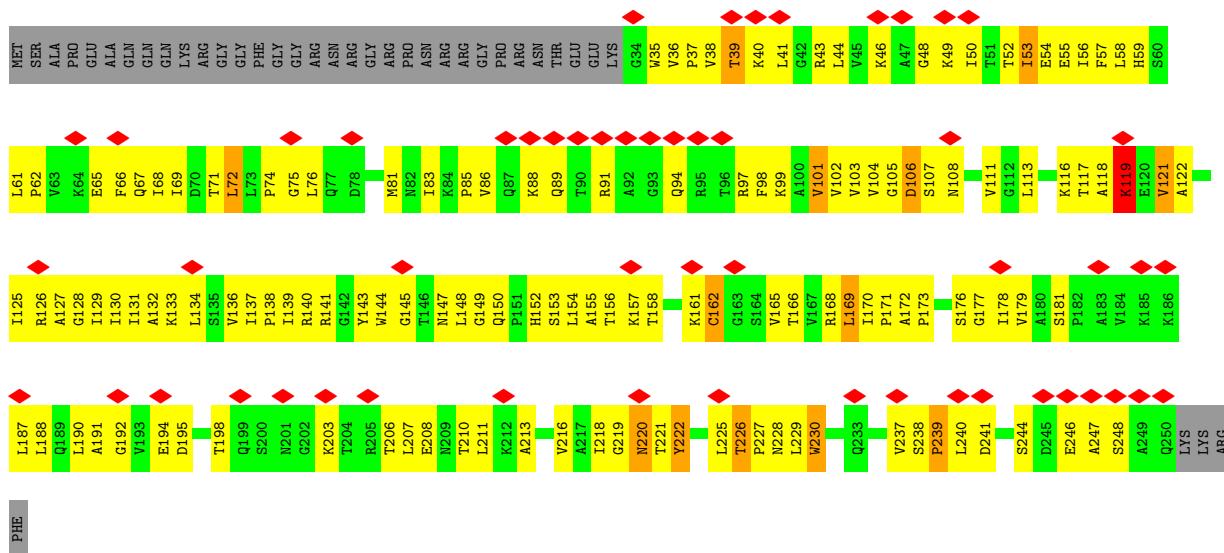




• Molecule 51: eS1 (yeast S1)

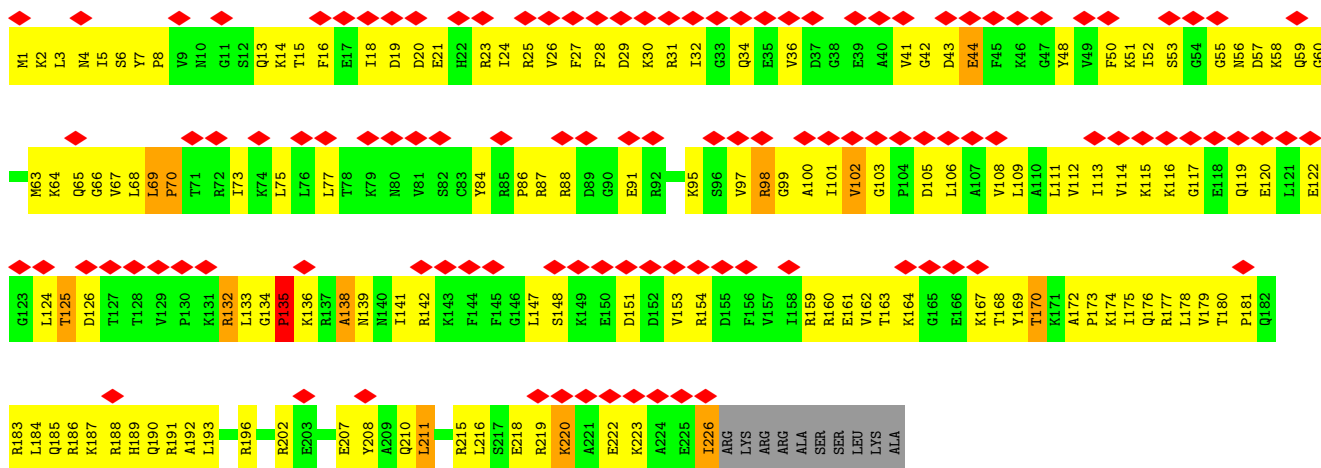


• Molecule 52: uS5 (yeast S2)

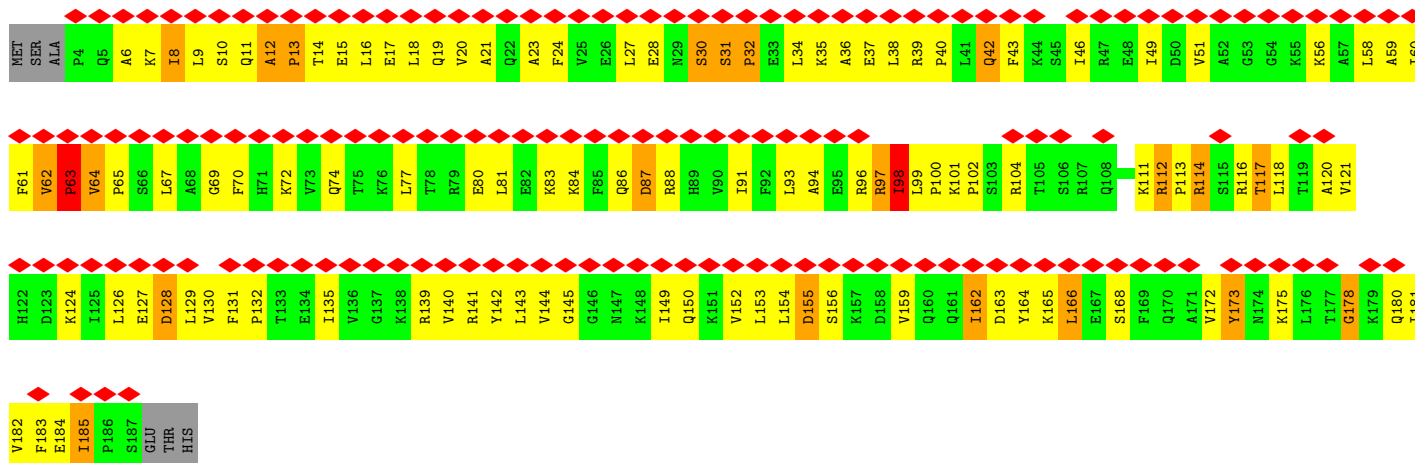
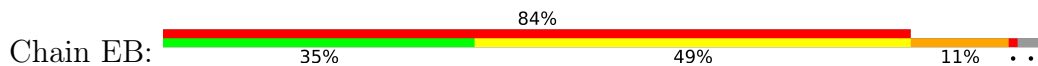




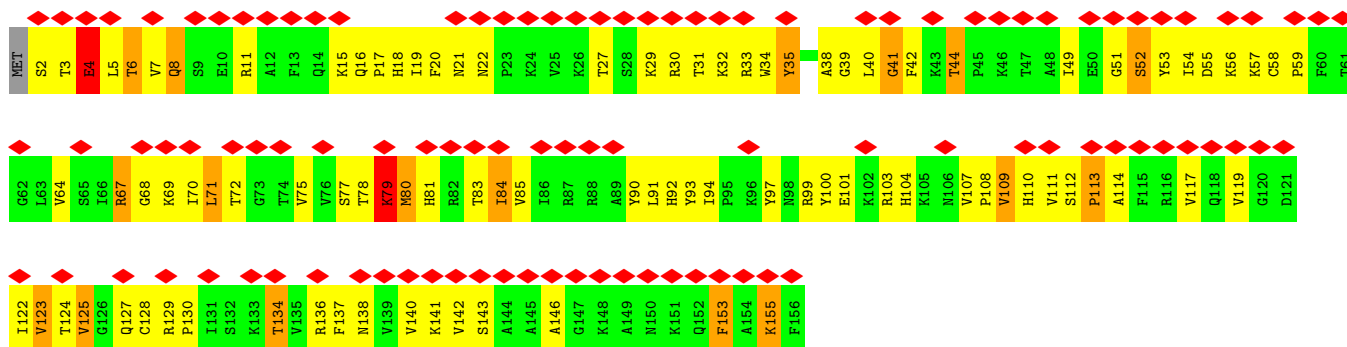
• Molecule 56: eS6 (yeast S6)



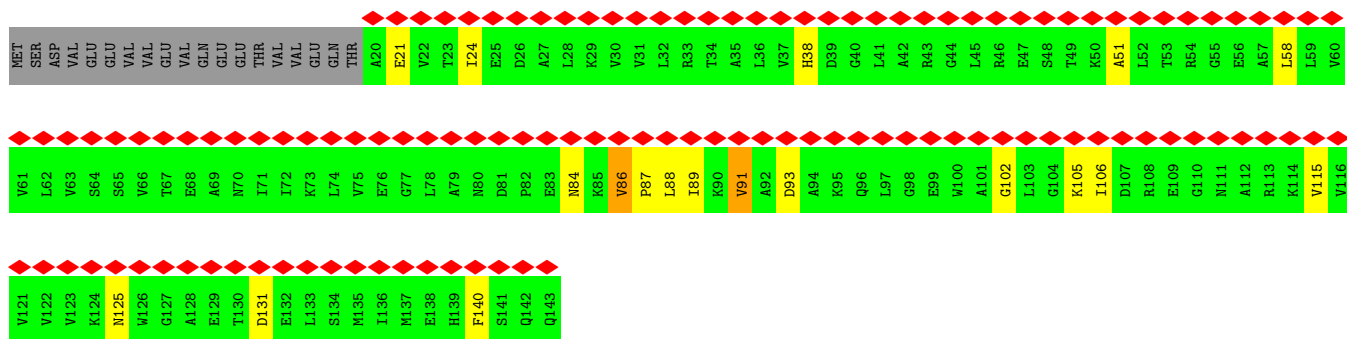
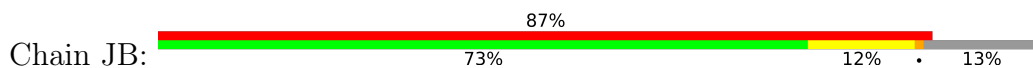
• Molecule 57: eS7 (yeast S7)



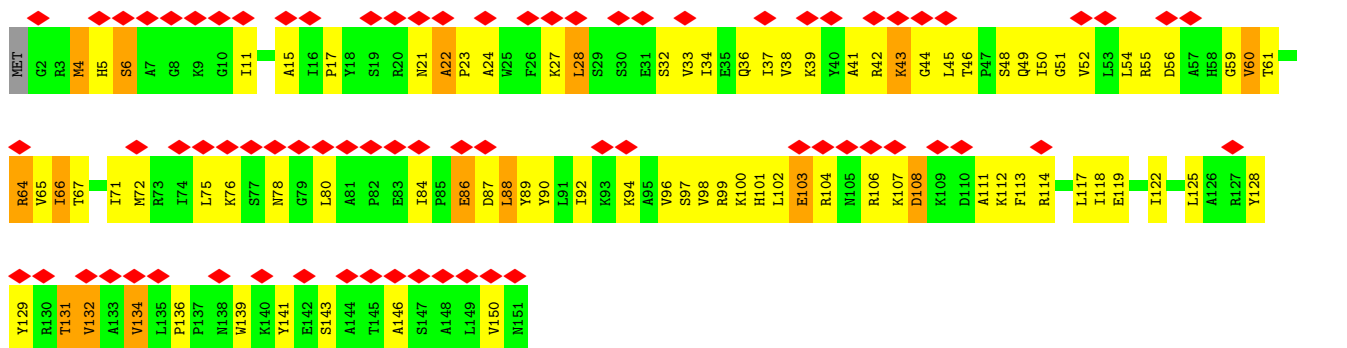
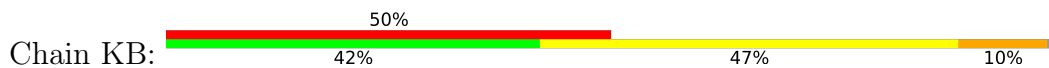
• Molecule 58: eS8 (yeast S8)



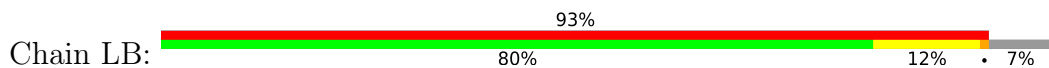
• Molecule 62: eS12 (yeast S12)

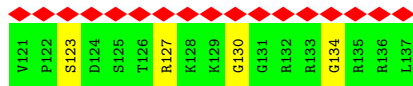
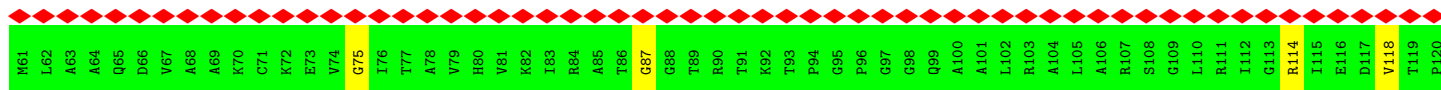


• Molecule 63: uS15 (yeast S13)

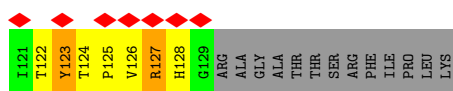
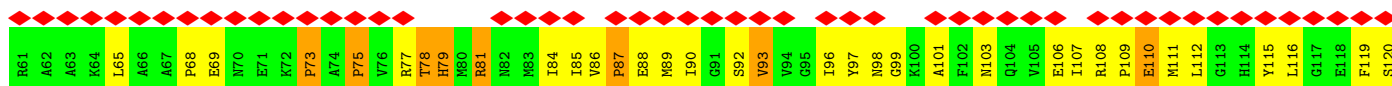
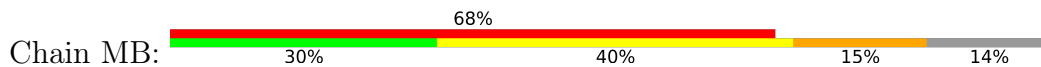


• Molecule 64: uS11 (yeast S14)

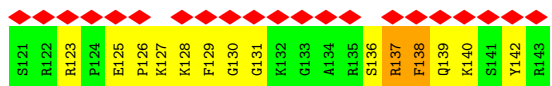
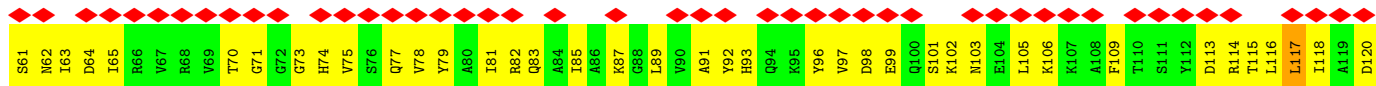
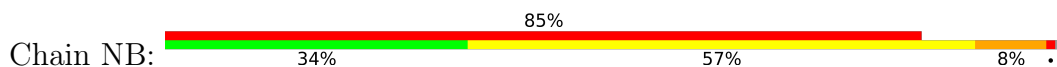




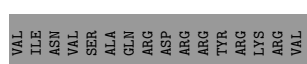
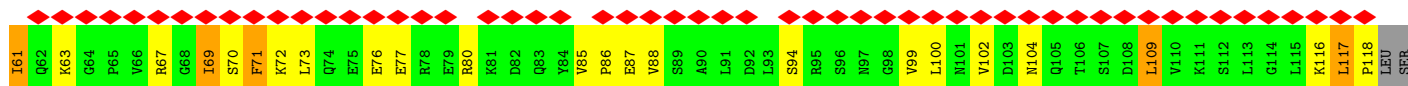
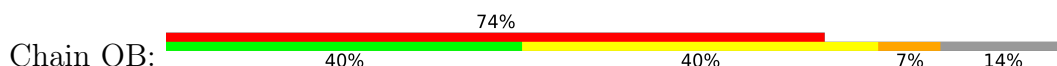
• Molecule 65: uS19 (yeast S15)



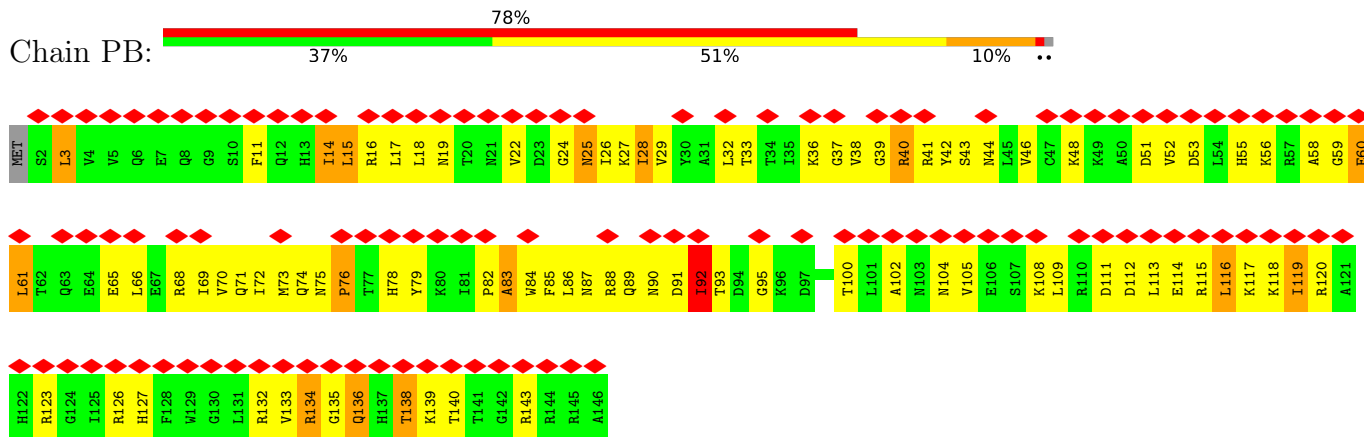
• Molecule 66: uS9 (yeast S16)



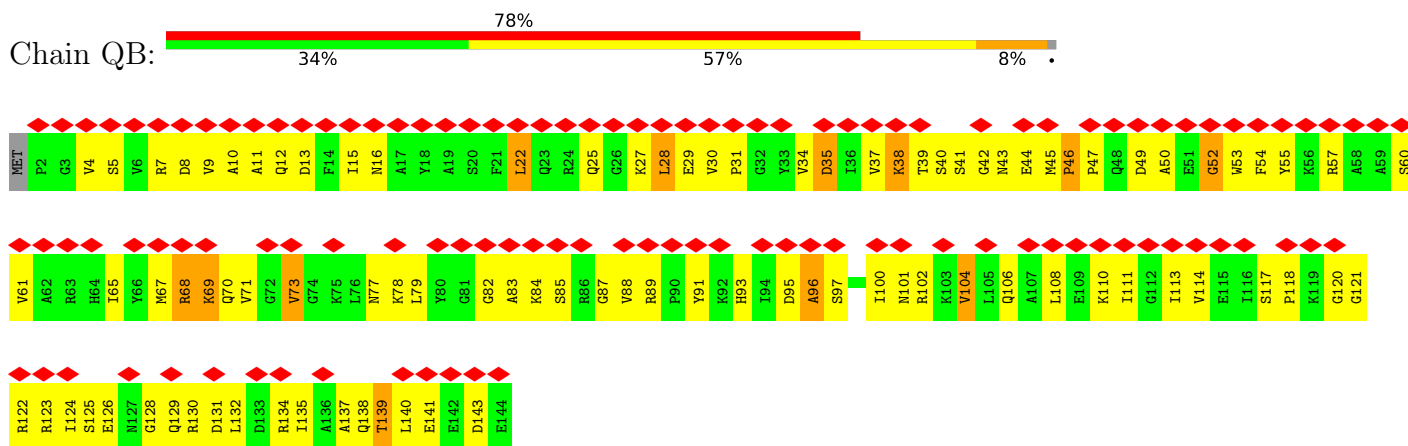
• Molecule 67: eS17 (yeast S17)



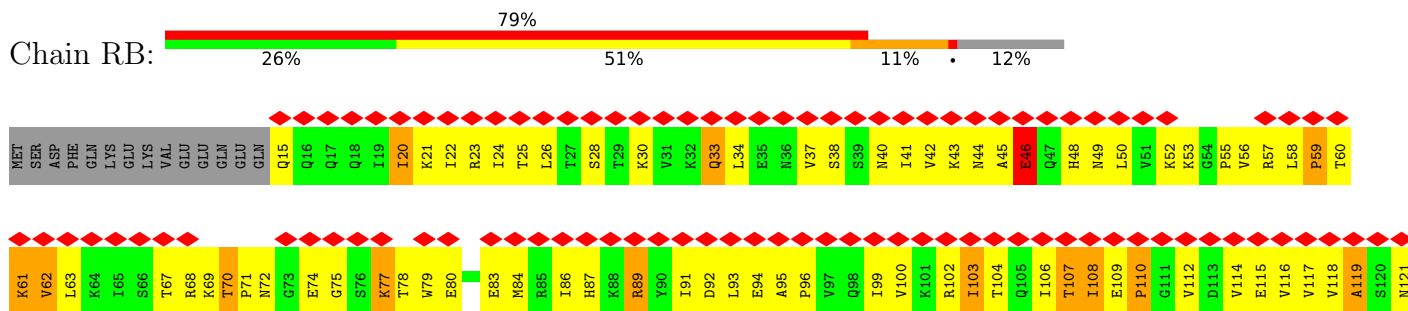
• Molecule 68: uS13 (yeast S18)



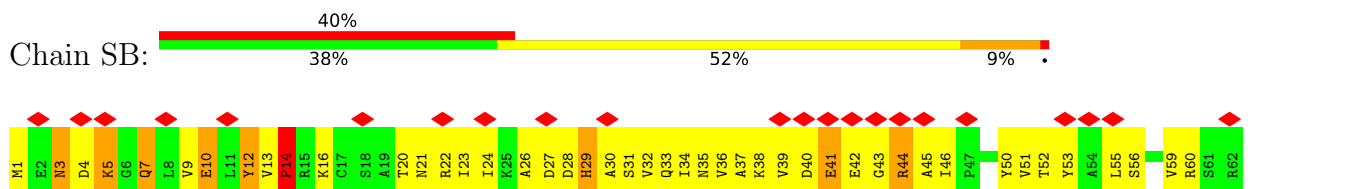
• Molecule 69: eS19 (yeast S19)

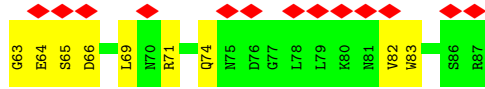


• Molecule 70: uS10 (yeast S20)

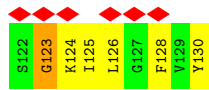
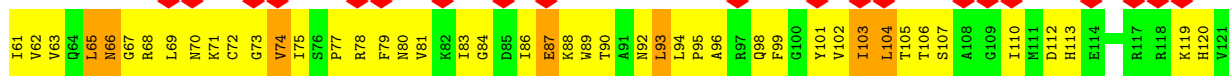
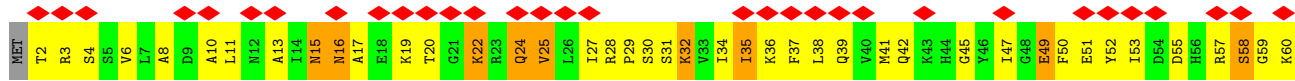


• Molecule 71: eS21 (yeast S21)

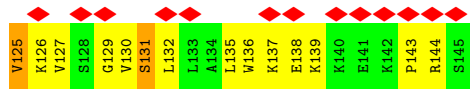
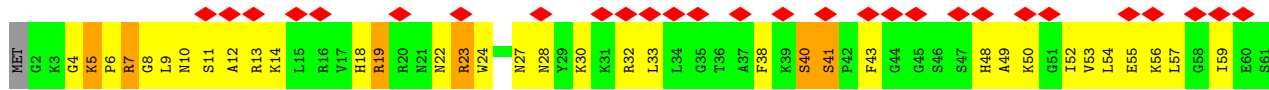




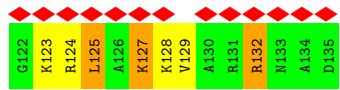
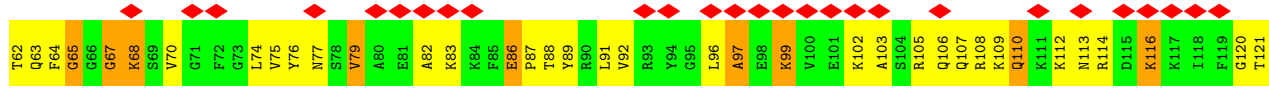
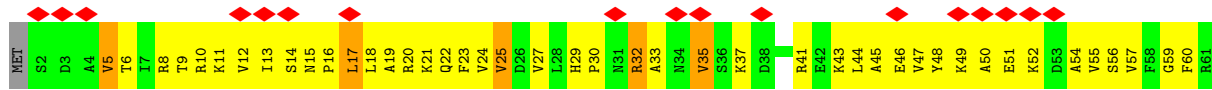
• Molecule 72: uS8 (yeast S22)



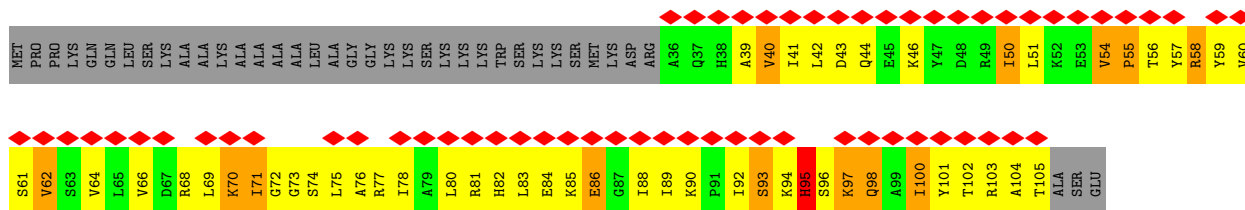
• Molecule 73: uS12 (yeast S23)



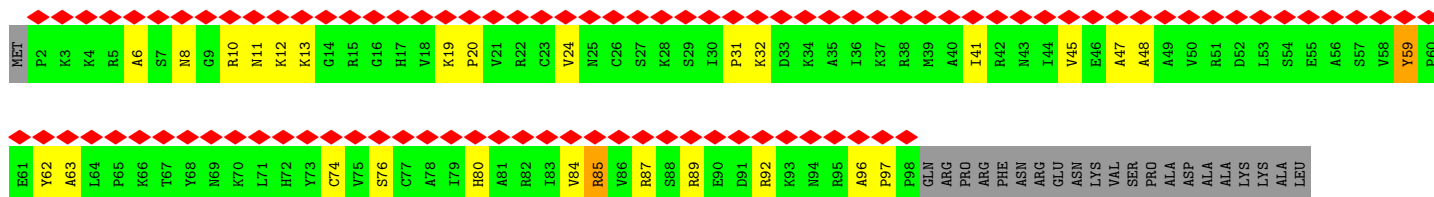
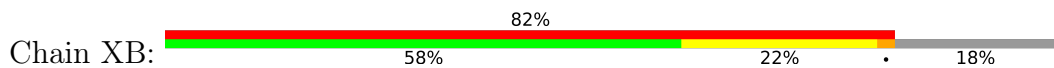
• Molecule 74: eS24 (yeast S24)



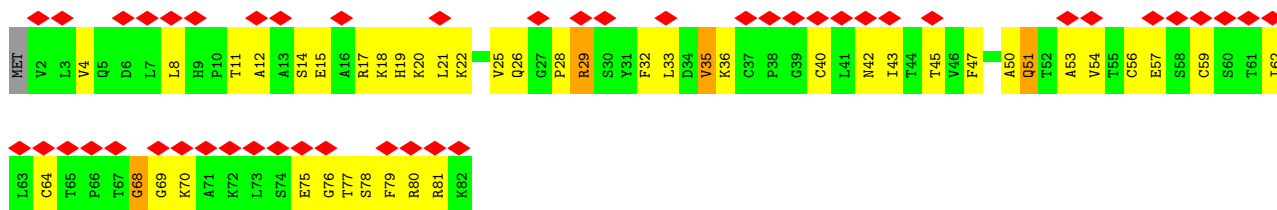
• Molecule 75: eS25 (yeast S25)



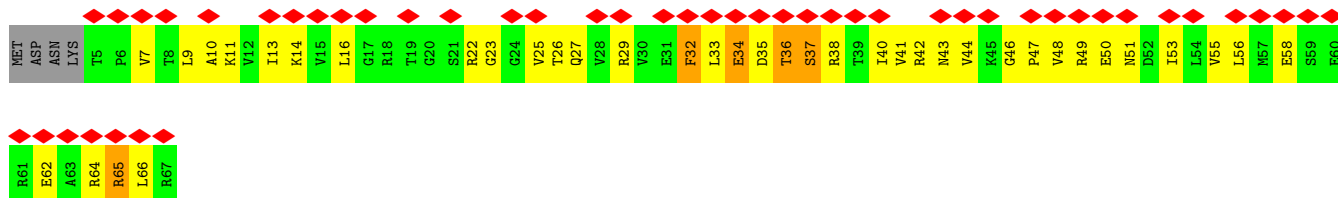
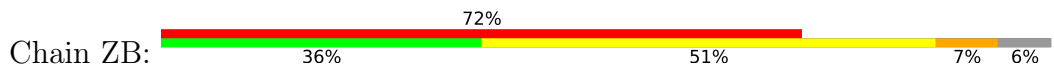
• Molecule 76: eS26 (yeast S26)



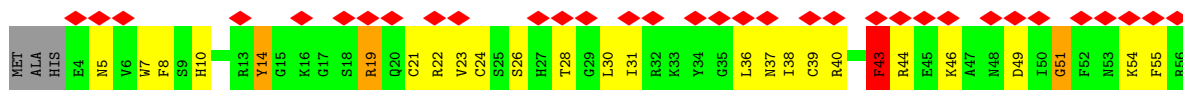
• Molecule 77: eS27 (yeast S27)



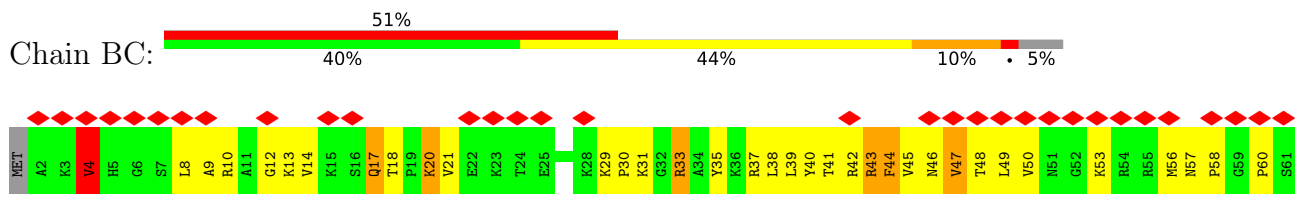
• Molecule 78: eS28 (yeast S28)



• Molecule 79: uS14 (yeast S29)

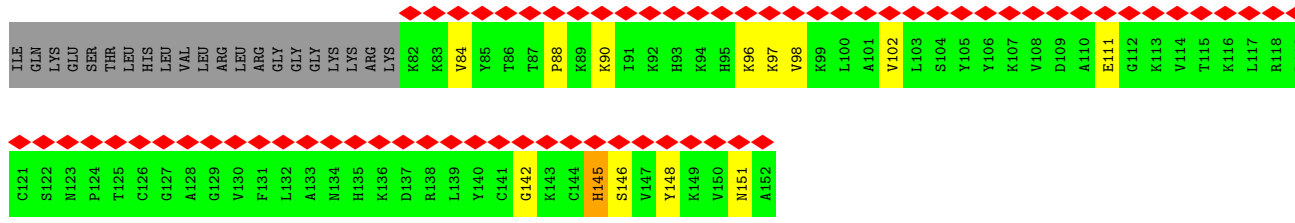
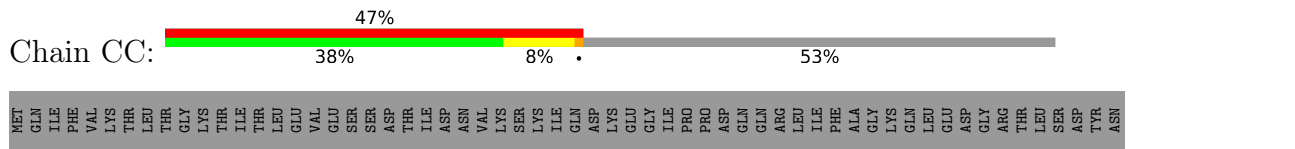


• Molecule 80: eS30 (yeast S30)

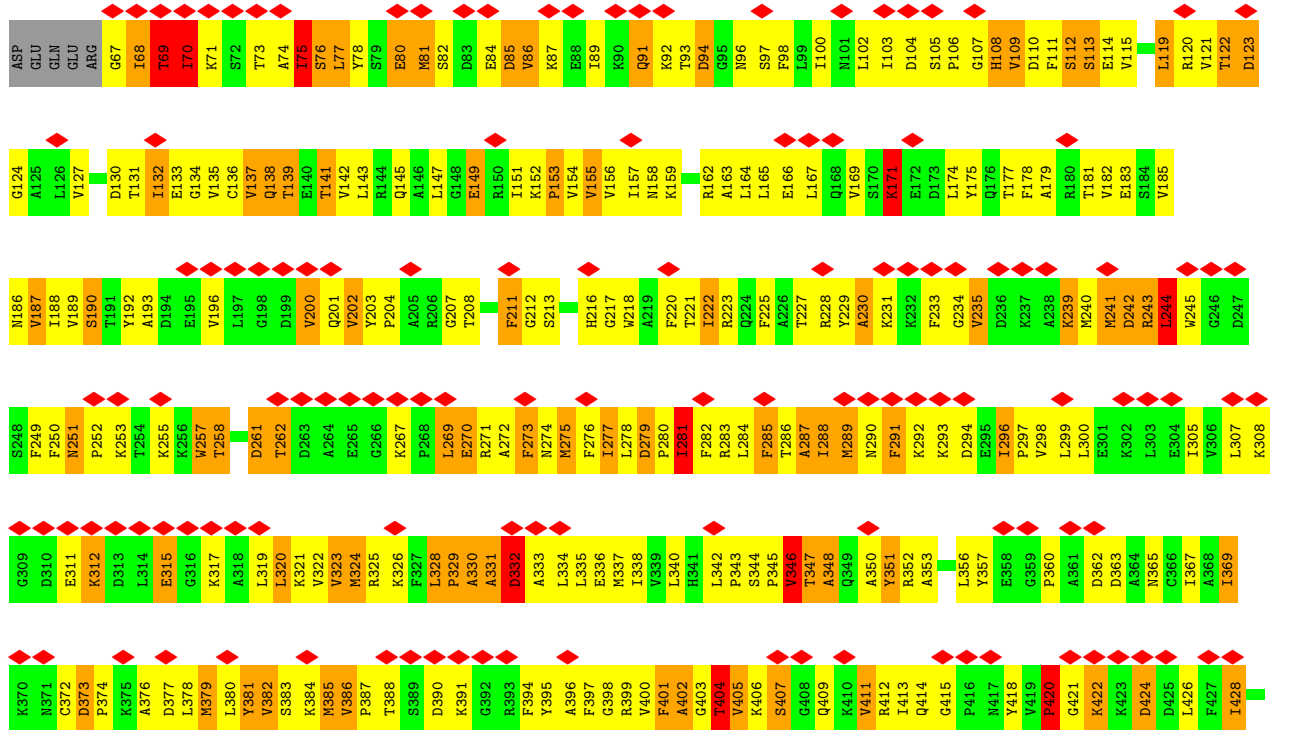
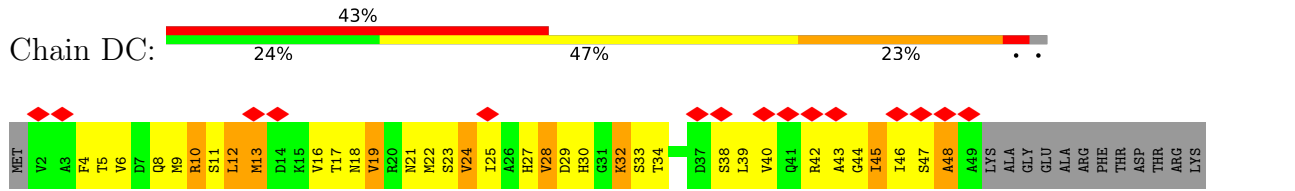


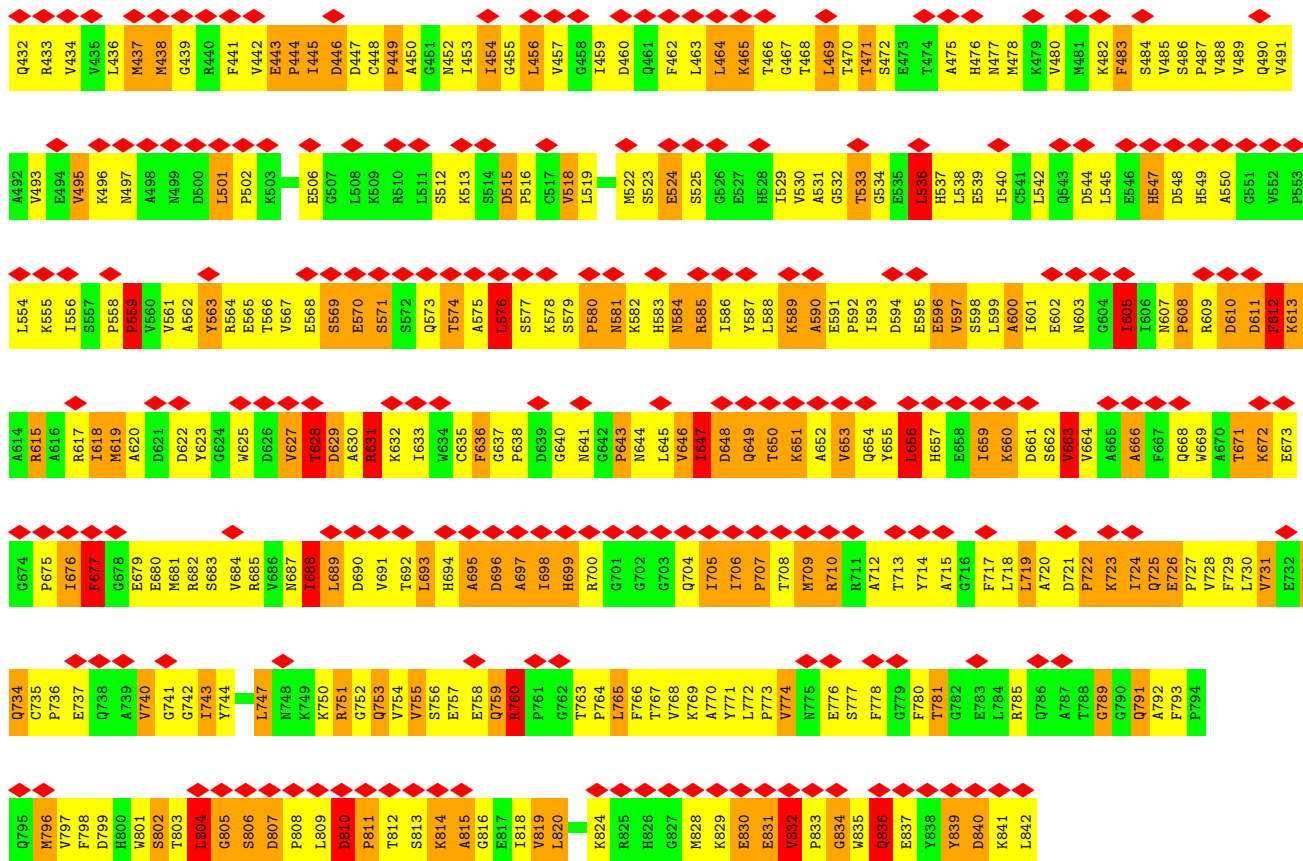
VAL
GLN

• Molecule 81: eS31 (yeast S31)

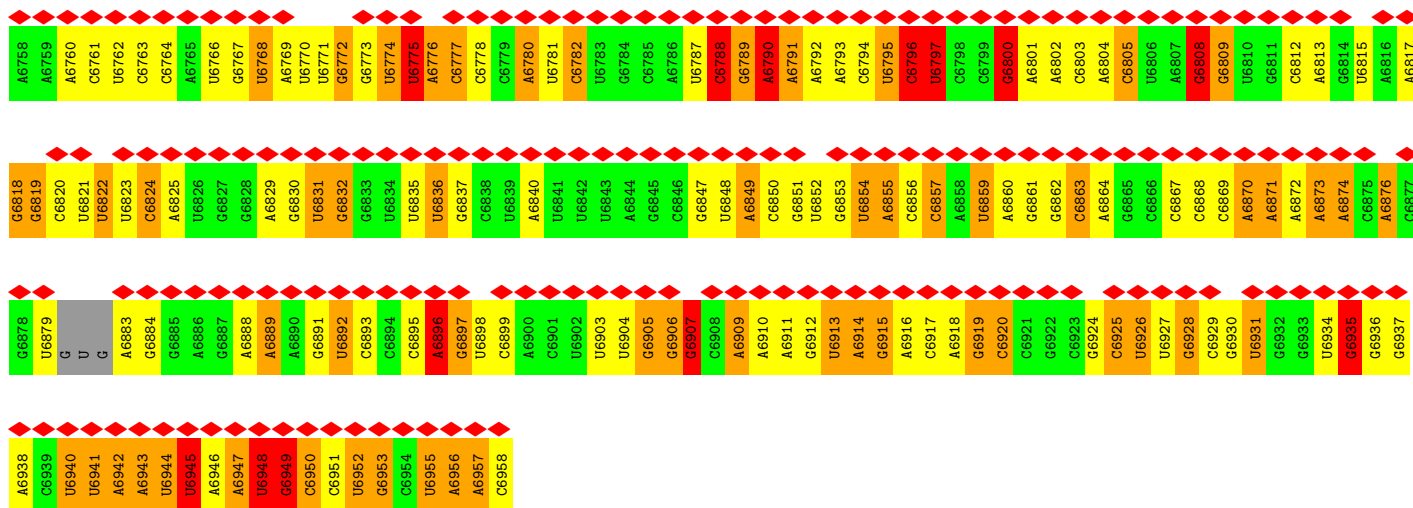
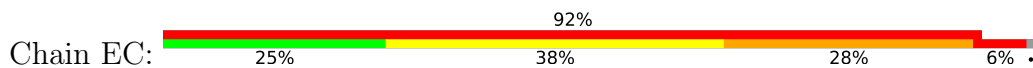


• Molecule 82: yeast eEF2





• Molecule 83: IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	59570	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	0.073	Depositor
Minimum map value	-0.027	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.02	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 i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, MG, DDE, SO1

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	0.72	0/41014	0.65	33/63809 (0.1%)
2	B	0.66	0/78631	0.65	35/122552 (0.0%)
3	C	0.65	0/3747	0.63	0/5832
4	D	0.65	0/2884	0.59	0/4491
5	E	2.89	181/1377 (13.1%)	1.25	8/1844 (0.4%)
6	F	1.21	5/1952 (0.3%)	1.00	5/2622 (0.2%)
7	G	1.07	2/3153 (0.1%)	0.88	5/4239 (0.1%)
8	H	1.22	6/2802 (0.2%)	1.02	11/3792 (0.3%)
9	I	1.14	1/2426 (0.0%)	1.00	8/3271 (0.2%)
10	J	1.35	3/1425 (0.2%)	1.03	7/1912 (0.4%)
11	K	1.21	1/1822 (0.1%)	1.05	7/2451 (0.3%)
12	L	1.19	3/1850 (0.2%)	1.00	7/2495 (0.3%)
13	M	1.21	2/1540 (0.1%)	0.94	2/2073 (0.1%)
14	N	1.30	3/1754 (0.2%)	0.90	2/2350 (0.1%)
15	O	1.09	0/1375	0.90	2/1842 (0.1%)
16	P	3.02	97/728 (13.3%)	1.35	10/975 (1.0%)
17	Q	1.21	2/1568 (0.1%)	1.02	6/2106 (0.3%)
18	R	1.33	1/1069 (0.1%)	1.03	5/1438 (0.3%)
19	S	1.13	2/1758 (0.1%)	1.03	15/2354 (0.6%)
20	T	1.10	2/1586 (0.1%)	1.04	9/2128 (0.4%)
21	U	1.16	6/1466 (0.4%)	0.93	7/1968 (0.4%)
22	V	1.19	1/1466 (0.1%)	1.00	4/1965 (0.2%)
23	W	1.13	1/1539 (0.1%)	1.13	11/2050 (0.5%)
24	X	1.27	1/1482 (0.1%)	1.06	10/1990 (0.5%)
25	Y	1.28	3/1301 (0.2%)	0.91	3/1743 (0.2%)
26	Z	1.08	2/812 (0.2%)	0.83	3/1099 (0.3%)
27	AA	1.17	0/1019	0.91	1/1369 (0.1%)
28	BA	1.26	0/521	0.90	0/691
29	CA	1.26	0/984	1.00	7/1325 (0.5%)
30	DA	1.31	4/1005 (0.4%)	1.04	5/1341 (0.4%)
31	EA	1.13	0/1119	0.94	2/1497 (0.1%)
32	FA	1.11	1/1205 (0.1%)	0.96	3/1612 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	GA	1.15	0/474	0.98	2/629 (0.3%)
34	HA	1.04	0/751	0.95	2/1008 (0.2%)
35	IA	1.06	0/904	0.88	2/1213 (0.2%)
36	JA	1.23	1/1041 (0.1%)	0.94	2/1394 (0.1%)
37	KA	1.06	0/869	1.00	5/1168 (0.4%)
38	LA	1.19	2/891 (0.2%)	1.06	7/1191 (0.6%)
39	MA	1.22	2/979 (0.2%)	0.98	1/1301 (0.1%)
40	NA	1.23	0/779	1.05	2/1034 (0.2%)
41	OA	1.27	3/697 (0.4%)	1.01	1/923 (0.1%)
42	PA	1.29	0/619	0.87	0/826
43	QA	1.16	1/444 (0.2%)	1.05	0/588
44	RA	1.30	1/424 (0.2%)	0.97	4/562 (0.7%)
45	SA	2.26	13/235 (5.5%)	1.32	2/300 (0.7%)
46	TA	1.21	0/861	0.87	1/1136 (0.1%)
47	UA	1.18	0/702	1.03	2/934 (0.2%)
48	VA	2.58	130/1498 (8.7%)	1.61	26/2025 (1.3%)
49	WA	1.43	5/2498 (0.2%)	0.84	3/3398 (0.1%)
50	XA	1.00	0/1653	0.96	9/2261 (0.4%)
51	YA	2.23	18/855 (2.1%)	1.13	4/1067 (0.4%)
52	ZA	1.05	0/1665	0.93	7/2263 (0.3%)
53	AB	1.33	2/1759 (0.1%)	0.90	3/2368 (0.1%)
54	BB	1.24	4/2110 (0.2%)	0.93	7/2839 (0.2%)
55	CB	1.37	1/1630 (0.1%)	0.99	8/2202 (0.4%)
56	DB	1.28	3/1844 (0.2%)	0.94	6/2464 (0.2%)
57	EB	1.39	3/1506 (0.2%)	0.95	3/2028 (0.1%)
58	FB	1.37	3/1515 (0.2%)	0.99	7/2021 (0.3%)
59	GB	1.06	0/1519	1.04	10/2035 (0.5%)
60	HB	1.46	5/837 (0.6%)	0.92	3/1131 (0.3%)
61	IB	1.42	3/1273 (0.2%)	0.90	4/1712 (0.2%)
62	JB	2.13	7/495 (1.4%)	1.21	3/617 (0.5%)
63	KB	1.33	1/1216 (0.1%)	1.00	3/1638 (0.2%)
64	LB	2.06	5/507 (1.0%)	1.12	0/632
65	MB	1.49	3/996 (0.3%)	1.00	4/1335 (0.3%)
66	NB	1.38	0/1126	0.92	0/1510
67	OB	1.17	0/844	1.40	12/1120 (1.1%)
68	PB	1.38	3/1212 (0.2%)	0.89	0/1628
69	QB	1.33	2/1131 (0.2%)	1.00	3/1517 (0.2%)
70	RB	1.49	2/866 (0.2%)	0.93	4/1169 (0.3%)
71	SB	1.08	0/694	0.93	3/935 (0.3%)
72	TB	1.12	1/1039 (0.1%)	0.99	5/1395 (0.4%)
73	UB	1.22	1/1140 (0.1%)	0.94	5/1518 (0.3%)
74	VB	1.23	0/1088	0.99	5/1449 (0.3%)
75	WB	1.38	3/571 (0.5%)	1.01	2/768 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	XB	2.18	9/387 (2.3%)	1.26	6/482 (1.2%)
77	YB	1.29	0/621	0.76	0/838
78	ZB	1.39	0/500	0.79	0/670
79	AC	1.34	0/454	0.88	1/602 (0.2%)
80	BC	1.29	0/483	1.02	1/643 (0.2%)
81	CC	1.93	1/283 (0.4%)	0.99	1/352 (0.3%)
82	DC	2.04	204/6521 (3.1%)	1.08	28/8830 (0.3%)
83	EC	1.53	2/4579 (0.0%)	0.94	29/7119 (0.4%)
All	All	1.08	774/227965 (0.3%)	0.81	481/334014 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	18
2	B	0	70
3	C	0	4
48	VA	0	2
82	DC	0	1
83	EC	0	9
All	All	0	104

The worst 5 of 774 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	CB	25	LEU	CA-C	12.41	1.58	1.52
16	P	88	PRO	CA-C	11.18	1.62	1.52
5	E	120	VAL	CA-C	9.32	1.62	1.52
16	P	106	LEU	CA-C	8.94	1.62	1.52
48	VA	80	VAL	CA-C	8.80	1.60	1.53

The worst 5 of 481 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	VA	108	PRO	CB-CA-C	-27.82	69.58	110.20
67	OB	73	LEU	N-CA-C	17.97	137.25	110.30
48	VA	106	ALA	N-CA-C	14.93	131.41	110.06
48	VA	181	PHE	N-CA-C	-12.93	99.26	112.97
48	VA	180	PRO	N-CA-C	12.48	129.96	114.35

There are no chirality outliers.

5 of 104 planarity outliers are listed below:

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

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	36760	0	18348	1440	0
2	B	70288	0	35262	2388	0
3	C	3354	0	1695	115	0
4	D	2580	0	1304	103	0
5	E	1359	0	1425	114	0
6	F	1918	0	1987	217	0
7	G	3082	0	3165	238	0
8	H	2750	0	2863	237	0
9	I	2376	0	2325	204	0
10	J	1401	0	1501	90	0
11	K	1785	0	1862	144	0
12	L	1818	0	1908	188	0
13	M	1519	0	1587	124	0
14	N	1718	0	1754	138	0
15	O	1354	0	1383	106	0
16	P	723	0	774	129	0
17	Q	1543	0	1608	147	0
18	R	1054	0	1149	90	0
19	S	1721	0	1779	165	0
20	T	1556	0	1659	102	0
21	U	1443	0	1485	101	0
22	V	1442	0	1543	124	0
23	W	1522	0	1617	106	0
24	X	1446	0	1487	159	0
25	Y	1277	0	1323	111	0
26	Z	796	0	812	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	AA	1004	0	1048	77	0
28	BA	509	0	537	37	0
29	CA	969	0	1036	85	0
30	DA	994	0	1081	110	0
31	EA	1093	0	1155	110	0
32	FA	1174	0	1215	122	0
33	GA	463	0	491	21	0
34	HA	743	0	797	94	0
35	IA	890	0	938	48	0
36	JA	1020	0	1090	61	0
37	KA	851	0	880	61	0
38	LA	881	0	949	106	0
39	MA	970	0	1078	110	0
40	NA	772	0	849	46	0
41	OA	682	0	687	59	0
42	PA	613	0	682	37	0
43	QA	437	0	475	44	0
44	RA	418	0	459	33	0
45	SA	234	0	284	12	0
46	TA	848	0	918	38	0
47	UA	695	0	738	55	0
48	VA	1473	0	1514	192	0
49	WA	2445	0	2401	219	0
50	XA	1612	0	1623	137	0
51	YA	856	0	226	2	0
52	ZA	1635	0	1723	137	0
53	AB	1734	0	1817	136	0
54	BB	2069	0	2154	268	0
55	CB	1610	0	1675	143	0
56	DB	1820	0	1918	156	0
57	EB	1481	0	1572	134	0
58	FB	1490	0	1525	154	0
59	GB	1494	0	1573	156	0
60	HB	817	0	804	80	0
61	IB	1245	0	1314	111	0
62	JB	496	0	141	0	0
63	KB	1193	0	1255	88	0
64	LB	508	0	151	2	0
65	MB	975	0	1017	95	0
66	NB	1106	0	1166	102	0
67	OB	836	0	827	61	0
68	PB	1193	0	1222	98	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	QB	1113	0	1124	92	0
70	RB	856	0	917	92	0
71	SB	685	0	672	67	0
72	TB	1022	0	1060	85	0
73	UB	1122	0	1196	106	0
74	VB	1074	0	1132	113	0
75	WB	563	0	603	60	0
76	XB	388	0	96	3	0
77	YB	611	0	633	42	0
78	ZB	498	0	535	48	0
79	AC	444	0	436	37	0
80	BC	475	0	525	50	0
81	CC	284	0	76	1	0
82	DC	6419	0	6493	680	0
83	EC	4105	0	2063	133	0
84	DC	28	0	12	5	0
85	DC	1	0	0	0	0
86	DC	35	0	42	3	0
All	All	212656	0	156225	11084	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 30.

The worst 5 of 11084 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:EC:6927:U:H3'	83:EC:6928:G:H5'	1.22	1.17
2:B:1235:U:H4'	2:B:1236:G:H5'	1.17	1.14
48:VA:108:PRO:HA	48:VA:179:SER:HA	1.14	1.13
1:A:230:C:H3'	1:A:231:U:H5''	1.31	1.12
58:FB:12:SER:HA	58:FB:18:ARG:HH21	1.10	1.11

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	165/217 (76%)	128 (78%)	27 (16%)	10 (6%)	1	12
6	F	250/254 (98%)	175 (70%)	61 (24%)	14 (6%)	1	13
7	G	384/387 (99%)	305 (79%)	64 (17%)	15 (4%)	2	20
8	H	359/362 (99%)	255 (71%)	70 (20%)	34 (10%)	0	6
9	I	294/297 (99%)	217 (74%)	58 (20%)	19 (6%)	1	11
10	J	173/176 (98%)	131 (76%)	34 (20%)	8 (5%)	2	17
11	K	220/244 (90%)	171 (78%)	40 (18%)	9 (4%)	2	19
12	L	231/256 (90%)	168 (73%)	44 (19%)	19 (8%)	0	8
13	M	189/191 (99%)	140 (74%)	39 (21%)	10 (5%)	1	14
14	N	207/221 (94%)	161 (78%)	36 (17%)	10 (5%)	2	16
15	O	167/174 (96%)	126 (75%)	26 (16%)	15 (9%)	0	7
16	P	92/165 (56%)	65 (71%)	20 (22%)	7 (8%)	1	8
17	Q	191/199 (96%)	142 (74%)	40 (21%)	9 (5%)	2	17
18	R	134/138 (97%)	107 (80%)	16 (12%)	11 (8%)	0	8
19	S	201/204 (98%)	150 (75%)	45 (22%)	6 (3%)	3	25
20	T	195/199 (98%)	158 (81%)	33 (17%)	4 (2%)	5	31
21	U	181/184 (98%)	150 (83%)	24 (13%)	7 (4%)	2	20
22	V	183/186 (98%)	133 (73%)	43 (24%)	7 (4%)	2	20
23	W	186/189 (98%)	153 (82%)	26 (14%)	7 (4%)	2	20
24	X	170/172 (99%)	131 (77%)	28 (16%)	11 (6%)	1	11
25	Y	157/160 (98%)	124 (79%)	21 (13%)	12 (8%)	1	8
26	Z	98/121 (81%)	72 (74%)	21 (21%)	5 (5%)	1	15
27	AA	134/137 (98%)	114 (85%)	19 (14%)	1 (1%)	18	51
28	BA	59/155 (38%)	47 (80%)	7 (12%)	5 (8%)	0	7
29	CA	119/142 (84%)	92 (77%)	19 (16%)	8 (7%)	1	11
30	DA	124/127 (98%)	88 (71%)	30 (24%)	6 (5%)	2	16
31	EA	133/136 (98%)	95 (71%)	27 (20%)	11 (8%)	0	7
32	FA	146/149 (98%)	105 (72%)	30 (20%)	11 (8%)	1	9
33	GA	56/59 (95%)	43 (77%)	10 (18%)	3 (5%)	1	14
34	HA	95/105 (90%)	71 (75%)	19 (20%)	5 (5%)	1	14

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	NB	139/143 (97%)	109 (78%)	21 (15%)	9 (6%)	1	11
67	OB	115/136 (85%)	85 (74%)	23 (20%)	7 (6%)	1	12
68	PB	143/146 (98%)	111 (78%)	22 (15%)	10 (7%)	1	10
69	QB	141/144 (98%)	120 (85%)	15 (11%)	6 (4%)	2	18
70	RB	105/121 (87%)	79 (75%)	21 (20%)	5 (5%)	2	16
71	SB	85/87 (98%)	61 (72%)	17 (20%)	7 (8%)	0	8
72	TB	127/130 (98%)	92 (72%)	29 (23%)	6 (5%)	2	17
73	UB	142/145 (98%)	98 (69%)	29 (20%)	15 (11%)	0	5
74	VB	132/135 (98%)	100 (76%)	26 (20%)	6 (4%)	2	17
75	WB	68/108 (63%)	51 (75%)	7 (10%)	10 (15%)	0	3
76	XB	95/119 (80%)	56 (59%)	26 (27%)	13 (14%)	0	3
77	YB	79/82 (96%)	53 (67%)	22 (28%)	4 (5%)	1	15
78	ZB	61/67 (91%)	44 (72%)	15 (25%)	2 (3%)	3	23
79	AC	51/56 (91%)	44 (86%)	6 (12%)	1 (2%)	6	32
80	BC	58/63 (92%)	34 (59%)	18 (31%)	6 (10%)	0	5
81	CC	69/152 (45%)	44 (64%)	14 (20%)	11 (16%)	0	2
82	DC	819/842 (97%)	628 (77%)	144 (18%)	47 (6%)	1	13
All	All	12207/13416 (91%)	9156 (75%)	2296 (19%)	755 (6%)	2	12

5 of 755 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	157/198 (79%)	129 (82%)	28 (18%)	2	10
6	F	194/196 (99%)	174 (90%)	20 (10%)	7	28
7	G	322/323 (100%)	292 (91%)	30 (9%)	8	31
8	H	288/289 (100%)	250 (87%)	38 (13%)	4	20
9	I	244/245 (100%)	226 (93%)	18 (7%)	13	37
10	J	152/153 (99%)	136 (90%)	16 (10%)	6	27
11	K	186/205 (91%)	168 (90%)	18 (10%)	8	30
12	L	191/208 (92%)	166 (87%)	25 (13%)	4	20
13	M	171/171 (100%)	156 (91%)	15 (9%)	9	32
14	N	180/187 (96%)	157 (87%)	23 (13%)	4	21
15	O	147/150 (98%)	134 (91%)	13 (9%)	9	32
16	P	81/136 (60%)	64 (79%)	17 (21%)	1	6
17	Q	154/159 (97%)	132 (86%)	22 (14%)	3	18
18	R	107/109 (98%)	94 (88%)	13 (12%)	5	22
19	S	175/176 (99%)	154 (88%)	21 (12%)	5	23
20	T	160/162 (99%)	152 (95%)	8 (5%)	22	48
21	U	145/146 (99%)	131 (90%)	14 (10%)	8	30
22	V	150/151 (99%)	141 (94%)	9 (6%)	17	44
23	W	153/154 (99%)	131 (86%)	22 (14%)	3	18
24	X	156/156 (100%)	137 (88%)	19 (12%)	5	22
25	Y	136/137 (99%)	120 (88%)	16 (12%)	5	23
26	Z	87/107 (81%)	81 (93%)	6 (7%)	14	39
27	AA	104/105 (99%)	87 (84%)	17 (16%)	2	14
28	BA	54/129 (42%)	50 (93%)	4 (7%)	13	37
29	CA	105/118 (89%)	91 (87%)	14 (13%)	4	20
30	DA	109/110 (99%)	97 (89%)	12 (11%)	6	26
31	EA	115/116 (99%)	98 (85%)	17 (15%)	3	17
32	FA	118/119 (99%)	106 (90%)	12 (10%)	7	28
33	GA	46/47 (98%)	42 (91%)	4 (9%)	9	33
34	HA	81/88 (92%)	70 (86%)	11 (14%)	3	19
35	IA	96/97 (99%)	89 (93%)	7 (7%)	13	38
36	JA	109/111 (98%)	99 (91%)	10 (9%)	8	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	KA	90/91 (99%)	86 (96%)	4 (4%)	25	51
38	LA	95/103 (92%)	81 (85%)	14 (15%)	3	17
39	MA	104/105 (99%)	91 (88%)	13 (12%)	4	22
40	NA	81/82 (99%)	74 (91%)	7 (9%)	10	33
41	OA	70/71 (99%)	65 (93%)	5 (7%)	13	38
42	PA	68/69 (99%)	64 (94%)	4 (6%)	18	44
43	QA	45/46 (98%)	39 (87%)	6 (13%)	4	20
44	RA	47/116 (40%)	44 (94%)	3 (6%)	16	42
45	SA	23/23 (100%)	20 (87%)	3 (13%)	4	21
46	TA	90/91 (99%)	87 (97%)	3 (3%)	33	58
47	UA	71/72 (99%)	62 (87%)	9 (13%)	4	21
48	VA	160/254 (63%)	131 (82%)	29 (18%)	2	10
49	WA	261/262 (100%)	243 (93%)	18 (7%)	14	39
50	XA	173/210 (82%)	157 (91%)	16 (9%)	8	32
52	ZA	176/205 (86%)	163 (93%)	13 (7%)	13	37
53	AB	182/195 (93%)	162 (89%)	20 (11%)	6	26
54	BB	221/222 (100%)	204 (92%)	17 (8%)	12	37
55	CB	173/191 (91%)	158 (91%)	15 (9%)	9	33
56	DB	193/201 (96%)	184 (95%)	9 (5%)	23	49
57	EB	165/170 (97%)	154 (93%)	11 (7%)	15	41
58	FB	150/161 (93%)	140 (93%)	10 (7%)	15	41
59	GB	158/166 (95%)	146 (92%)	12 (8%)	12	37
60	HB	89/98 (91%)	82 (92%)	7 (8%)	11	36
61	IB	136/137 (99%)	126 (93%)	10 (7%)	13	37
63	KB	127/128 (99%)	117 (92%)	10 (8%)	11	36
65	MB	103/118 (87%)	96 (93%)	7 (7%)	14	40
66	NB	117/119 (98%)	107 (92%)	10 (8%)	10	34
67	OB	82/124 (66%)	77 (94%)	5 (6%)	17	43
68	PB	128/129 (99%)	119 (93%)	9 (7%)	14	39
69	QB	115/116 (99%)	109 (95%)	6 (5%)	21	47
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%)	69 (93%)	5 (7%)	14	40
72	TB	110/111 (99%)	98 (89%)	12 (11%)	6	26
73	UB	119/120 (99%)	111 (93%)	8 (7%)	15	41
74	VB	112/113 (99%)	104 (93%)	8 (7%)	13	38
75	WB	61/89 (68%)	54 (88%)	7 (12%)	5	24
77	YB	70/71 (99%)	68 (97%)	2 (3%)	37	60
78	ZB	56/60 (93%)	53 (95%)	3 (5%)	20	46
79	AC	47/49 (96%)	43 (92%)	4 (8%)	10	34
80	BC	51/54 (94%)	45 (88%)	6 (12%)	5	23
82	DC	699/714 (98%)	615 (88%)	84 (12%)	5	23
All	All	9865/10602 (93%)	8892 (90%)	973 (10%)	10	29

5 of 973 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	EA	46	ILE
80	BC	20	LYS
44	RA	85	LEU
78	ZB	34	GLU
82	DC	663	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 302 such sidechains are listed below:

Mol	Chain	Res	Type
63	KB	62	GLN
82	DC	259	ASN
65	MB	128	HIS
71	SB	7	GLN
82	DC	791	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1676/1798 (93%)	327 (19%)	11 (0%)
2	B	3265/3396 (96%)	538 (16%)	31 (0%)
3	C	157/158 (99%)	26 (16%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	D	120/121 (99%)	11 (9%)	0
83	EC	186/201 (92%)	77 (41%)	5 (2%)
All	All	5404/5674 (95%)	979 (18%)	47 (0%)

5 of 979 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	25	C
1	A	26	A
1	A	34	G
1	A	45	U

5 of 47 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	2248	C
2	B	2818	U
2	B	2263	C
2	B	2513	U
2	B	3218	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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	2.65	6 (33%)	17,28,30	2.09	5 (29%)

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	-	5/20/21/23	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	CD2-CG	7.93	1.53	1.36
82	DC	699	DDE	CBW-CBI	4.78	1.61	1.53
82	DC	699	DDE	CB-CG	3.04	1.58	1.49
82	DC	699	DDE	CBW-NCB	2.86	1.60	1.54
82	DC	699	DDE	CAT-CE1	2.36	1.53	1.49

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	DC	699	DDE	CAU-CAT-CE1	6.02	136.85	114.38
82	DC	699	DDE	CD2-NE2-CE1	2.81	109.90	107.55
82	DC	699	DDE	CAU-CBW-CBI	-2.66	106.01	111.22
82	DC	699	DDE	CD2-CG-ND1	-2.38	104.07	108.87
82	DC	699	DDE	OAG-CBI-NAD	2.14	126.82	123.04

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
82	DC	699	DDE	O-C-CA-CB
82	DC	699	DDE	OAG-CBI-CBW-NCB
82	DC	699	DDE	OAG-CBI-CBW-CAU
82	DC	699	DDE	CA-CB-CG-CD2
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 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	2.29	16 (47%)	38,64,64	2.06	10 (26%)
84	GDP	DC	901	85	29,30,30	1.69	4 (13%)	45,47,47	1.79	13 (28%)

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	-	-	2/21/104/104	0/7/5/5
84	GDP	DC	901	85	-	0/16/32/32	0/3/3/3

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	DC	901	GDP	PA-O3A	4.90	1.64	1.59
84	DC	901	GDP	PB-O1B	3.96	1.62	1.50
86	DC	903	SO1	O17-C52	3.91	1.46	1.40
86	DC	903	SO1	O56-C52	-3.73	1.32	1.41
86	DC	903	SO1	C1-C5	3.72	1.59	1.50

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	DC	903	SO1	C12-C6-C10	-6.22	103.05	107.92
86	DC	903	SO1	C25-C22-C24	4.99	129.50	113.64
84	DC	901	GDP	C2-N3-C4	4.58	120.19	112.30
84	DC	901	GDP	C5-C4-N3	-4.40	121.39	128.39
86	DC	903	SO1	C10-C6-C2	3.61	108.39	104.12

There are no chirality outliers.

All (2) torsion outliers are listed below:

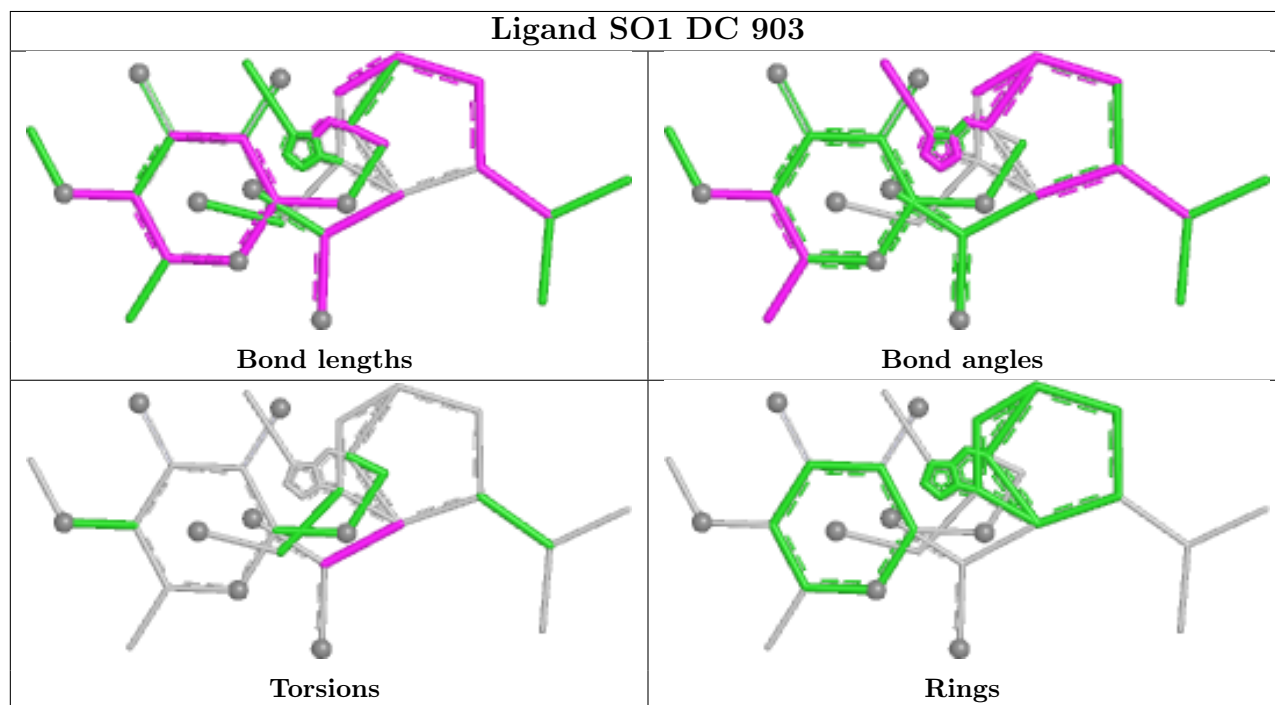
Mol	Chain	Res	Type	Atoms
86	DC	903	SO1	C2-C1-C5-O14
86	DC	903	SO1	C2-C1-C5-O15

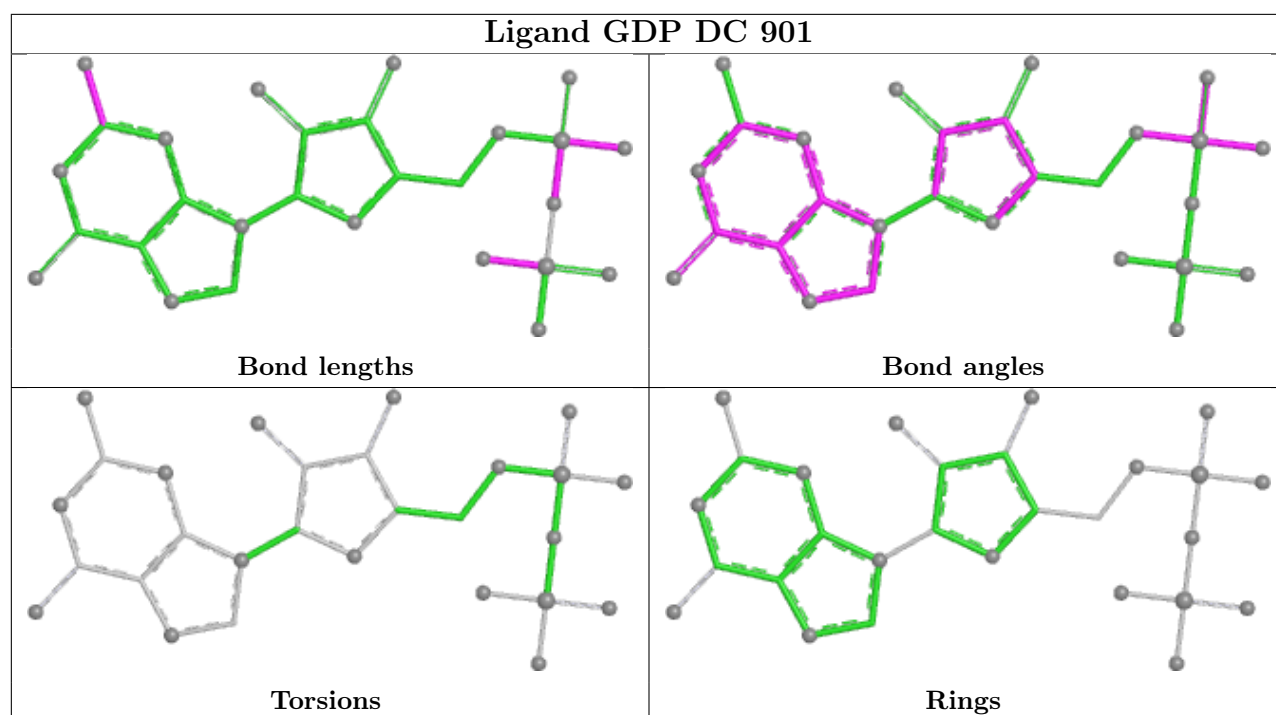
There are no ring outliers.

2 monomers are involved in 8 short contacts:

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

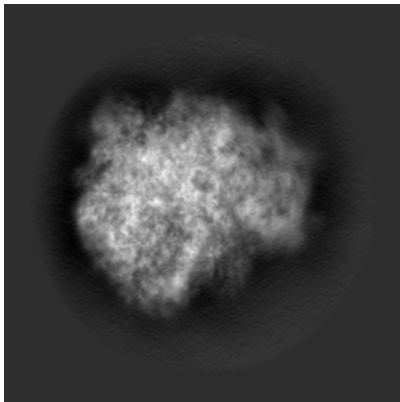
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6644. These allow visual inspection of the internal detail of the map and identification of artifacts.

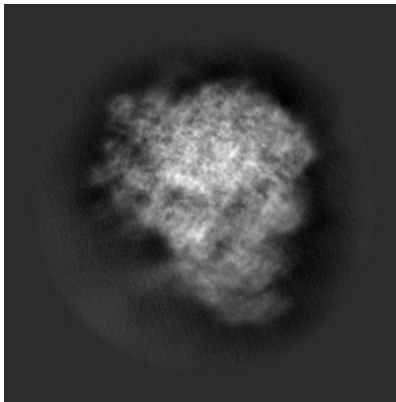
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

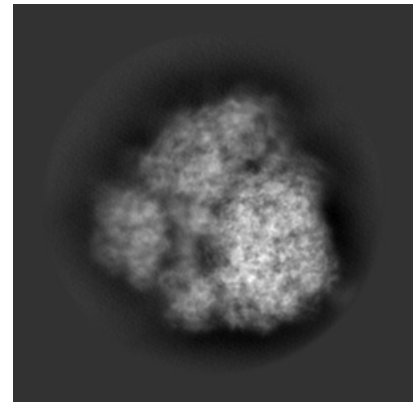
6.1.1 Primary map



X



Y

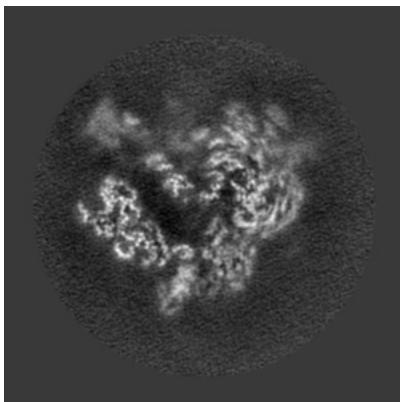


Z

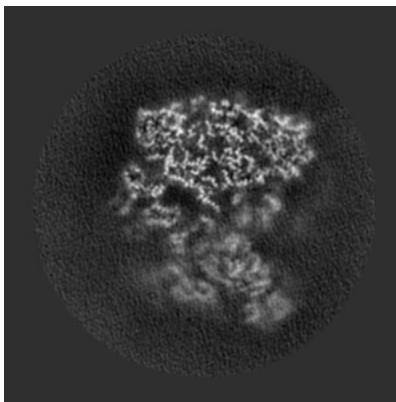
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

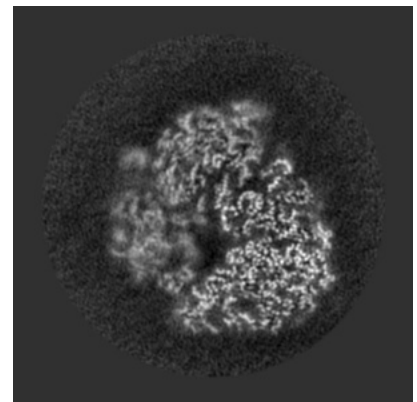
6.2.1 Primary map



X Index: 256



Y Index: 256

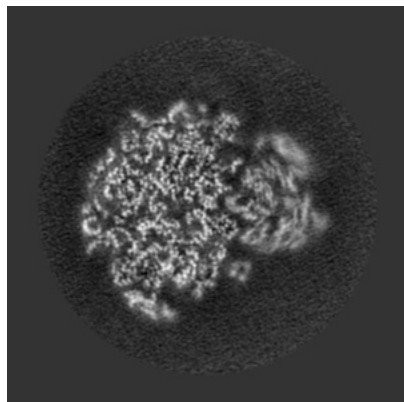


Z Index: 256

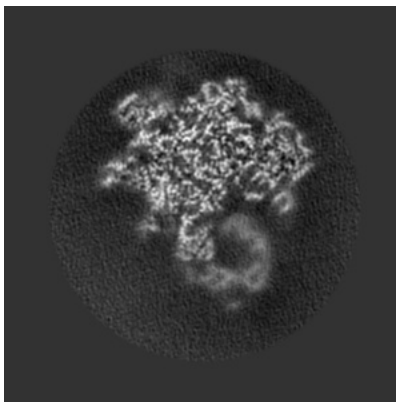
The images above show central slices of the map in three orthogonal directions.

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

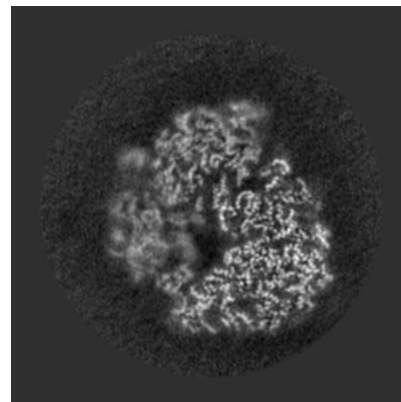
6.3.1 Primary map



X Index: 290



Y Index: 163

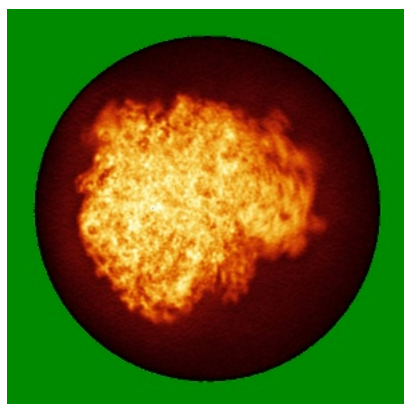


Z Index: 255

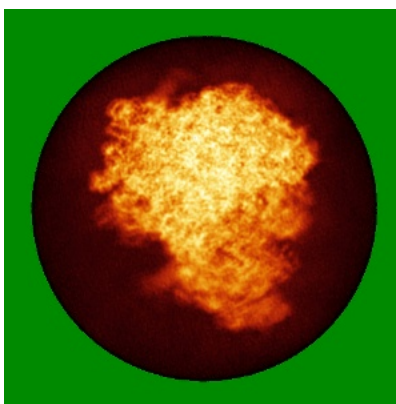
The images above show the largest variance slices of the map in three orthogonal directions.

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

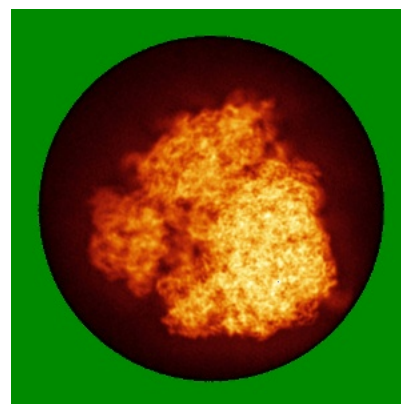
6.4.1 Primary map



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 [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

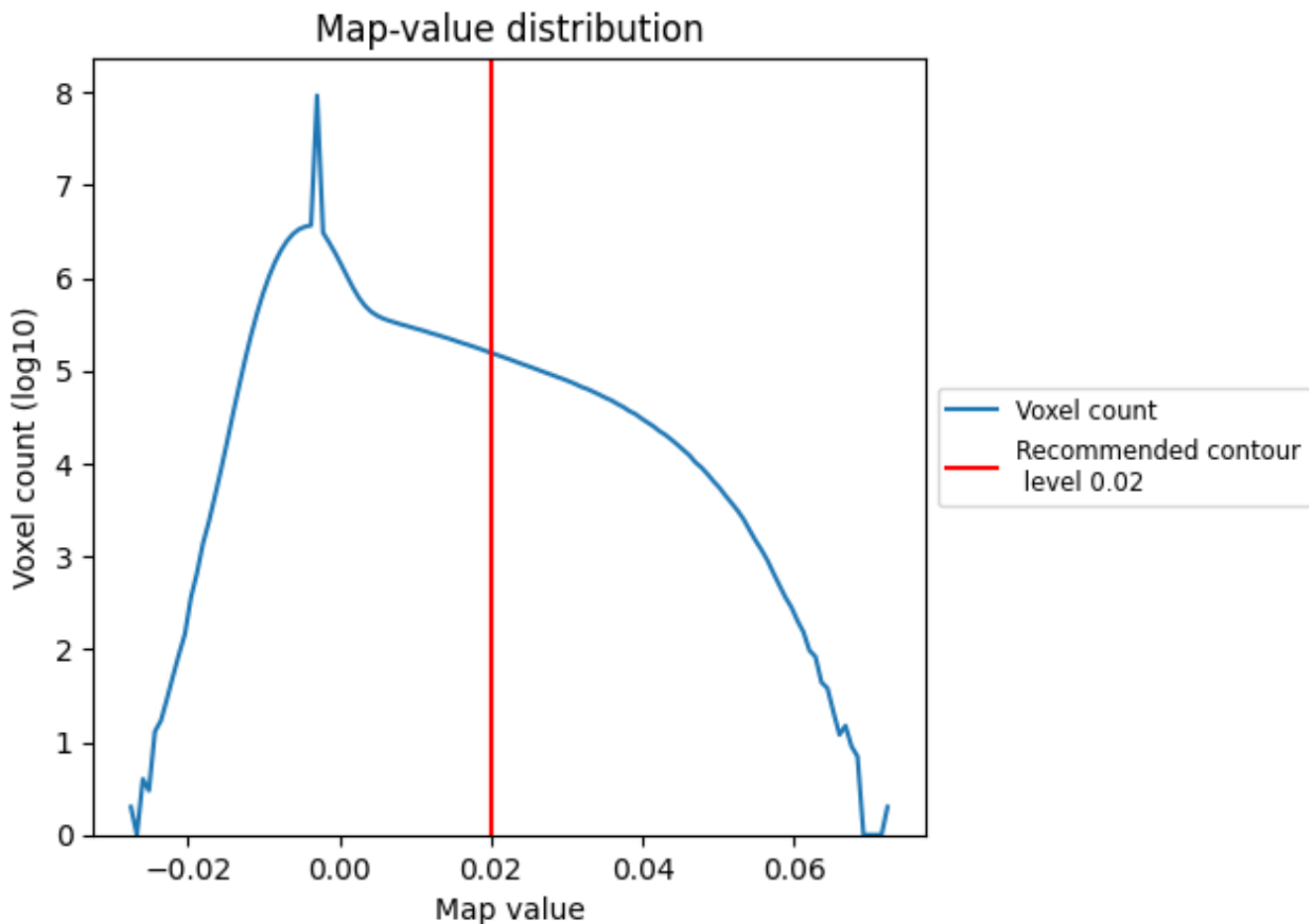
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

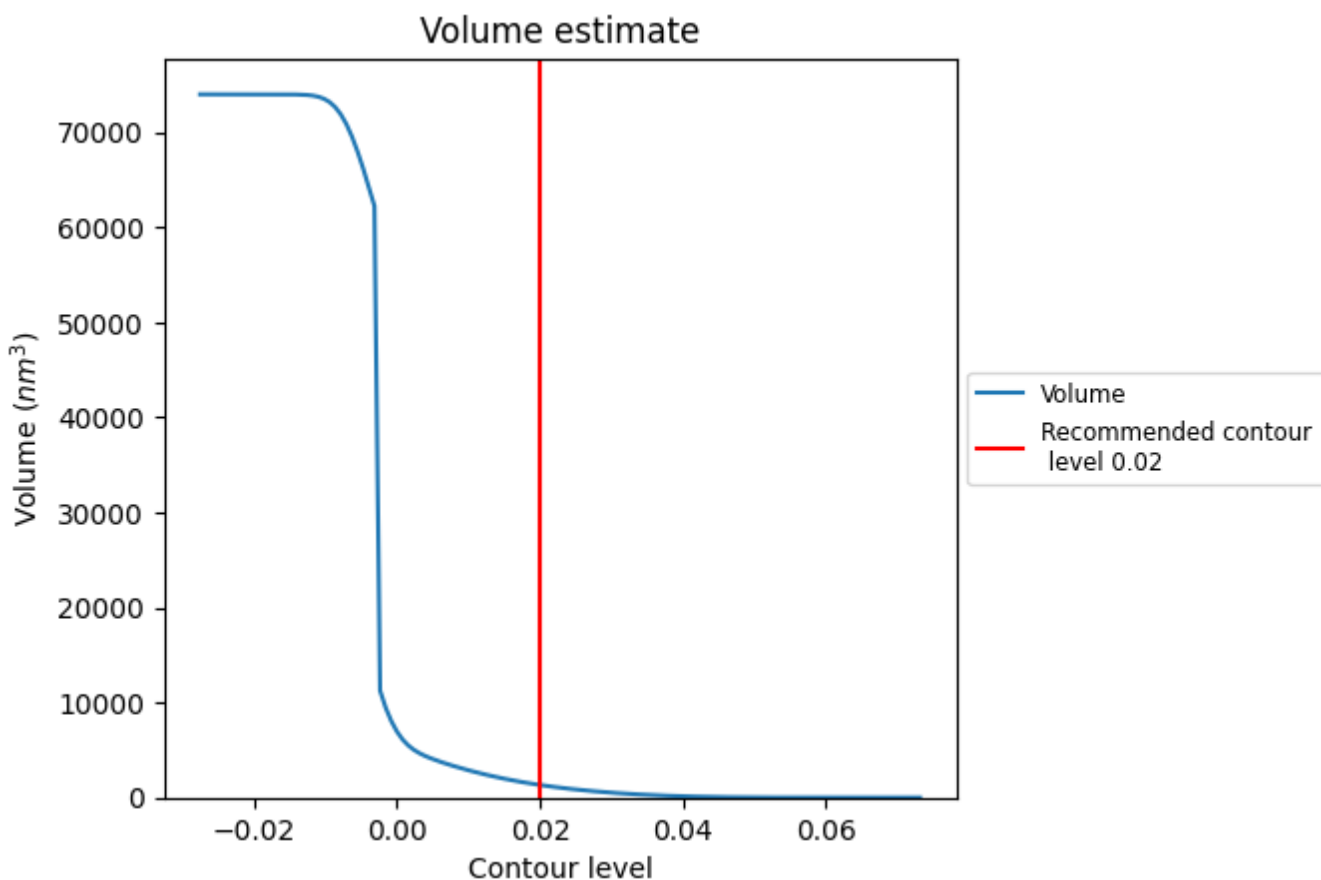
This section contains the results of statistical analysis of the map.

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.

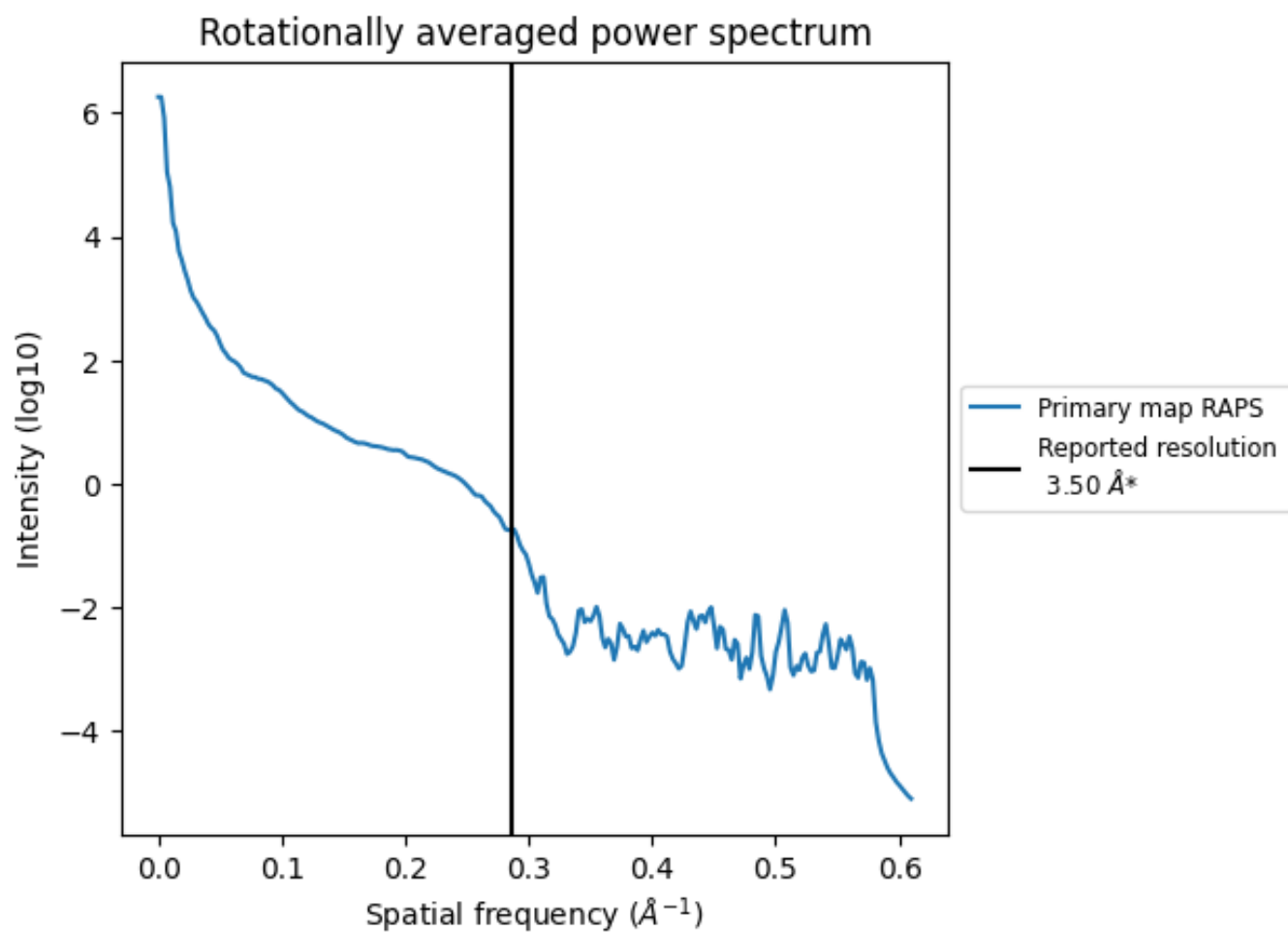
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1328 nm³; this corresponds to an approximate mass of 1200 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.286\AA^{-1}

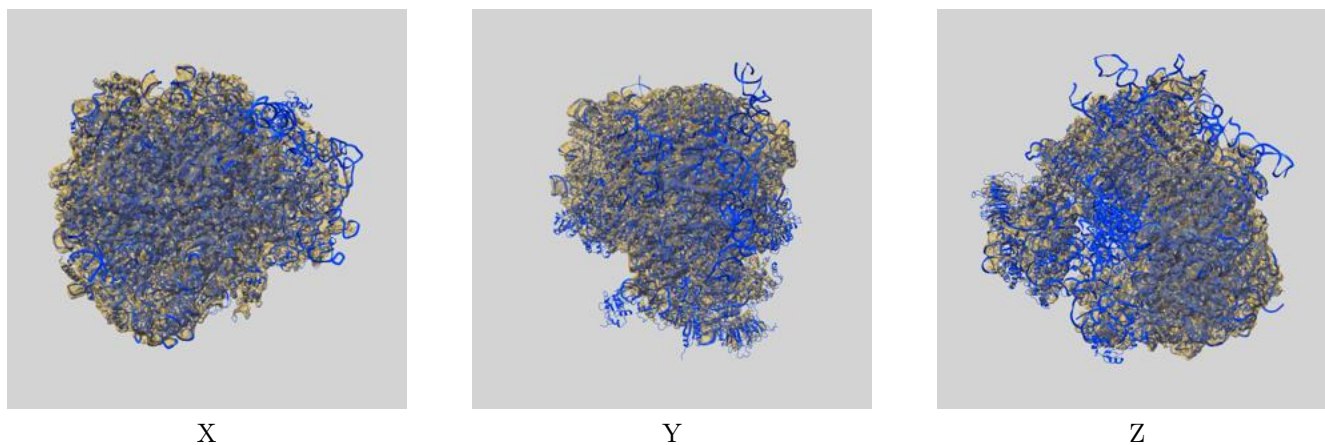
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

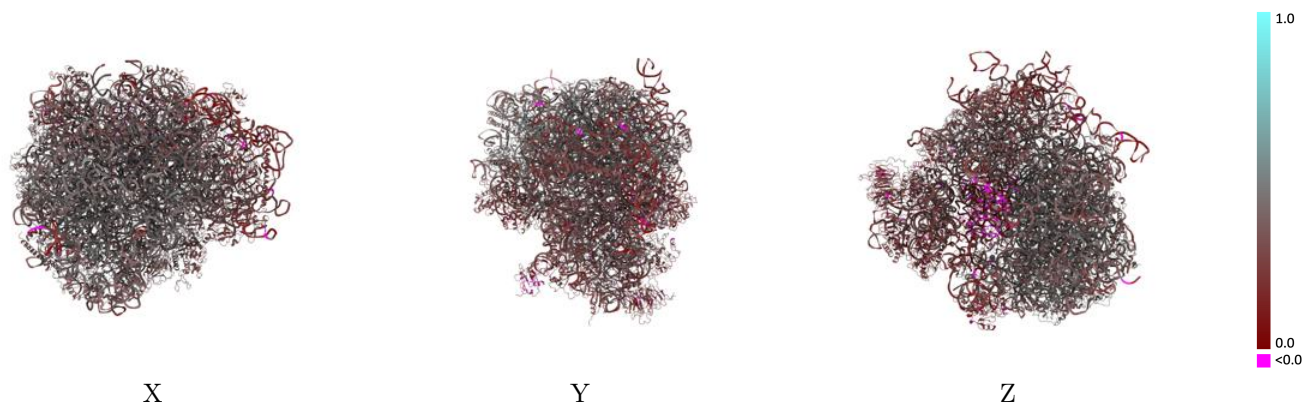
This section contains information regarding the fit between EMDB map EMD-6644 and PDB model 5JUP. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



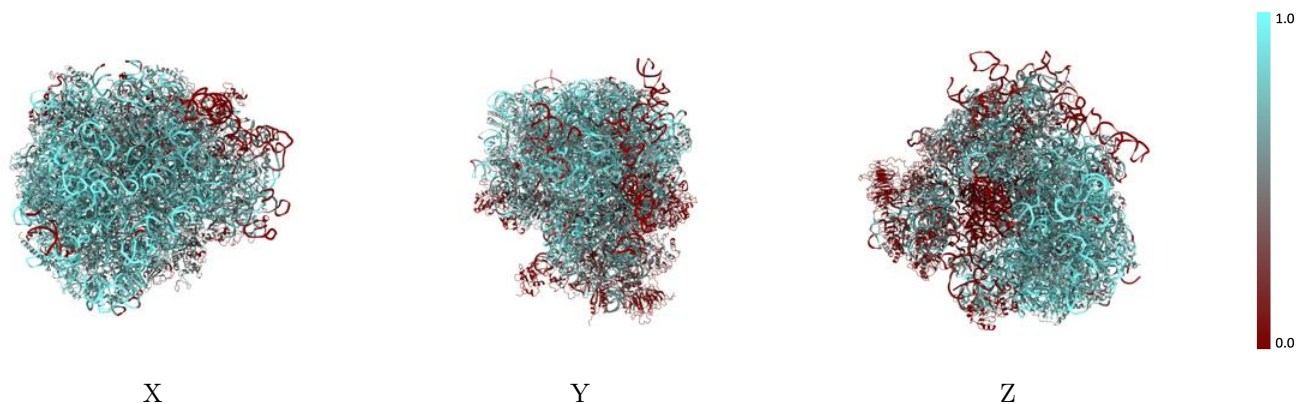
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



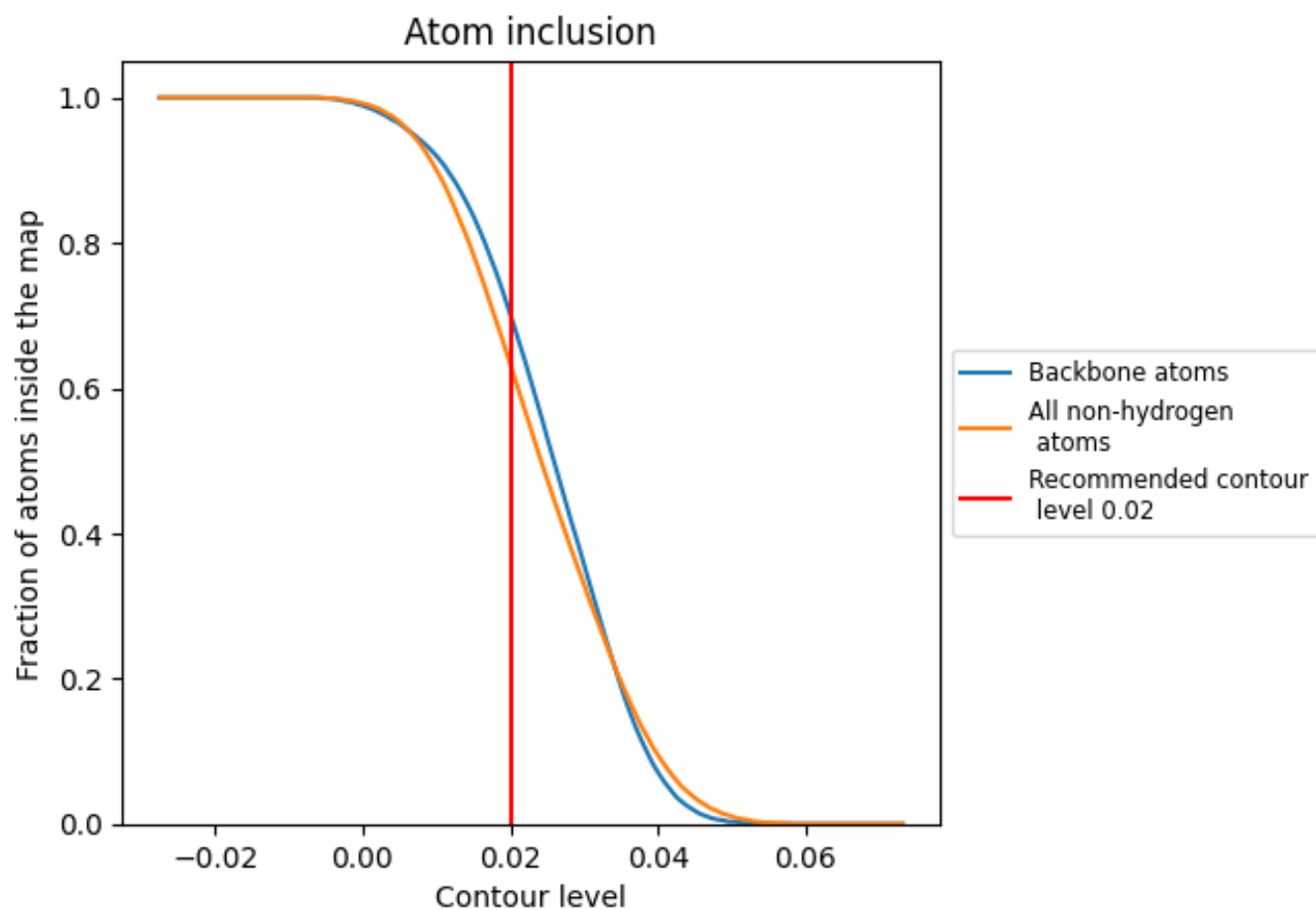
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 63% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6330	 0.3620
A	 0.6430	 0.3080
AA	 0.5450	 0.4530
AB	 0.2350	 0.3110
AC	 0.3690	 0.3020
B	 0.8560	 0.4010
BA	 0.6150	 0.4350
BB	 0.5190	 0.3280
BC	 0.3490	 0.3350
C	 0.8950	 0.4130
CA	 0.5560	 0.4100
CB	 0.1770	 0.2580
CC	 0.0000	 0.1720
D	 0.9470	 0.3960
DA	 0.6790	 0.4090
DB	 0.4000	 0.2980
DC	 0.4300	 0.3220
E	 0.0300	 0.2420
EA	 0.5750	 0.3780
EB	 0.1380	 0.3160
EC	 0.1210	 0.2040
F	 0.6110	 0.4330
FA	 0.6960	 0.4450
FB	 0.4060	 0.3340
G	 0.6590	 0.4470
GA	 0.6120	 0.4240
GB	 0.5330	 0.3340
H	 0.7050	 0.4390
HA	 0.6550	 0.3880
HB	 0.2920	 0.2580
I	 0.6570	 0.3720
IA	 0.6720	 0.4330
IB	 0.3190	 0.3480
J	 0.6010	 0.3960
JA	 0.6730	 0.4560

















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Chain	Atom inclusion	Q-score
JB	 0.0000	 0.1650
K	 0.6730	 0.4200
KA	 0.6180	 0.4520
KB	 0.4070	 0.3250
L	 0.5950	 0.3770
LA	 0.5800	 0.4110
LB	 0.0000	 0.1200
M	 0.6180	 0.4160
MA	 0.6190	 0.3790
MB	 0.2060	 0.2590
N	 0.5790	 0.4060
NA	 0.6720	 0.3970
NB	 0.1640	 0.2610
O	 0.6150	 0.3640
OA	 0.6650	 0.4450
OB	 0.1730	 0.2620
P	 0.0930	 0.1920
PA	 0.1620	 0.3450
PB	 0.1870	 0.2730
Q	 0.6870	 0.4160
QA	 0.6800	 0.4420
QB	 0.2340	 0.2730
R	 0.6740	 0.4040
RA	 0.6730	 0.4290
RB	 0.1010	 0.3020
S	 0.6450	 0.4320
SA	 0.0000	 0.1530
SB	 0.4660	 0.3660
T	 0.6380	 0.4300
TA	 0.6380	 0.4430
TB	 0.4400	 0.3670
U	 0.6790	 0.4440
UA	 0.5780	 0.4140
UB	 0.3740	 0.3860
V	 0.7170	 0.4420
VA	 0.0970	 0.2630
VB	 0.4520	 0.2820
W	 0.5080	 0.3770
WA	 0.1040	 0.2650
WB	 0.1340	 0.2470
X	 0.6310	 0.4300
XA	 0.3140	 0.3290

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Chain	Atom inclusion	Q-score
XB	 0.0000	 0.1230
Y	 0.6530	 0.4420
YA	 0.0000	 0.1290
YB	 0.3320	 0.3360
Z	 0.5550	 0.3800
ZA	 0.5150	 0.3800
ZB	 0.2150	 0.2810