



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:59 PM UTC

PDB ID : 5JUJ / pdb_00005juj
EMDB ID : EMD-6647
Title : Saccharomyces cerevisiae 80S ribosome bound with elongation factor eEF2-GDP-sordarin and Taura Syndrome Virus IRES, Structure V (least rotated 40S subunit)
Authors : Abeyrathne, P.; Koh, C.S.; Grant, T.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2016-05-10
Resolution : 4.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

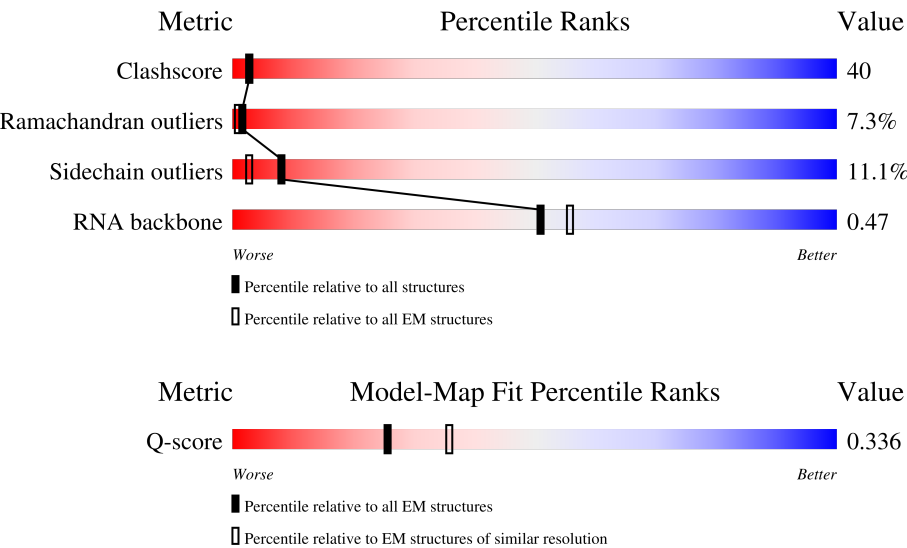
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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

Mol	Chain	Length	Quality of chain
1	A	1798	15% 22% 61% 15% ..
2	B	3396	8% 20% 62% 14% ..
3	C	158	21% 64% 14% .

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Mol	Chain	Length	Quality of chain
4	D	121	
5	E	217	
6	F	254	
7	G	387	
8	H	362	
9	I	297	
10	J	176	
11	K	244	
12	L	256	
13	M	191	
14	N	221	
15	O	174	
16	P	165	
17	Q	199	
18	R	138	
19	S	204	
20	T	199	
21	U	184	
22	V	186	
23	W	189	
24	X	172	
25	Y	160	
26	Z	121	
27	AA	137	
28	BA	155	

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Mol	Chain	Length	Quality of chain
29	CA	142	
30	DA	127	
31	EA	136	
32	FA	149	
33	GA	59	
34	HA	105	
35	IA	113	
36	JA	130	
37	KA	107	
38	LA	121	
39	MA	120	
40	NA	100	
41	OA	88	
42	PA	78	
43	QA	51	
44	RA	128	
45	SA	25	
46	TA	106	
47	UA	92	
48	VA	312	
49	WA	319	
50	XA	252	
51	YA	255	
52	ZA	254	
53	AB	240	

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

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Mol	Chain	Length	Quality of chain
79	AC	56	36%25%61%9%5%
80	BC	63	54%46%41%6%5%
81	CC	152	47%39%8%53%
82	DC	842	45%21%49%25%. .
83	EC	201	83%35%34%21%8%. .

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 215045 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1781	Total	C	N	O	P	0	0
			37658	16811	6630	12436	1781		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	YA	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
64	LB	127	Total	C	N	O	S	0	0
			942	578	186	175	3		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
76	XB	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

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

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

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

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

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

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

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

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

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

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

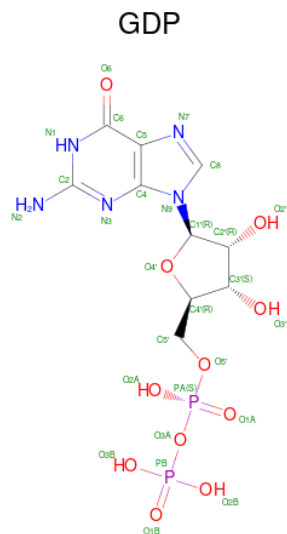
- Molecule 82 is a protein called yeast eEF2.

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

- Molecule 83 is a RNA chain called IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	EC	198	Total	C	N	O	P	0	0
			3968	1753	669	1348	198		

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



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

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

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

- Molecule 86 is [1R-(1.ALPHA.,3A.BETA.,4.BETA.,4A.BETA.,7.BETA.,7A.ALPHA.,8A.BETA.)]8A-[(6-DEOXY-4-O-METHYL-BETA-D-ALTROPYRANOSYLOXY)METHYL]-4-FORMYL-4,4A,5,6,7,7A,8,8A-OCTAHYDRO-7-METHYL-3-(1-METHYLETHYL)-1,4-METHANO-S-INDACENE-3A(1H)-CARBOXYLIC ACID (CCD ID: SO1) (formula: C₂₇H₄₂O₈).

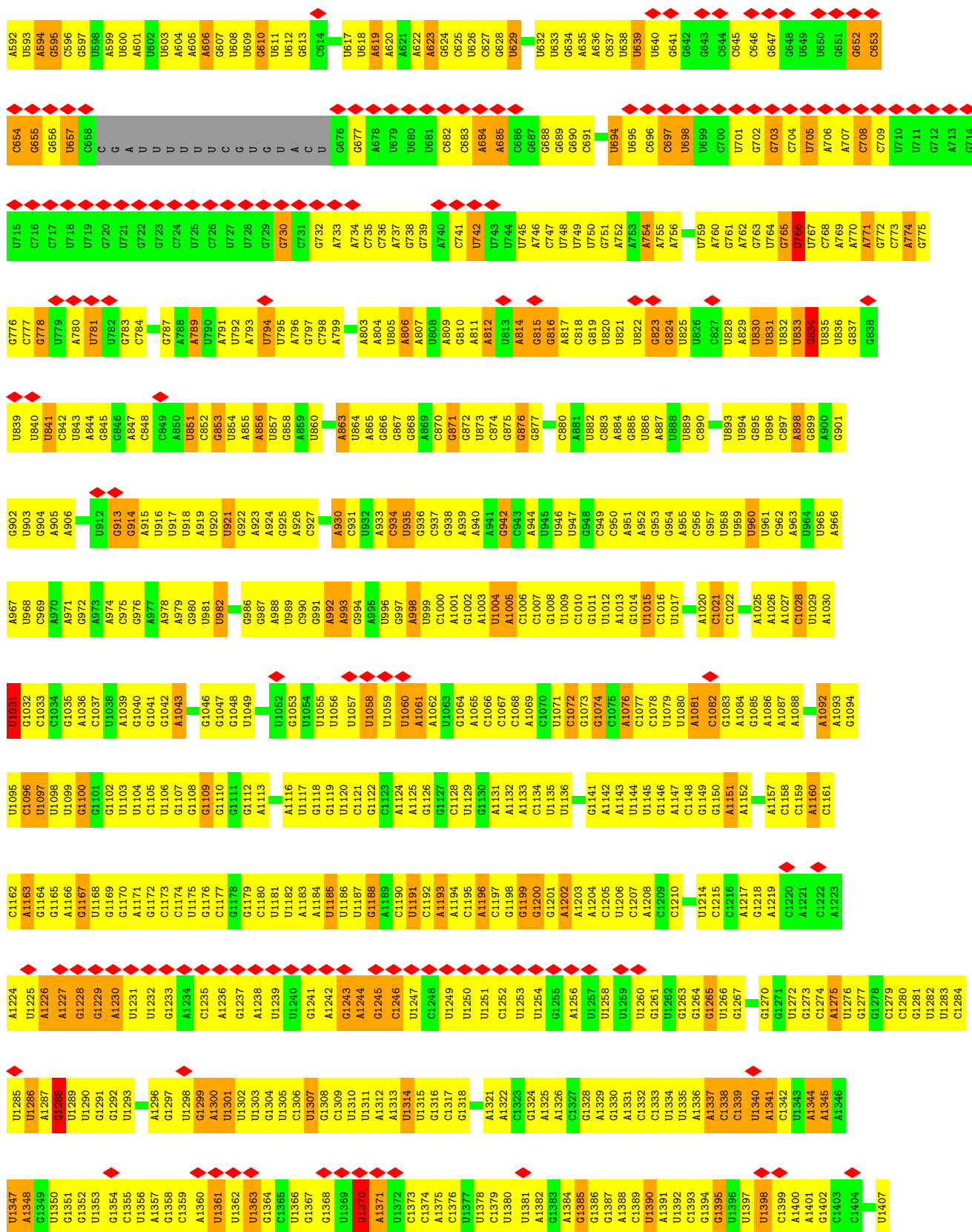


3 Residue-property plots

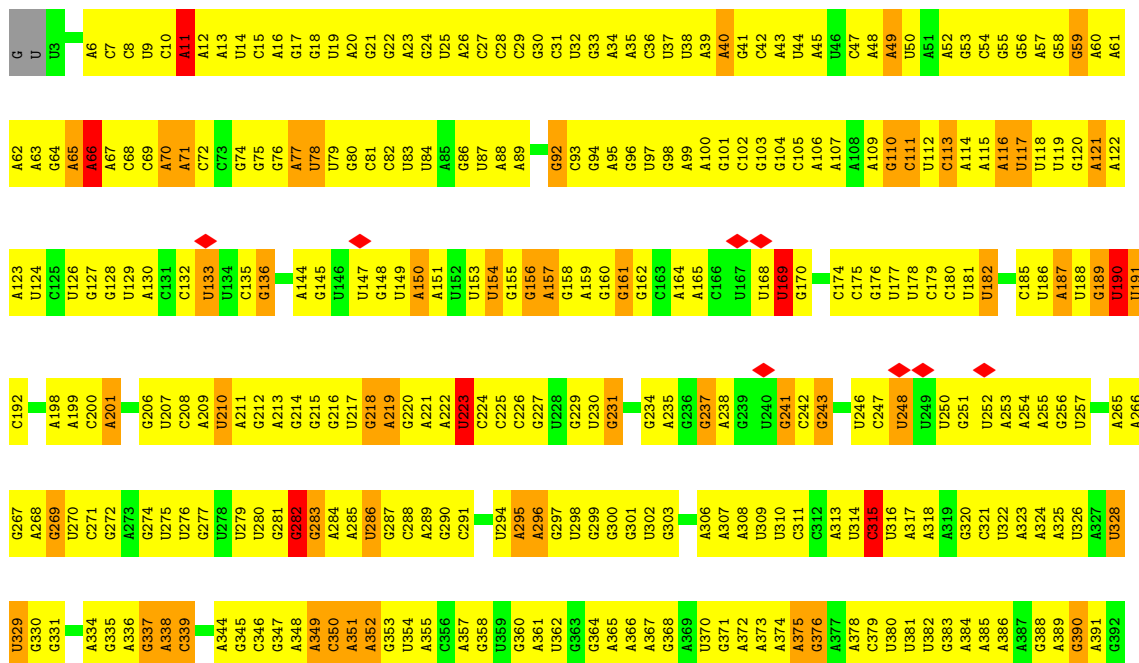
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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





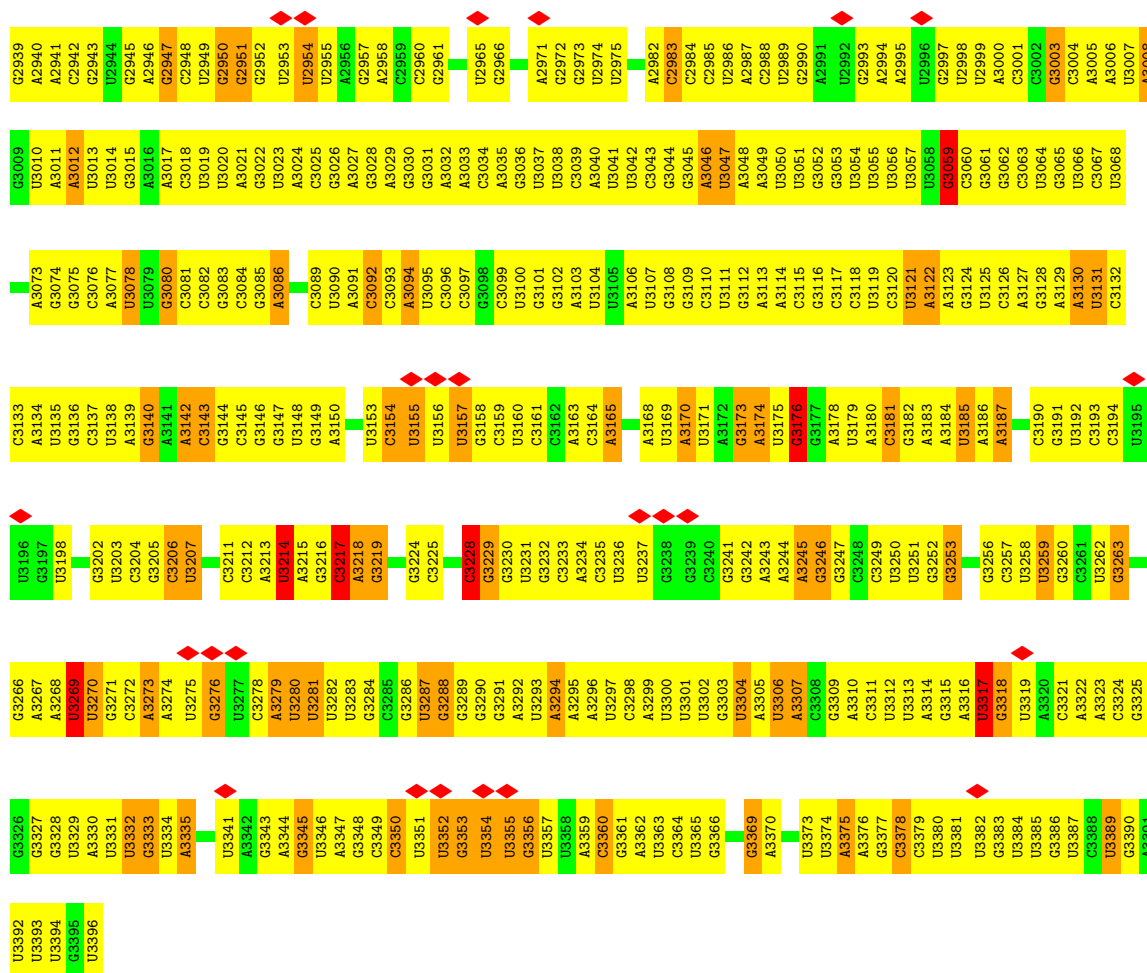
- Molecule 2: 25S ribosomal RNA



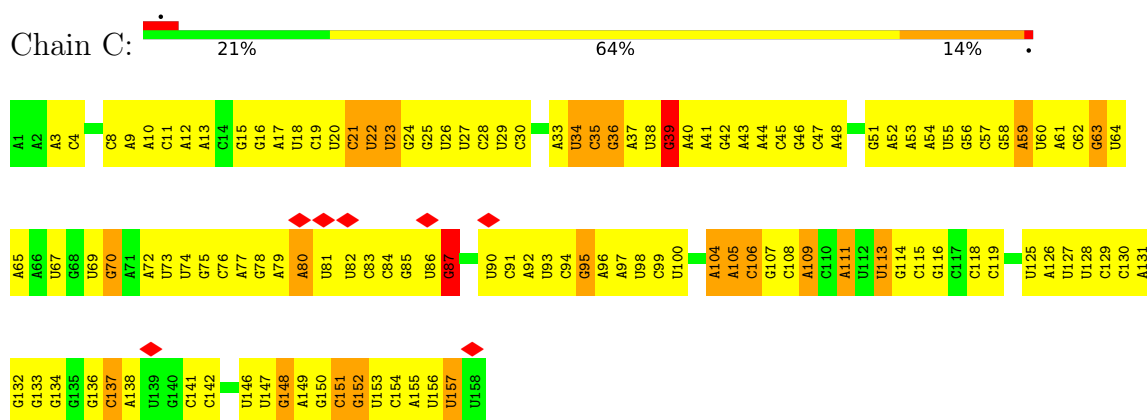


U2043	G	A1922	G1860	A1797	A1731	C1865	G1604	A1539	G1473	C1411	U1348	C1284
U2044	C	C1923	G1861	A1798	U1732	G1666	A1605	U1540	A1474	G1412	G1349	G1285
G2045	U	U1925	U1862	A1799	G1733	A1867	U1607	G1541	A1475	G1413	A1350	A1286
U2046	G	U1926	U1863	A1800	C1738	C1669	U1608	A1546	C1478	G1414	U1351	A1287
A2047	C	G1927	C1866	U1801	U1739	C1670	C1609	U1547	U1479	U1415	A1352	U1288
G2048	U	U1928	A1867	C1803	U1740	C1671	G1610	U1549	G1480	G1417	U1353	A1290
A2049	U	G1929	A1868	A1804	A1741	U1672	G1611	C1550	A1481	A1418	G1354	A1291
C2050	G	A1930	C1869	A1805	U1742	G1673	A1612	C1551	A1482	A1419	G1354	A1292
U2051	U	U1931	A1870	A1806	G1743	G1674	A1613	U1552	G1483	C1420	U1356	U1293
G2052	G	A1932	U1871	G1807	G1745	G1675	C1614	U1553	U1484	G1421	G1357	U1294
C2053	G	A1933	C1872	G1808	U1746	G1676	G1615	U1554	G1487	C1422	G1358	G1295
U2054	A	U1934	U1873	A1809	G1747	A1677	U1616	U1555	G1488	C1423	C1359	C1296
C2055	C	G1935	A1874	A1810	G1748	A1678	G1617	C1556	G1489	C1424	U1299	U1299
C2056	U	G1936	G1875	G1811	A1749	A1679	U1620	A1557	A1489	U1425	G1360	G1300
U2057	G	U1937	G1876	G1812	A1750	U1680	A1621	A1558	A1490	G1426	U1361	A1301
U2058	C	U1938	G1877	A1813	G1751	U1682	U1622	A1559	A1491	U1427	A1362	A1302
G2059	U	U1939	U1879	U1815	A1752	A1883	G1623	U1560	G1492	A1428	G1363	G1306
U2060	G	G1940	A1880	A1816	G1753	U1684	G1624	G1561	G1493	G1429	C1364	U1308
C2061	U	U1941	A1881	A1817	G1754	C1685	G1625	C1562	U1494	U1430	G1365	A1309
U2062	G	U1942	G1882	G1817	C1755	U1686	A1626	C1563	U1495	U1431	A1366	G1307
G2063	U	C1943	A1883	U1818	A1756	U1687	U1627	U1564	C1496	C1432	G1367	A1308
U2064	G	U1944	U1884	U1819	G1757	U1688	C1628	U1565	C1497	A1433	U1368	U1309
U2065	G	A1945	U1885	U1820	C1758	U1689	U1629	A1566	A1498	G1434	G1370	G1310
C2066	G	U1946	A1886	C1821	G1759	C1690	U1630	U1567	A1499	A1435	G1371	G1311
U2067	C	A1947	A1887	U1822	A1760	U1691	G1631	U1568	G1500	U1436	C1372	C1312
G2068	G	G1948	U1888	A1823	C1761	U1692	A1632	U1569	C1502	C1437	G1373	G1313
C2069	U	U1949	G1889	U1824	G1762	C1693	G1633	U1570	A1503	U1438	A1374	C1314
U2070	G	U1950	U1890	G1825	U1763	U1694	G1634	U1571	A1504	U1439	U1384	U1315
C2071	G	A1891	A1891	C1826	U1764	U1695	G1635	A1571	C1505	G1441	C1385	C1316
U2072	C	U1892	U1892	C1827	U1765	A1697	A1637	U1572	A1506	U1442	A1378	A1317
G2073	U	A1893	U1893	A1828	G1766	U1703	A1638	G1573	U1507	U1443	G1380	A1318
C2074	C	A1894	A1894	G1829	U1767	U1704	C1639	U1574	C1508	U1444	A1381	G1319
U2075	G	A1895	A1895	U1830	G1768	U1705	G1640	A1575	A1509	U1445	G1382	C1320
C2076	G	G1905	G1905	U1831	C1770	C1706	U1641	G1576	G1510	U1446	U1384	U1322
U2077	U	U1906	C1906	C1832	U1771	A1707	A1642	G1577	G1511	U1447	C1386	G1323
G2078	C	U1907	C1907	G1833	U1772	C1708	A1643	C1578	G1514	U1448	A1386	U1324
A2079	A	U1908	A1908	U1834	C1773	C1709	A1644	A1580	A1515	A1449	G1387	U1325
C2080	G	A1909	A1909	C1835	C1774	C1710	U1645	C1581	C1516	G1450	U1388	A1326
U2081	G	U1910	G1910	U1836	G1775	C1711	G1646	C1582	G1525	C1458	C1327	C1328
C2082	C	C1911	A1911	G1837	U1776	G1712	A1647	A1583	G1526	A1461	U1397	U1336
G2083	A	U1912	U1912	U1782	G1777	U1716	A1648	U1584	G1527	A1462	A1399	A1337
C2084	C	G1913	G1913	U1783	U1778	U1717	U1649	A1588	G1528	U1463	C1398	C1338
U2085	U	A1914	A1914	G1784	C1779	G1718	U1650	C1585	G1529	G1464	G1400	C1339
A2086	A	U1915	U1915	U1785	A1787	G1719	G1651	C1586	A1593	A1465	C1396	G1340
C2087	C	U1916	U1916	U1786	G1788	U1720	G1652	A1587	G1591	G1466	C1397	C1342
U2088	G	C1917	C1917	G1787	U1789	U1721	A1656	C1588	G1592	A1467	G1404	A1343
A2089	A	U1918	U1918	C1788	U1790	U1722	C1657	A1594	A1593	U1470	U1405	G1346
C2090	U	G1919	G1919	G1789	C1791	U1723	U1659	U1595	U1533	U1471	G1408	G1347
U2091	U	U1920	U1920	U1791	G1792	U1724	C1660	C1596	A1534	A1472	U1410	
C2092	C	A1921	A1921	C1792	U1793	C1725	G1662	G1598	A1535			
U2093	U			C1793	G1794	G1728	C1663	U1601	G1536			
G2094	G			U1795	G1795	A1729	G1664	A1602	A1537			
C2095	C							A1603	G1538			
U2096	U											
C2097	C											
G2098	G											
A2099	A											
C2100	C											
U2101	U											
C2102	C											

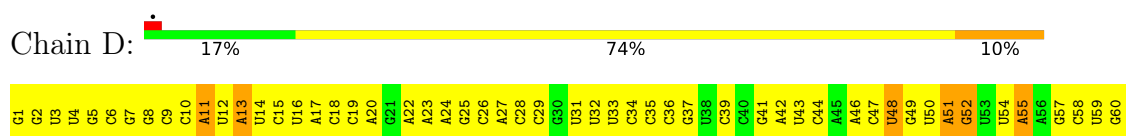


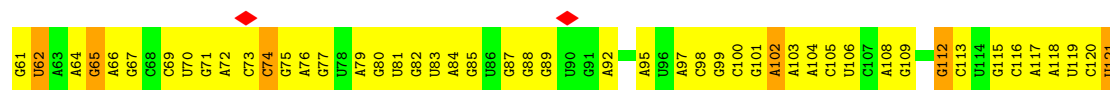


• Molecule 3: 5.8S ribosomal RNA

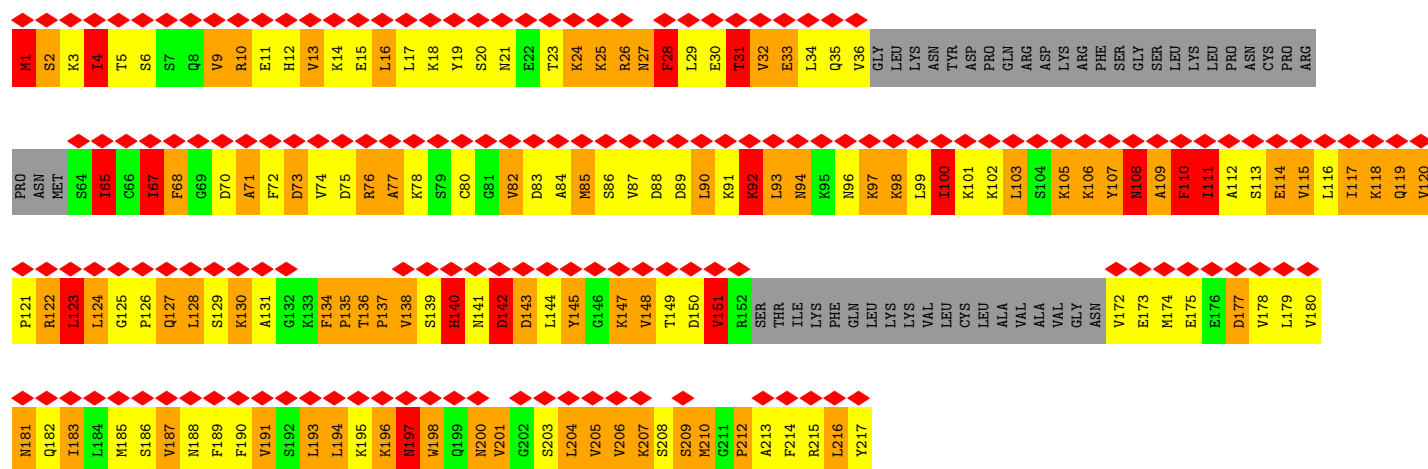
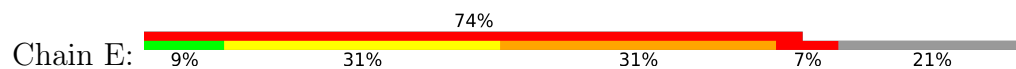


• Molecule 4: 5S ribosomal RNA

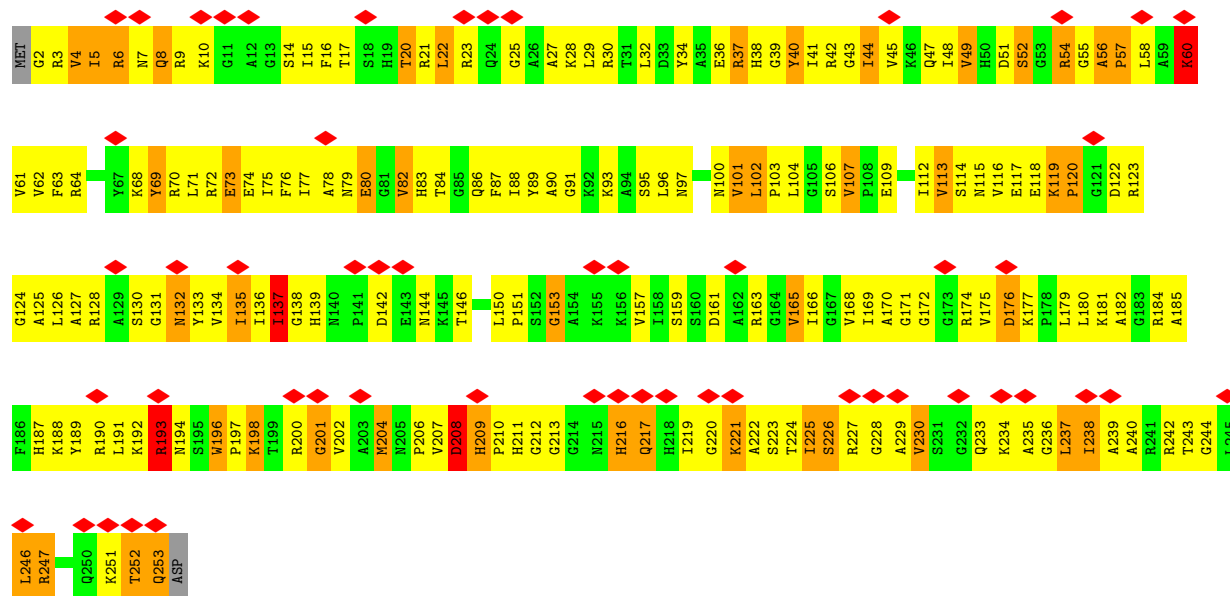




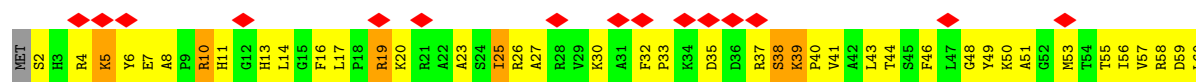
• Molecule 5: uL1 (yeast L1)

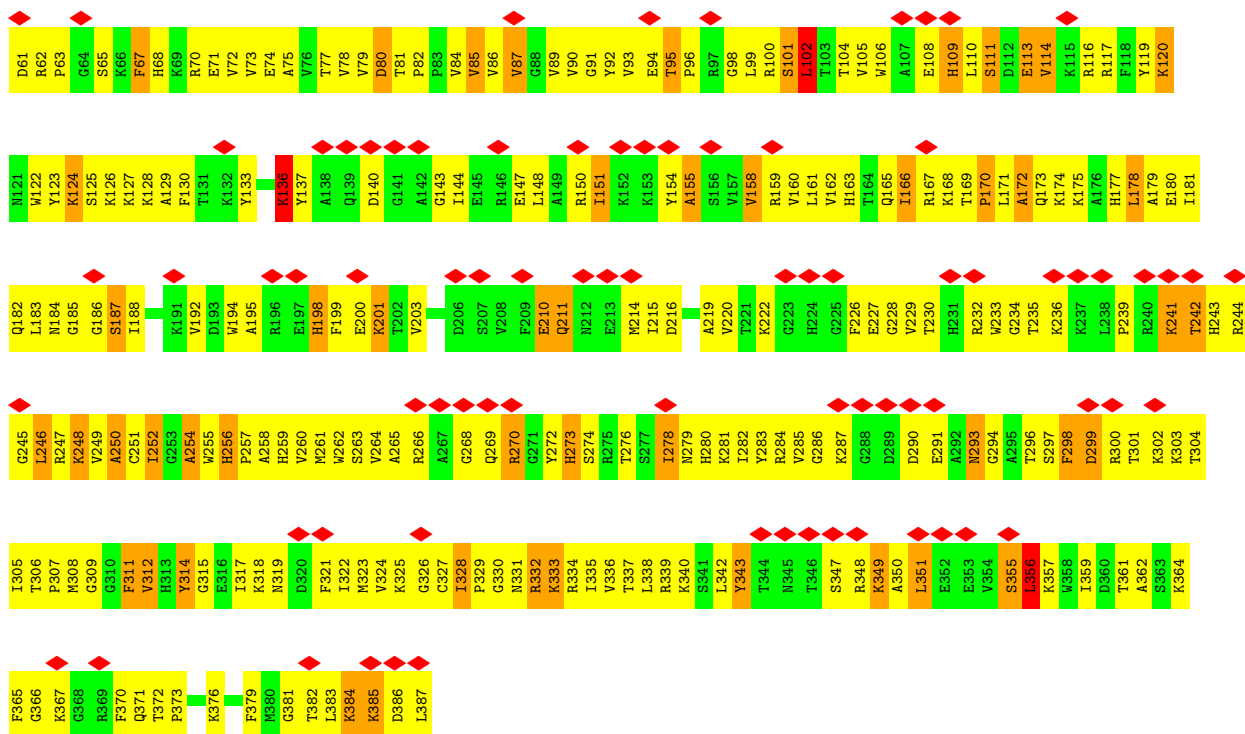


• Molecule 6: uL2 (yeast L2)

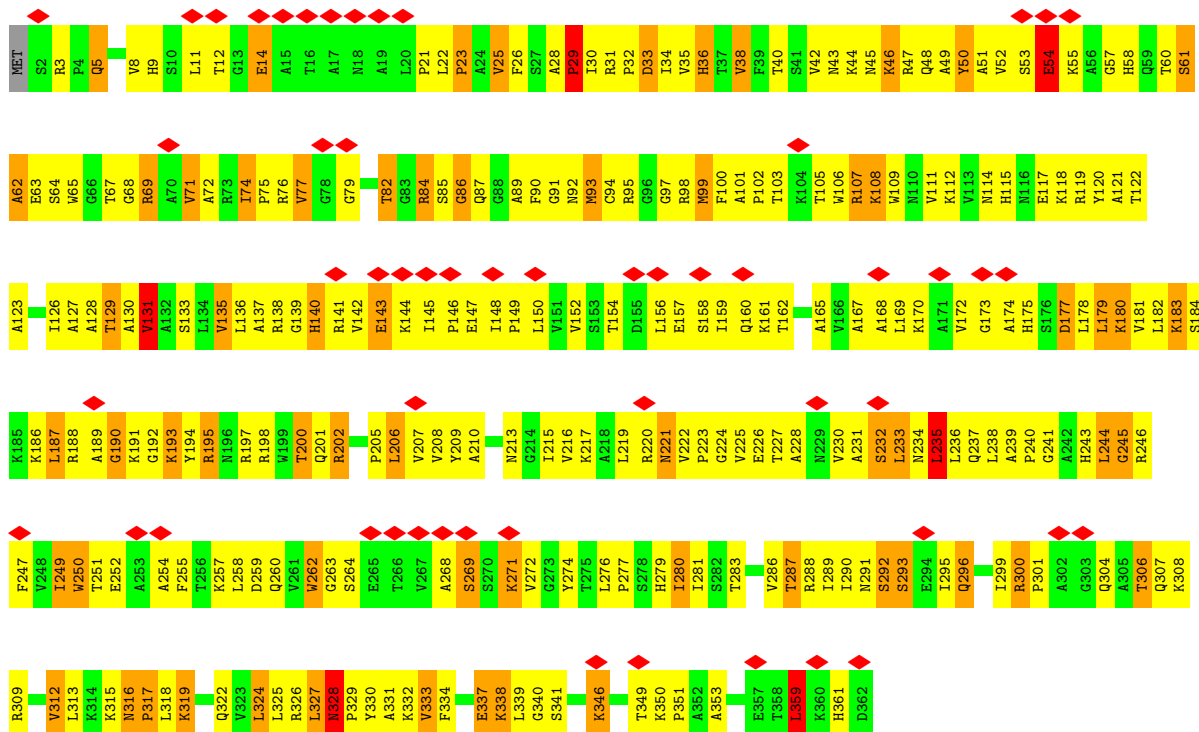


• Molecule 7: uL3 (yeast L3)

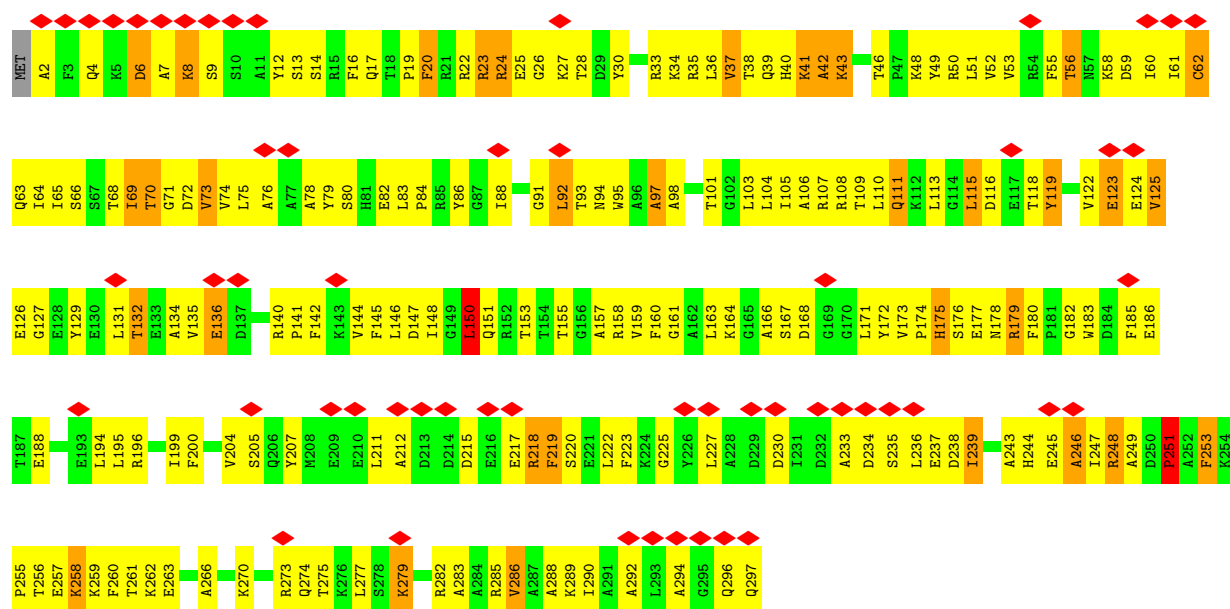




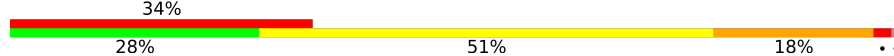
• Molecule 8: uL4 (yeast L4)

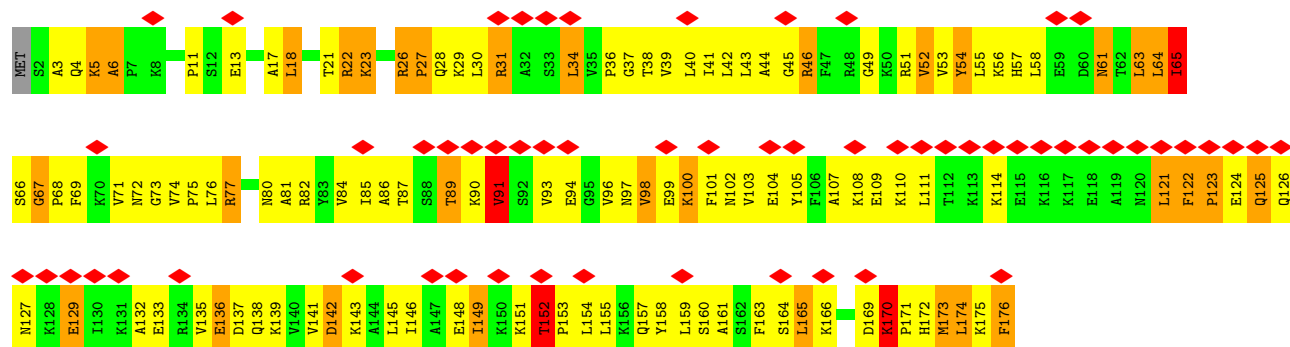


Chain I: 

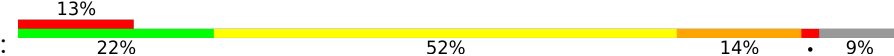


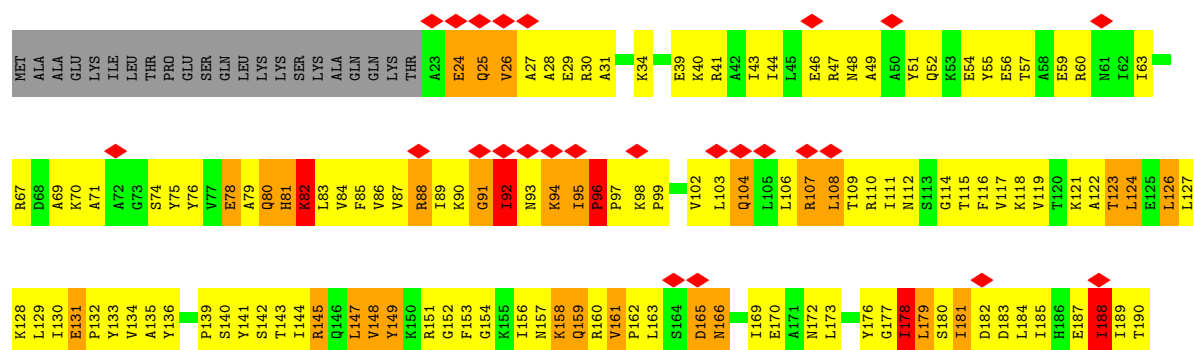
• Molecule 10: eL6 (yeast L6)

Chain J: 



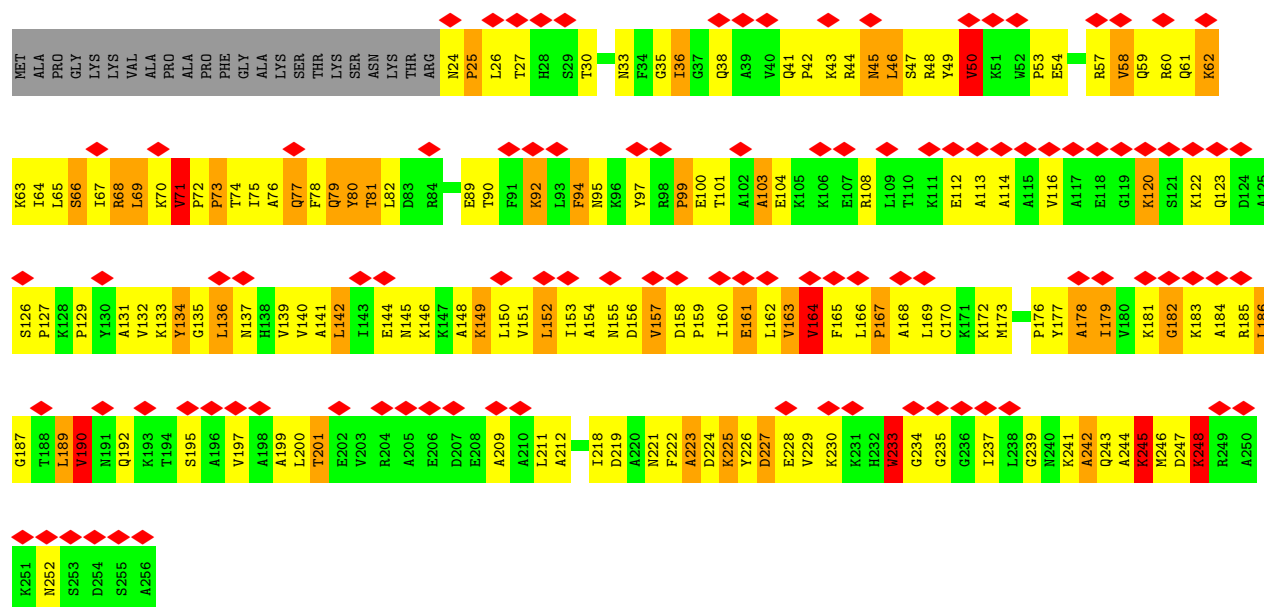
• Molecule 11: uL30 (yeast L7)

Chain K: 

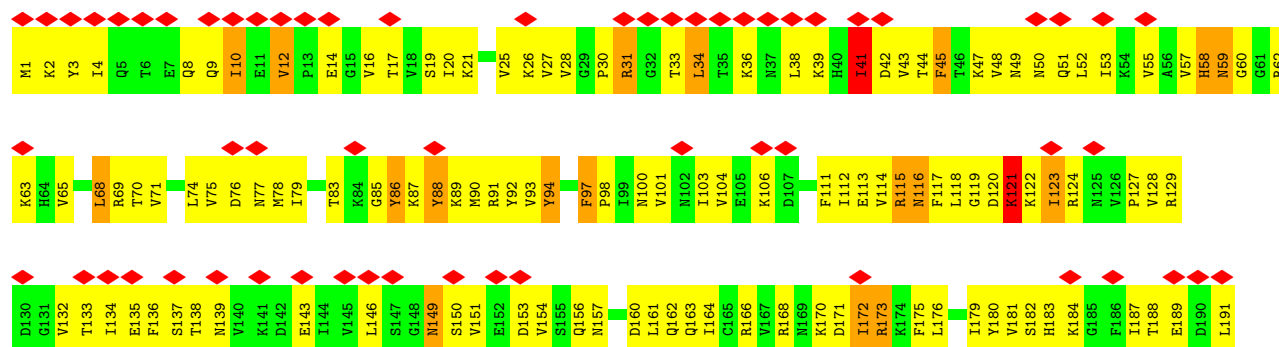




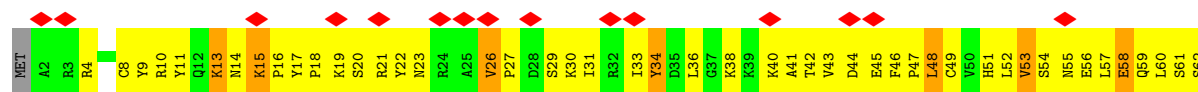
• Molecule 12: eL8 (yeast L8)

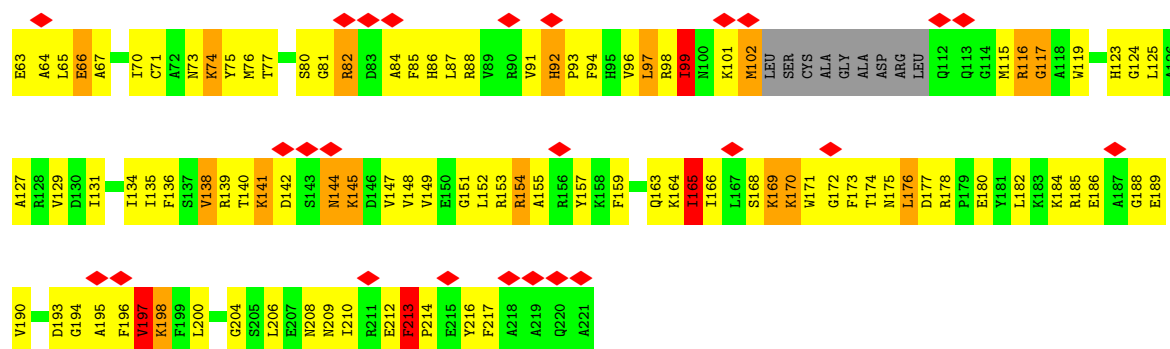


• Molecule 13: uL6 (yeast L9)

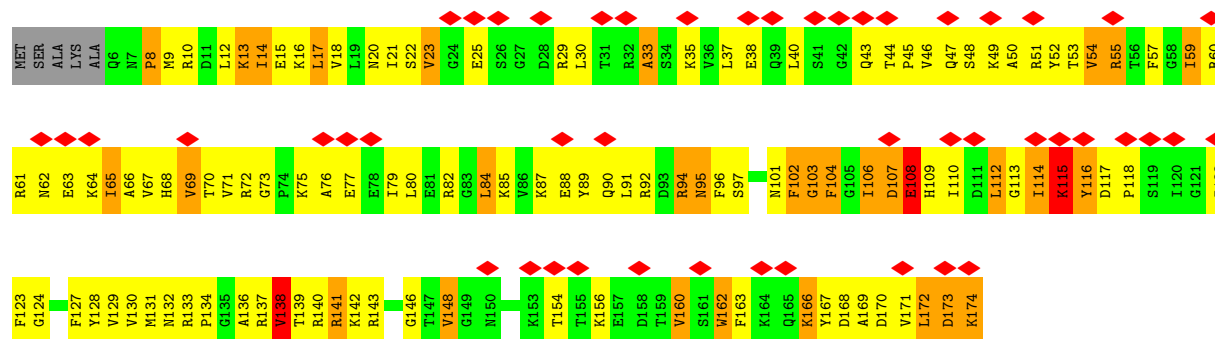


• Molecule 14: uL16 (yeast L10)

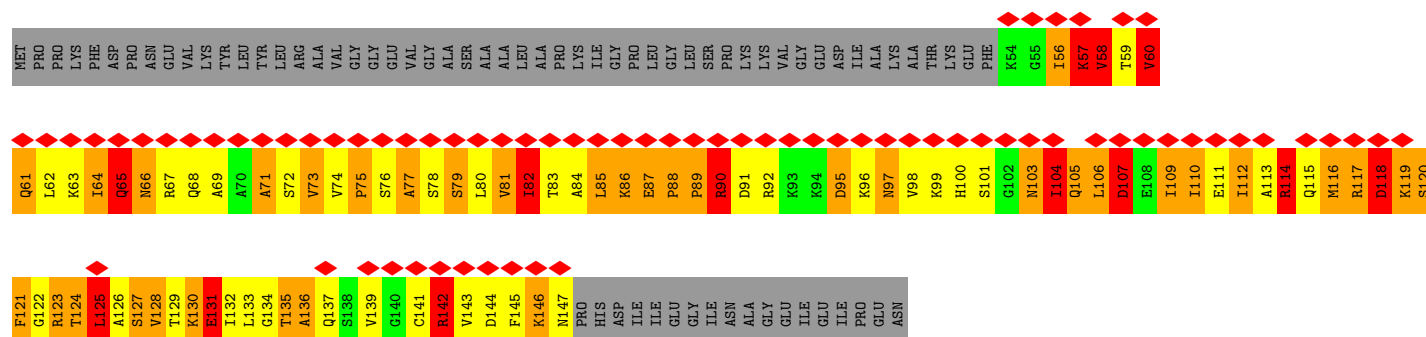
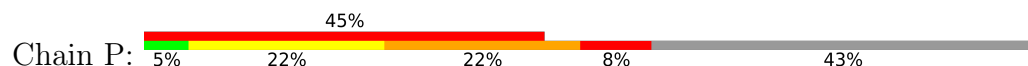




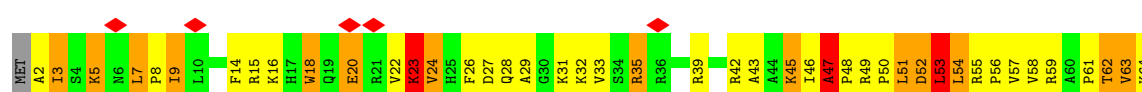
• Molecule 15: uL5 (yeast L11)

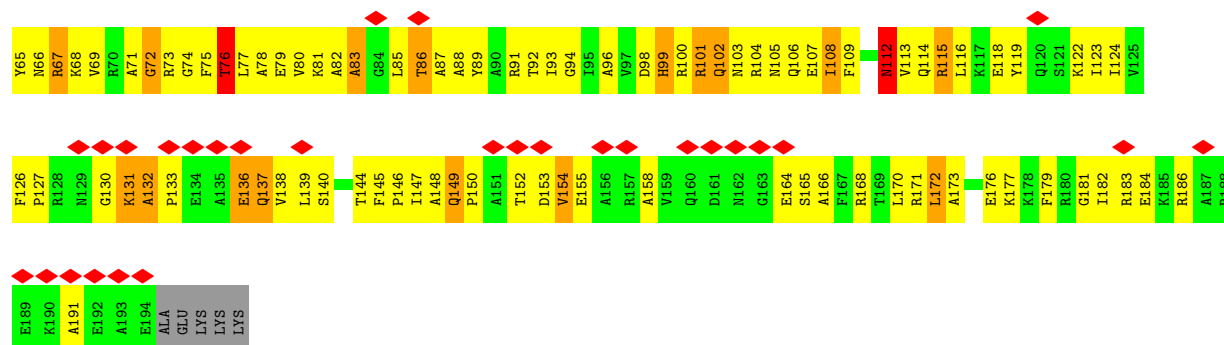


• Molecule 16: uL11 (yeast L12)

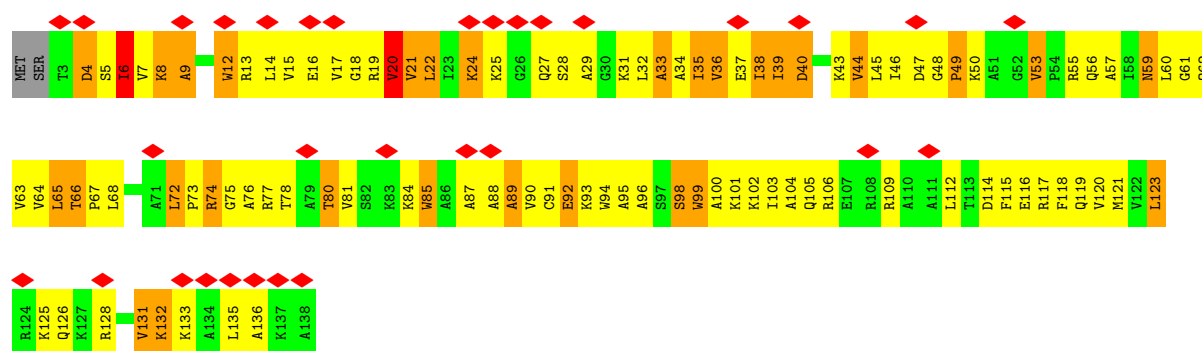


• Molecule 17: eL13 (yeast L13)

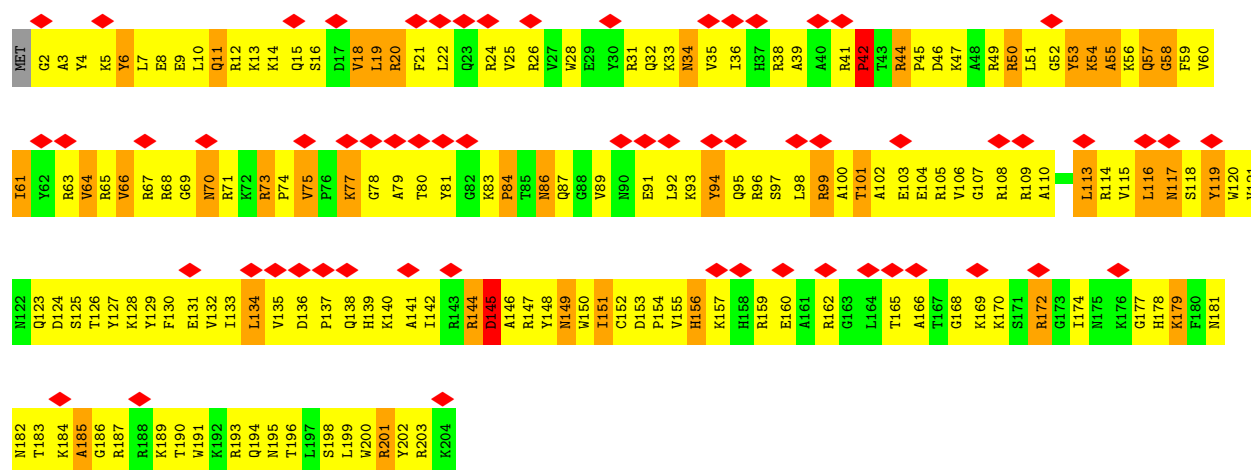




• Molecule 18: eL14 (yeast L14)

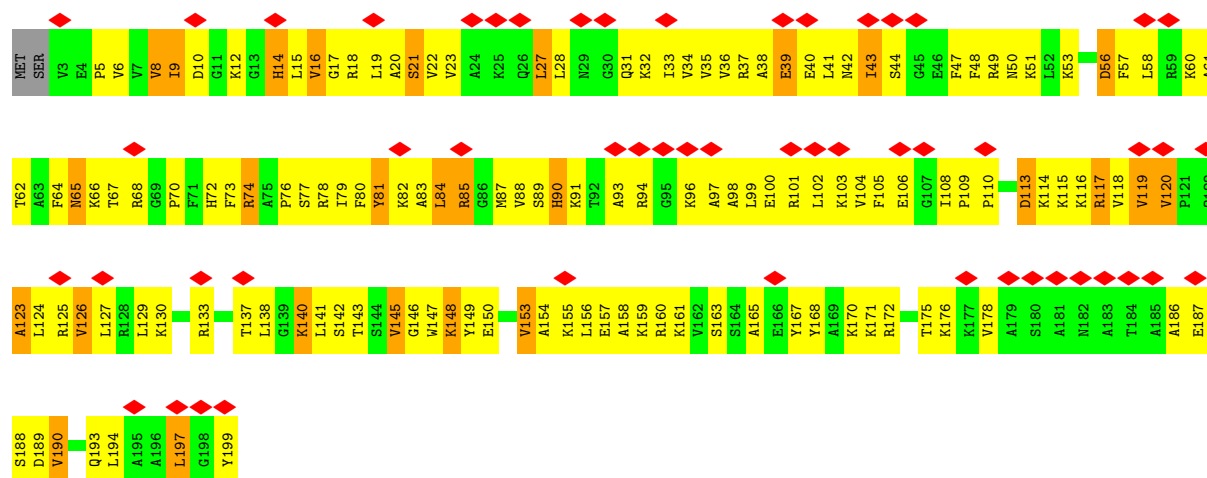


• Molecule 19: eL15 (yeast L15)

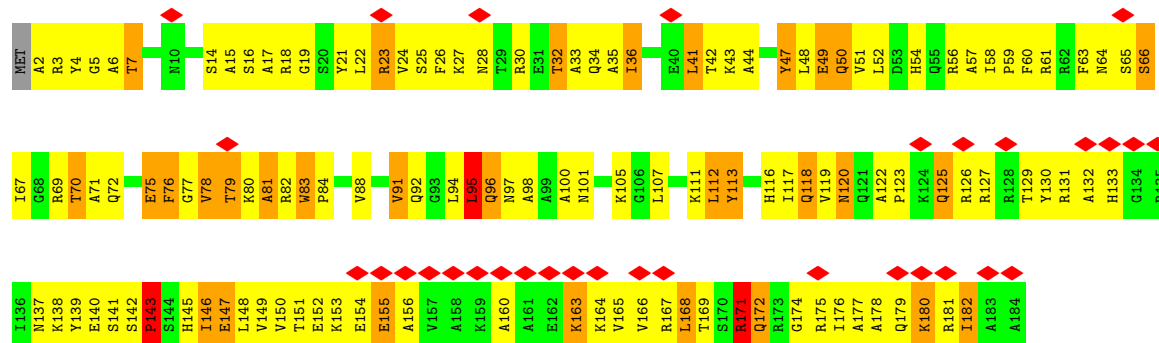


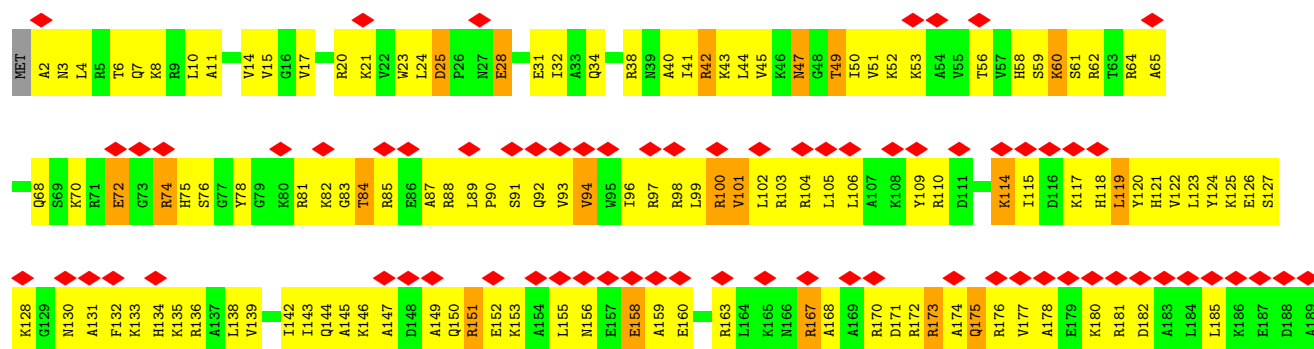
• Molecule 20: uL13 (yeast L16)



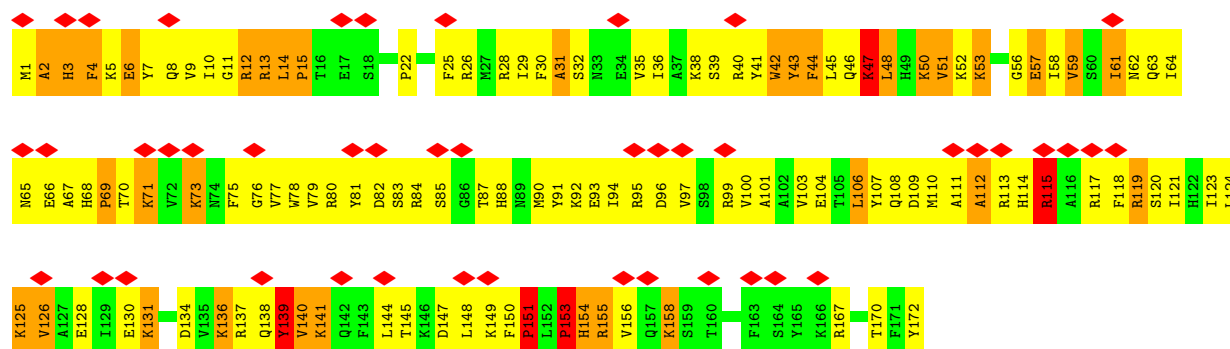


• Molecule 21: uL22 (yeast L17)

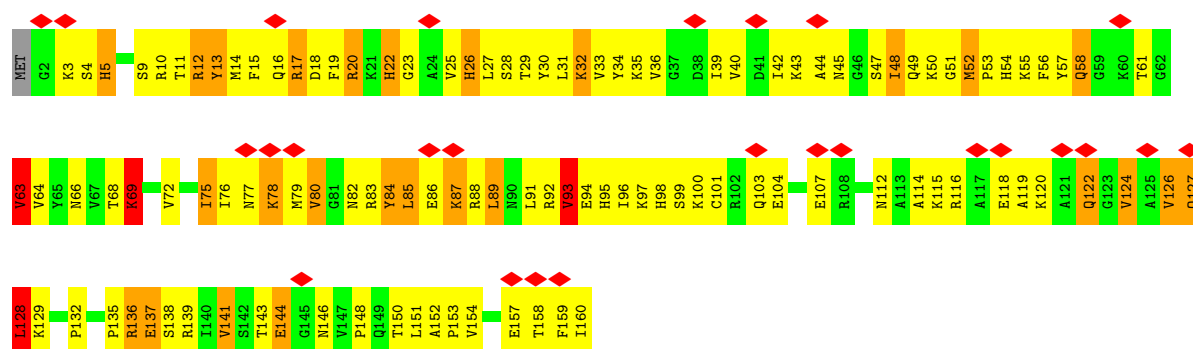




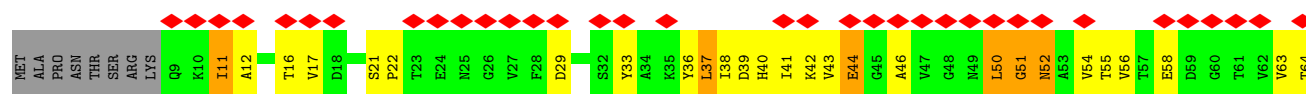
• Molecule 24: eL20 (yeast L20)

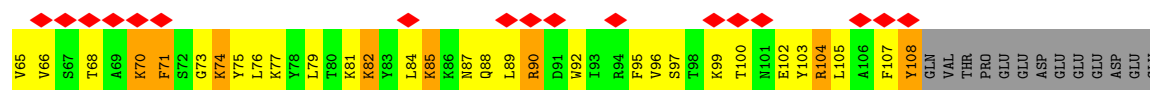


• Molecule 25: eL21 (yeast L21)

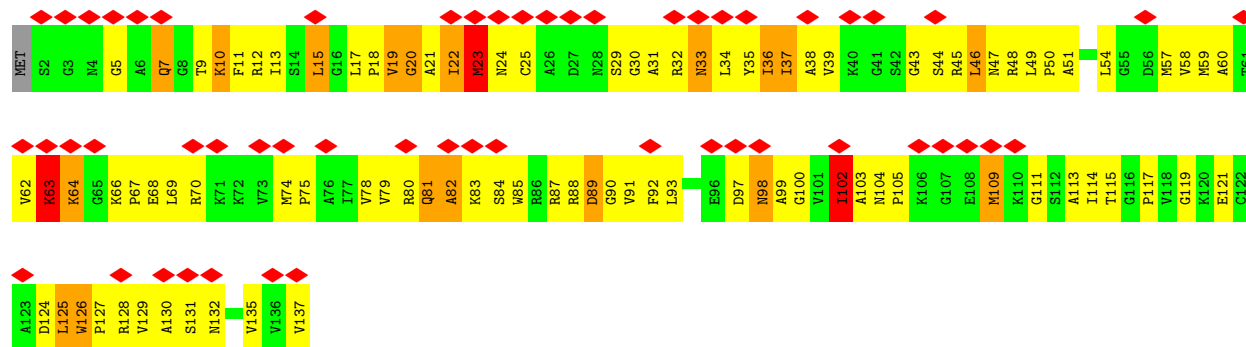


• Molecule 26: eL22 (yeast L22)

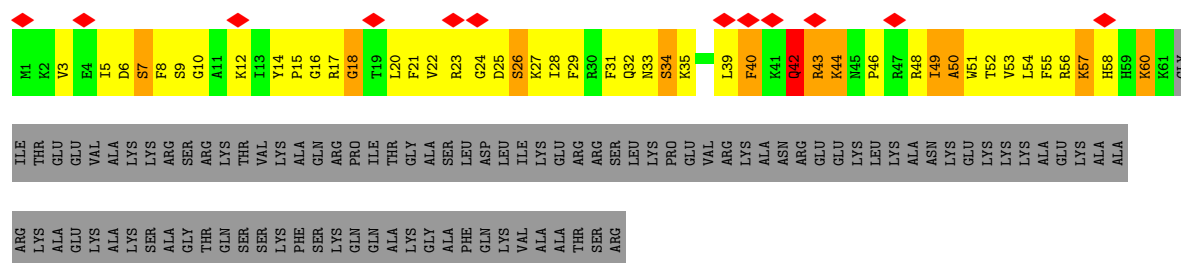
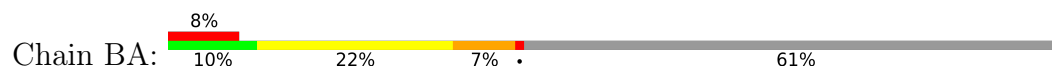




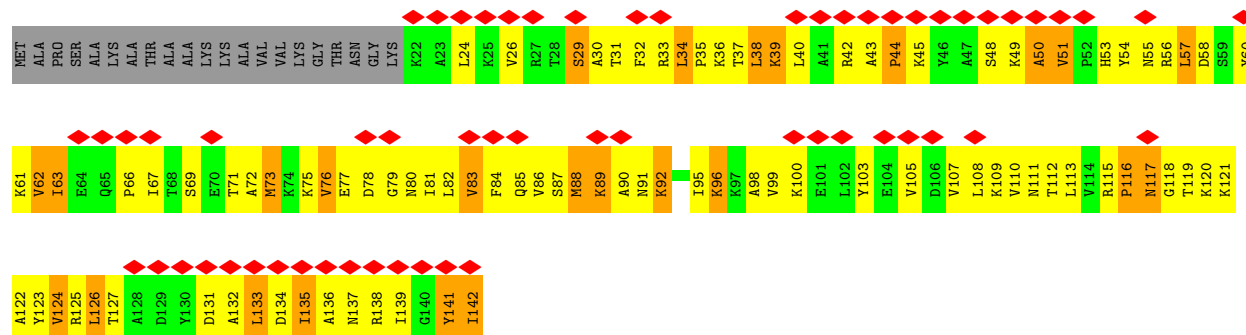
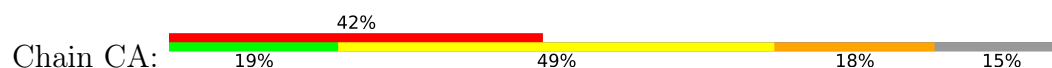
• Molecule 27: uL14 (yeast L23)



• Molecule 28: eL24 (yeast L24)

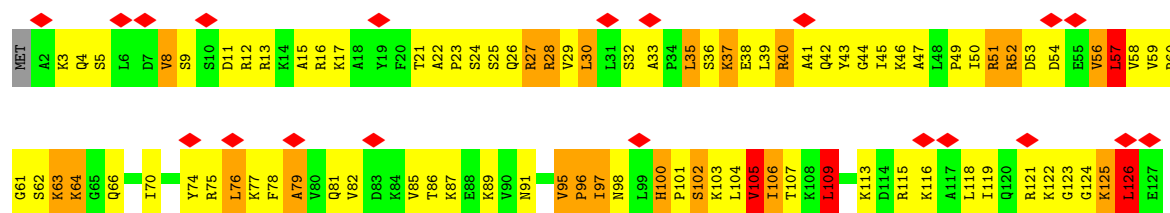


• Molecule 29: uL23 (yeast L25)

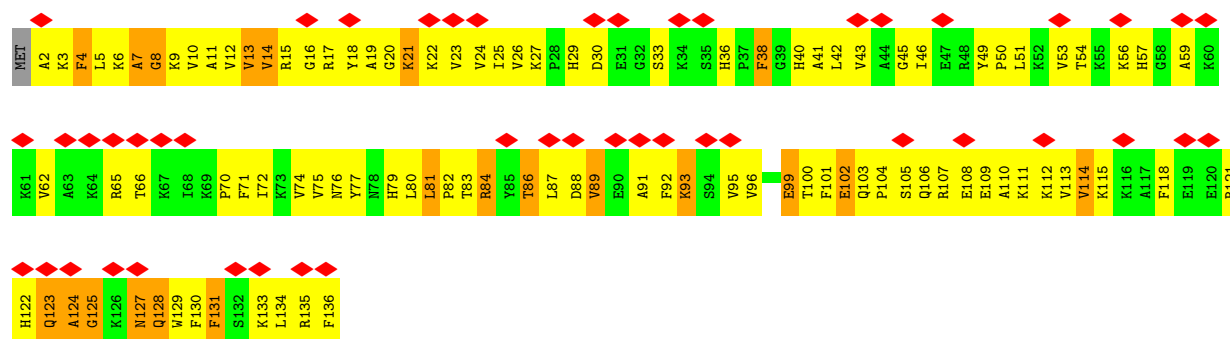


• Molecule 30: uL24 (yeast L26)

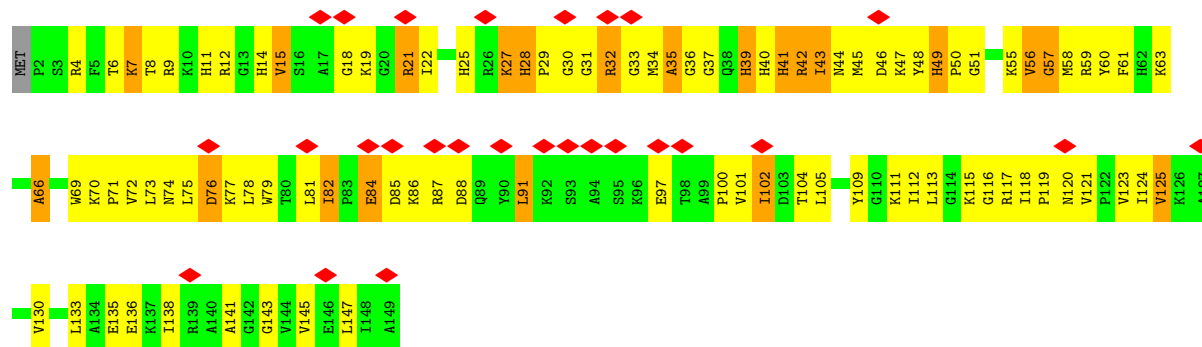




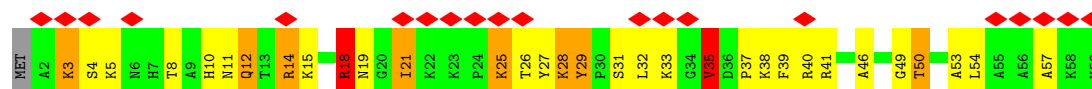
• Molecule 31: eL27 (yeast L27)



• Molecule 32: uL15 (yeast L28)

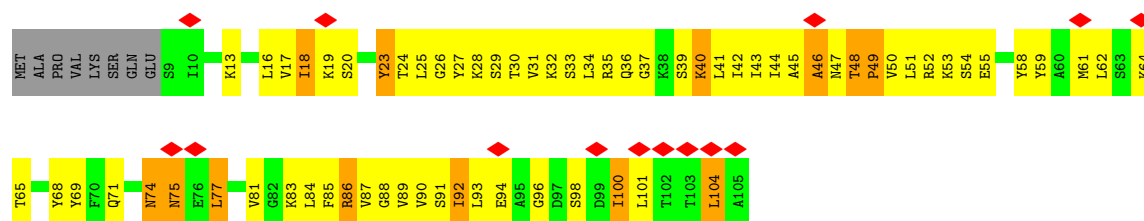


• Molecule 33: eL29 (yeast L29)

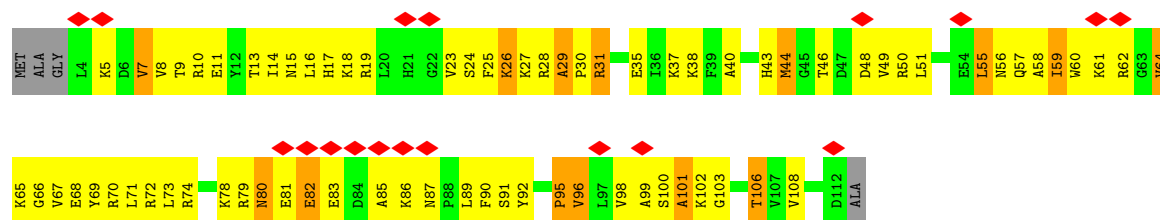


• Molecule 34: eL30 (yeast L30)

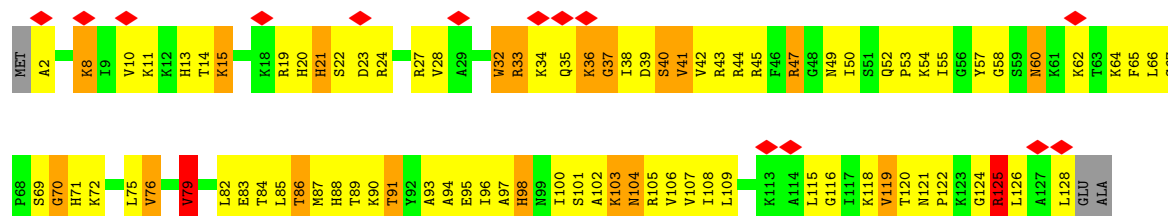




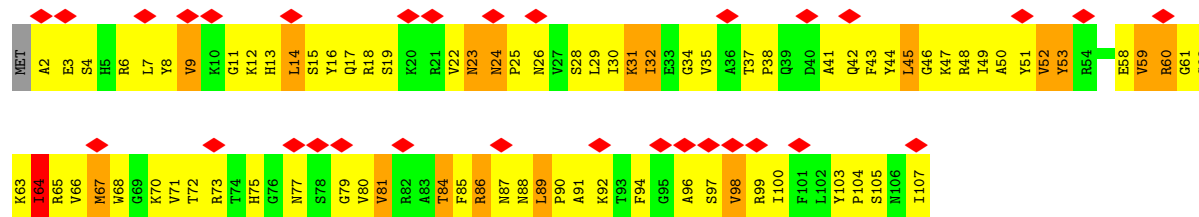
• Molecule 35: eL31 (yeast L31)



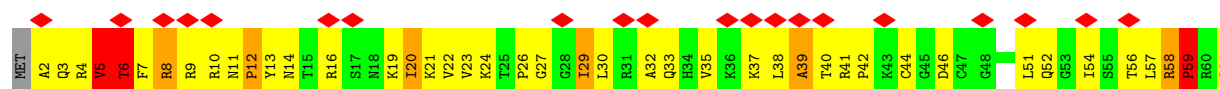
• Molecule 36: eL32 (yeast L32)

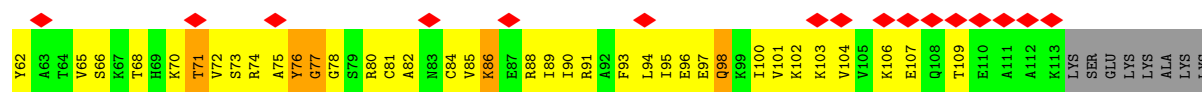


• Molecule 37: eL33 (yeast L33)

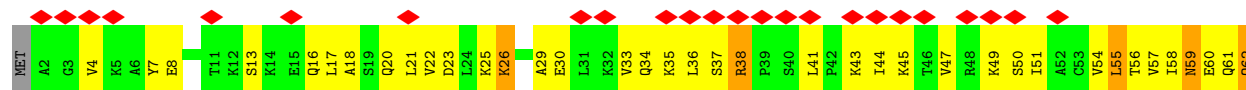


• Molecule 38: eL34 (yeast L34)





• Molecule 39: uL29 (yeast L35)



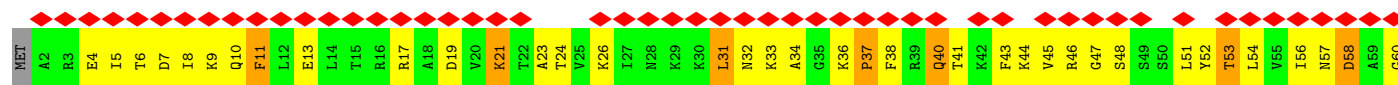
• Molecule 40: eL36 (yeast L36)



• Molecule 41: eL37 (yeast L37)

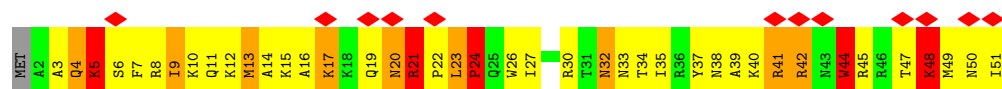
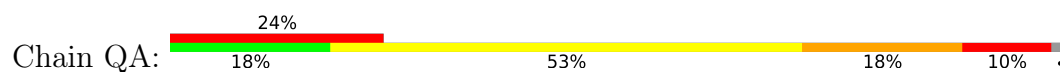


• Molecule 42: eL38 (yeast L38)

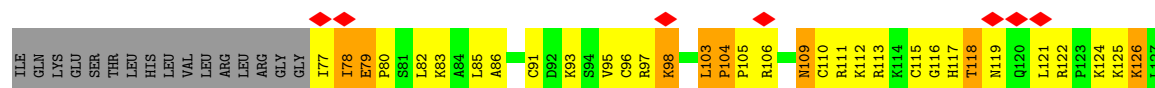
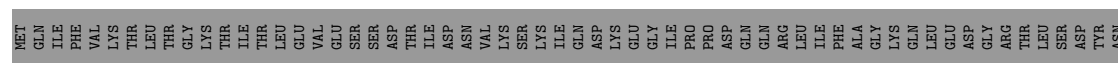
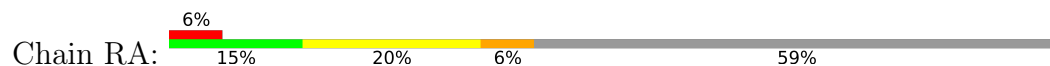


• Molecule 43: eL39 (yeast L39)

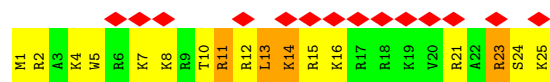




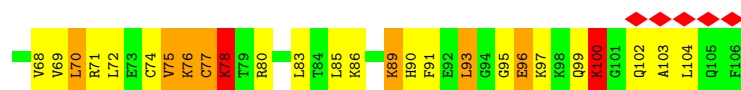
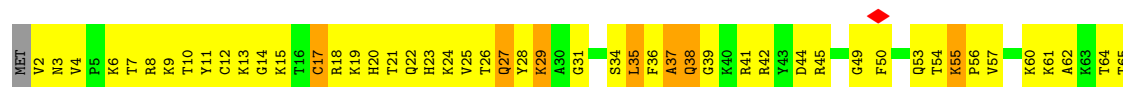
• Molecule 44: eL40 (yeast L40)



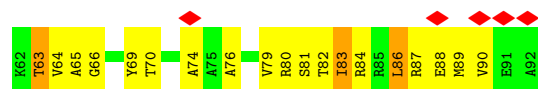
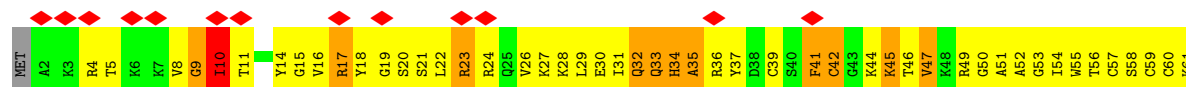
• Molecule 45: eL41 (yeast L41)



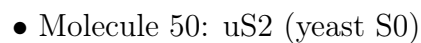
• Molecule 46: eL42 (yeast L42)

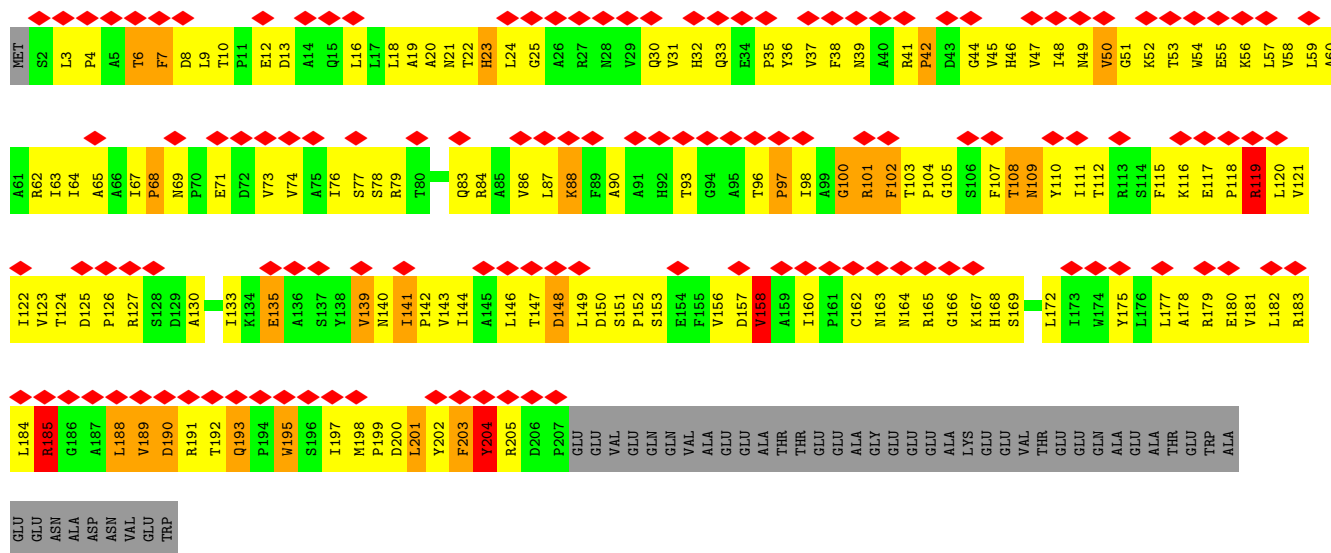


• Molecule 47: eL43 (yeast L43)

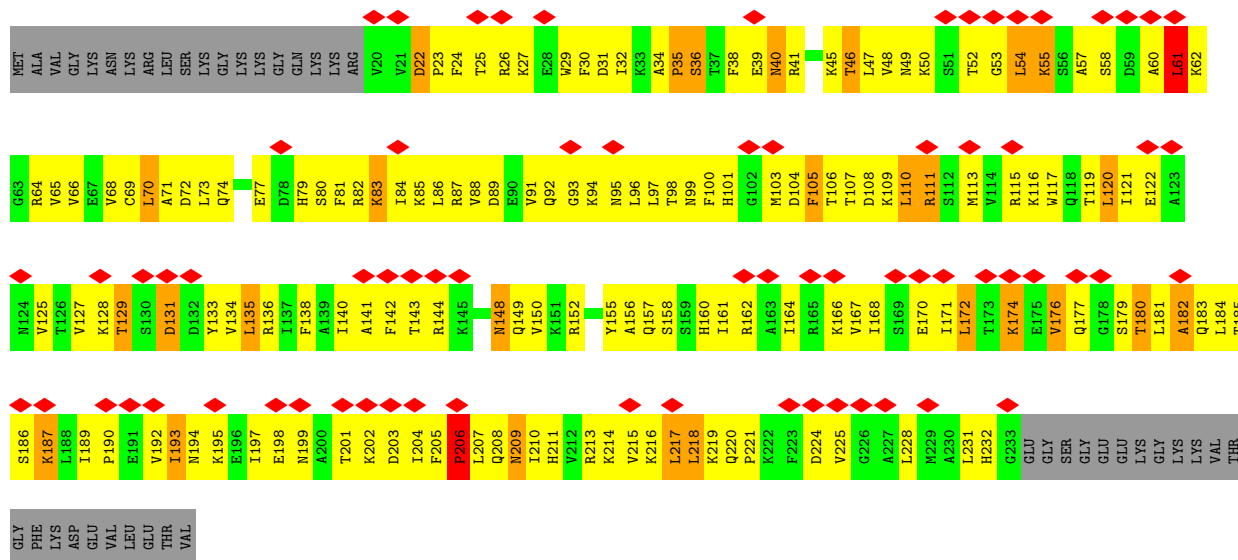


• Molecule 48: uL10 (yeast P0)

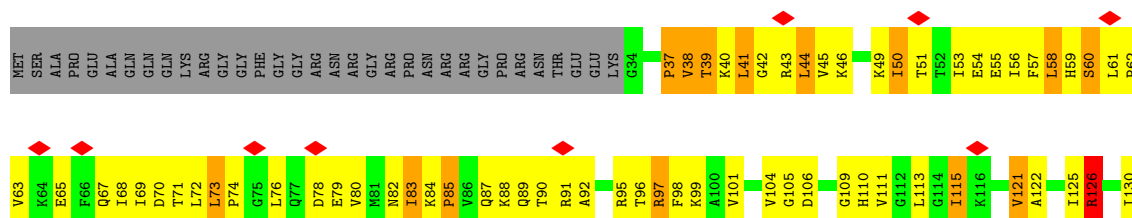


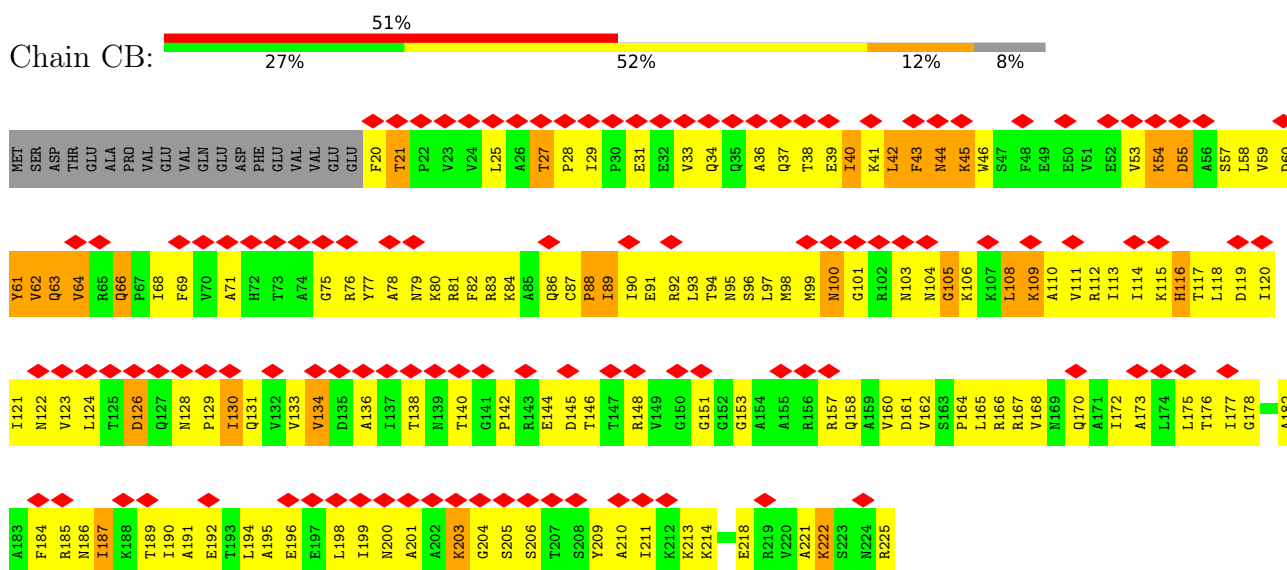


• Molecule 51: eS1 (yeast S1)

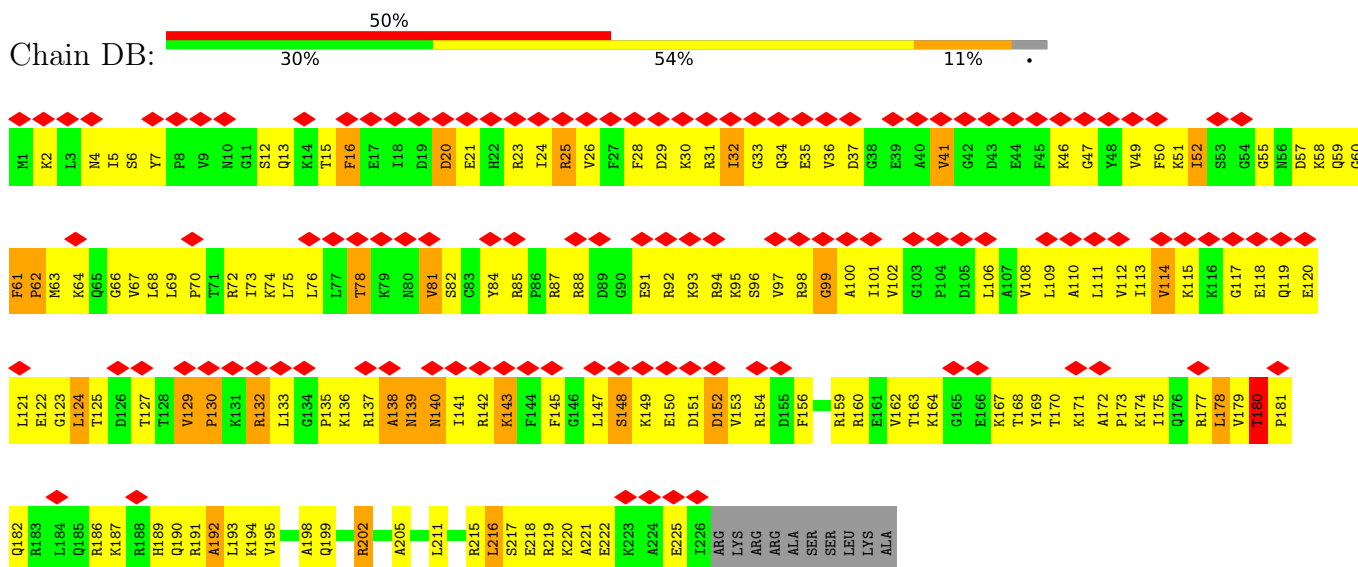


• Molecule 52: uS5 (yeast S2)

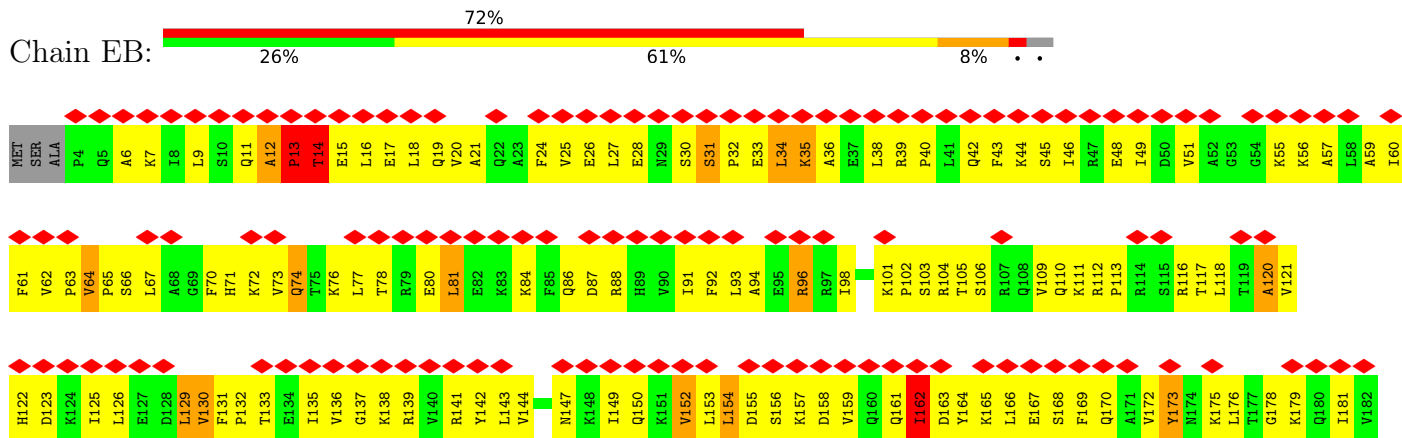


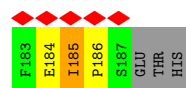


• Molecule 56: eS6 (yeast S6)

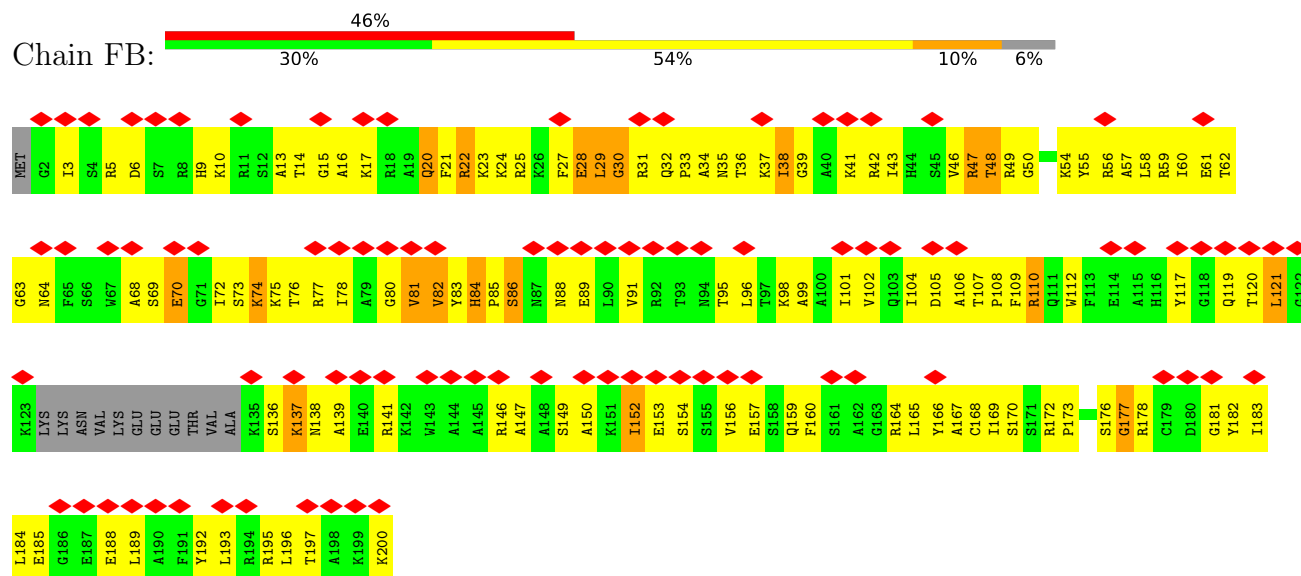


• Molecule 57: eS7 (yeast S7)

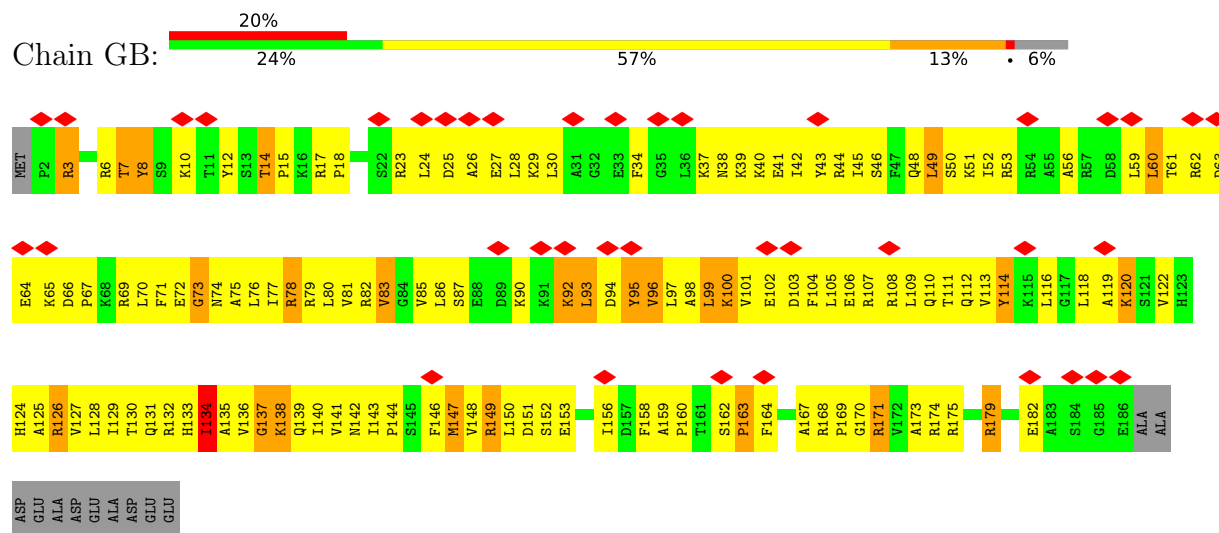




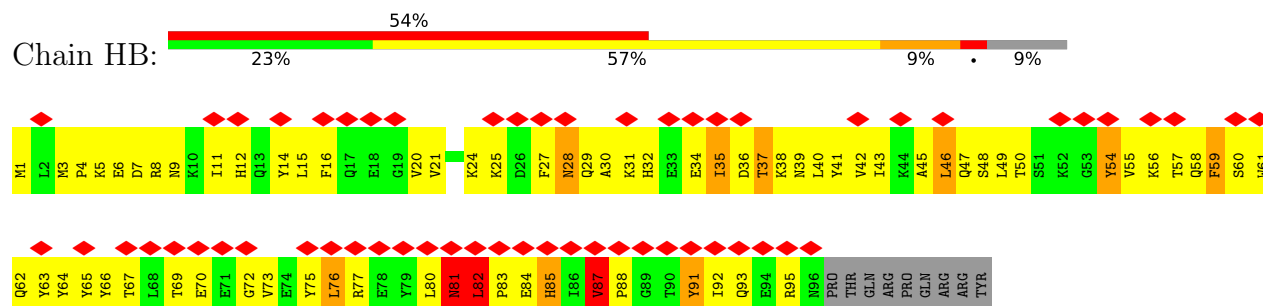
• Molecule 58: eS8 (yeast S8)

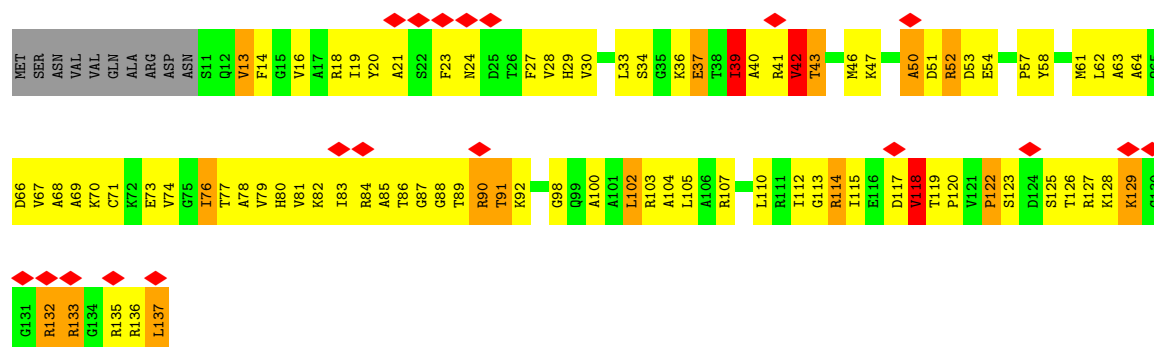


• Molecule 59: uS4 (yeast S9)

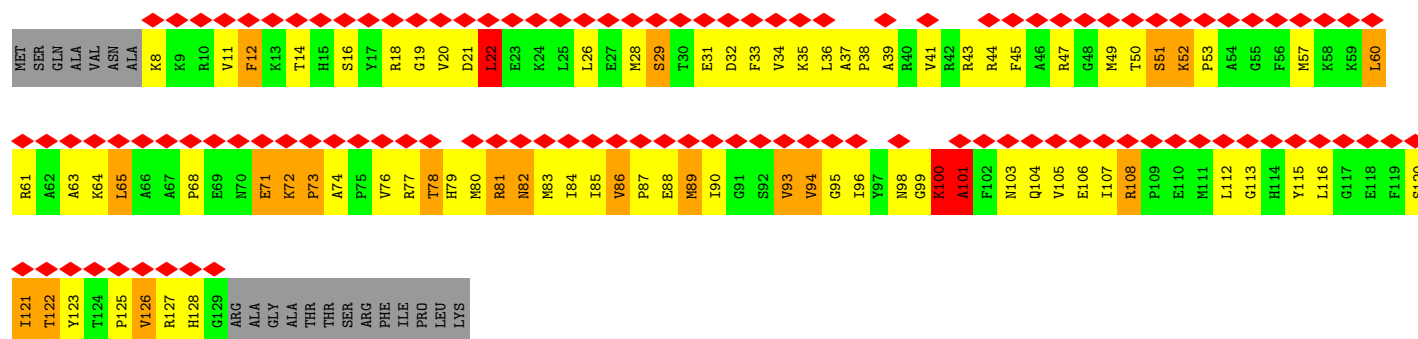
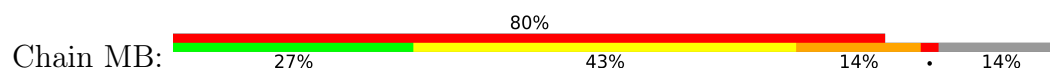


• Molecule 60: eS10 (yeast S10)





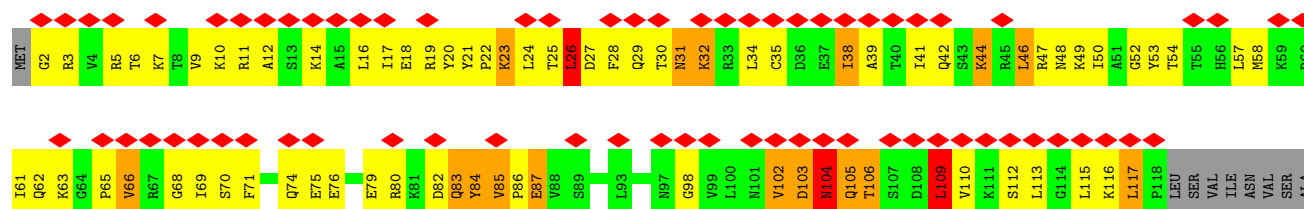
• Molecule 65: uS19 (yeast S15)



• Molecule 66: uS9 (yeast S16)



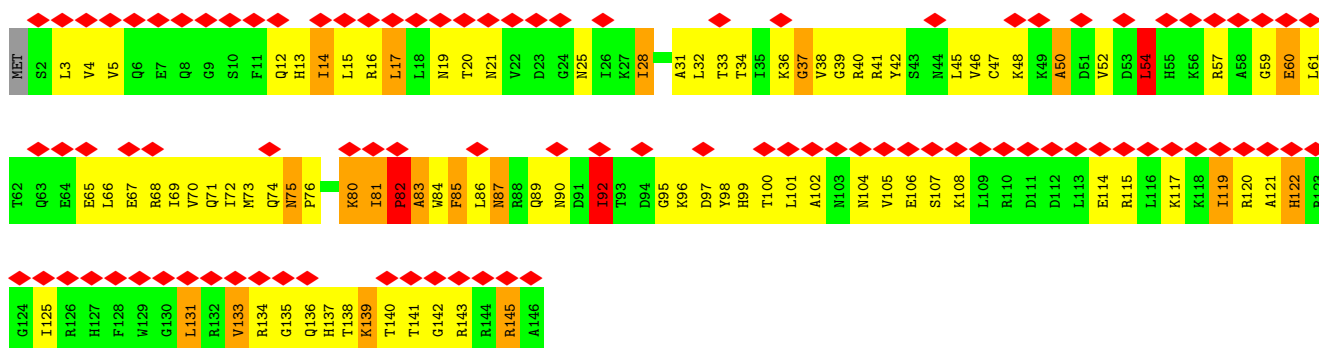
• Molecule 67: eS17 (yeast S17)



GLN
ARG
ASP
ARG
ARG
TYR
ARG
LYS
VAL

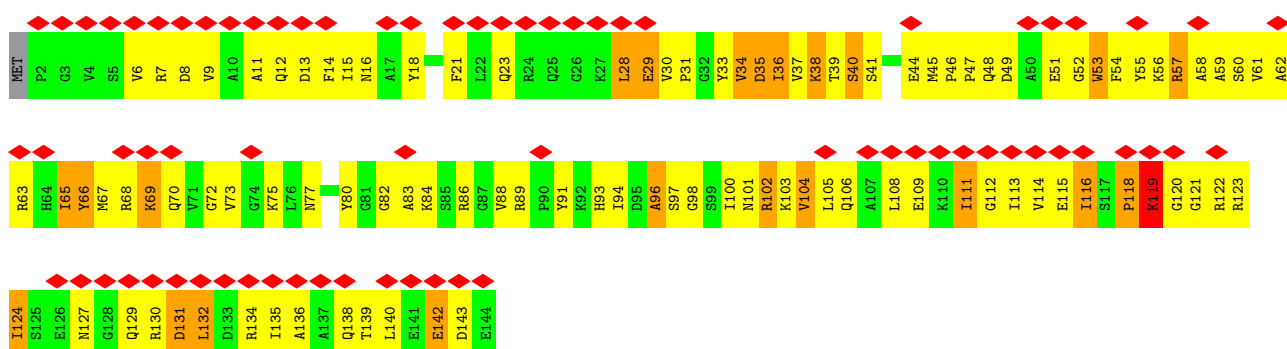
• Molecule 68: uS13 (yeast S18)

Chain PB: 

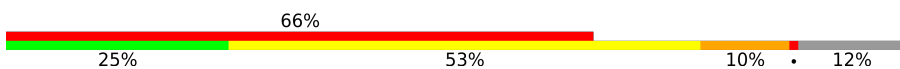


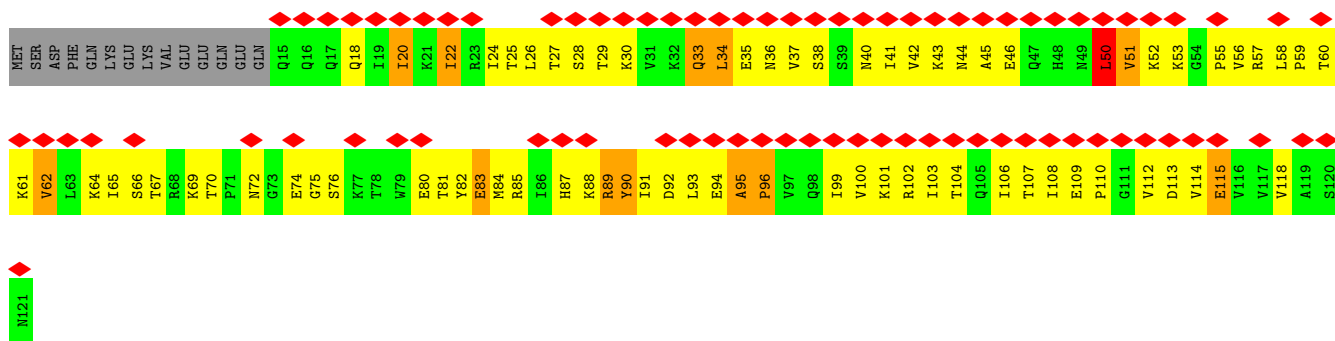
• Molecule 69: eS19 (yeast S19)

Chain QB: 



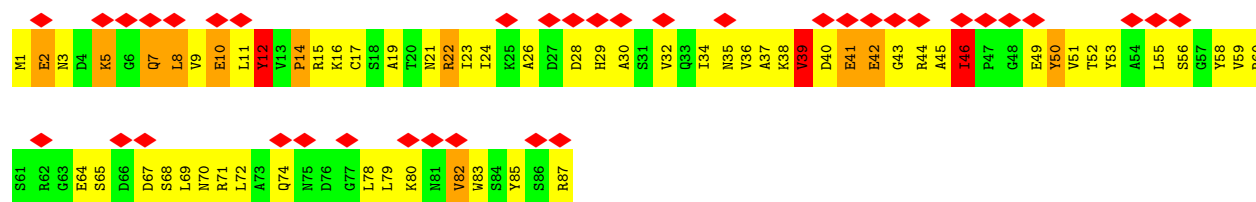
• Molecule 70: uS10 (yeast S20)

Chain RB: 

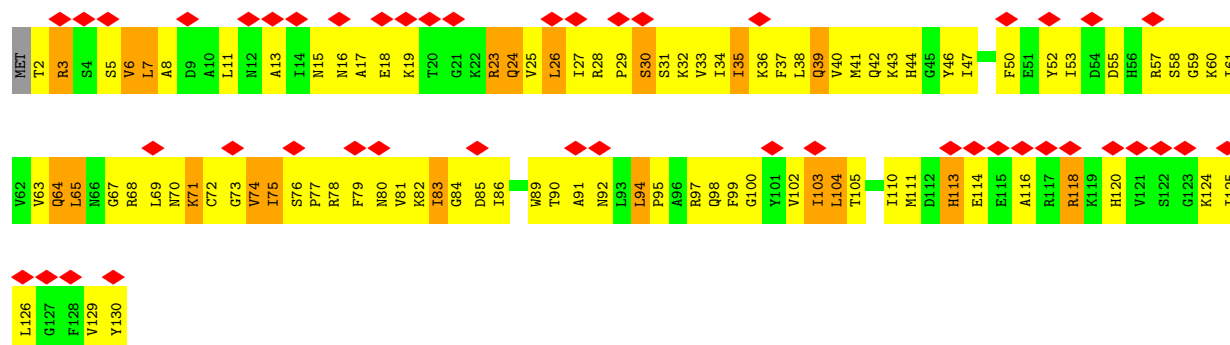


• Molecule 71: eS21 (yeast S21)

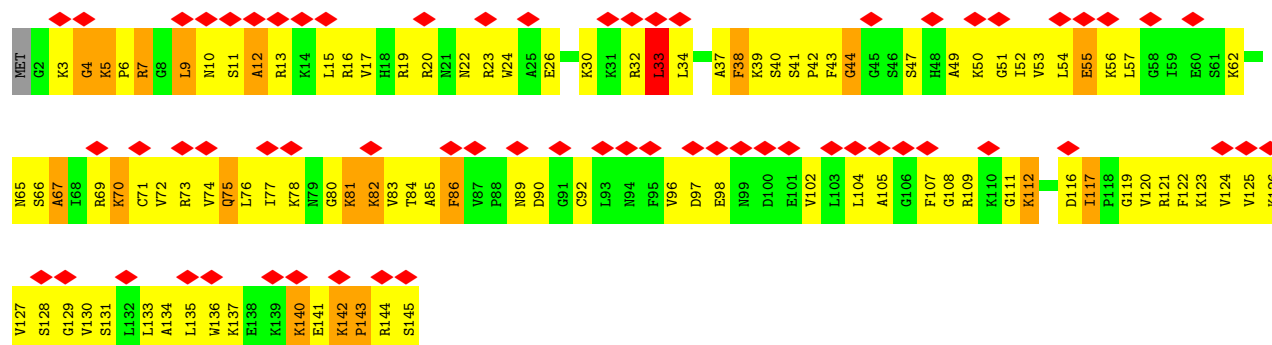
Chain SB: 



• Molecule 72: uS8 (yeast S22)



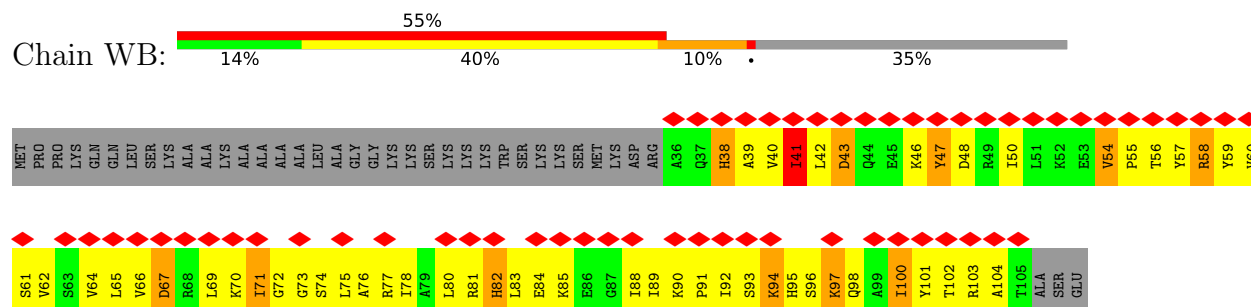
• Molecule 73: uS12 (yeast S23)



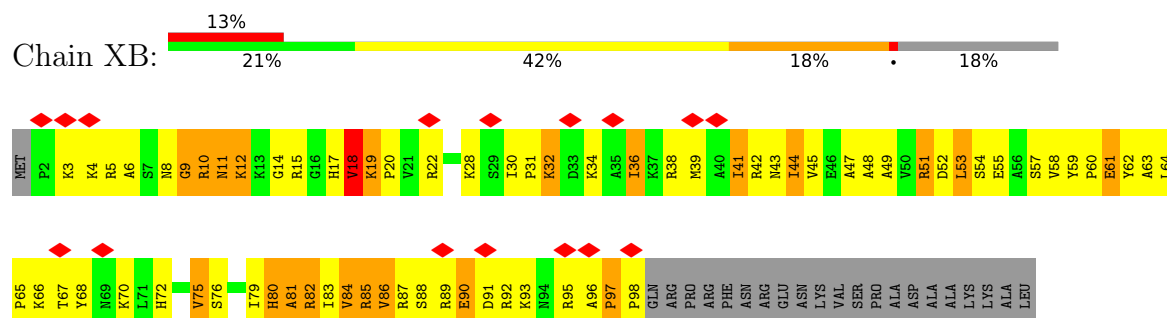
• Molecule 74: eS24 (yeast S24)



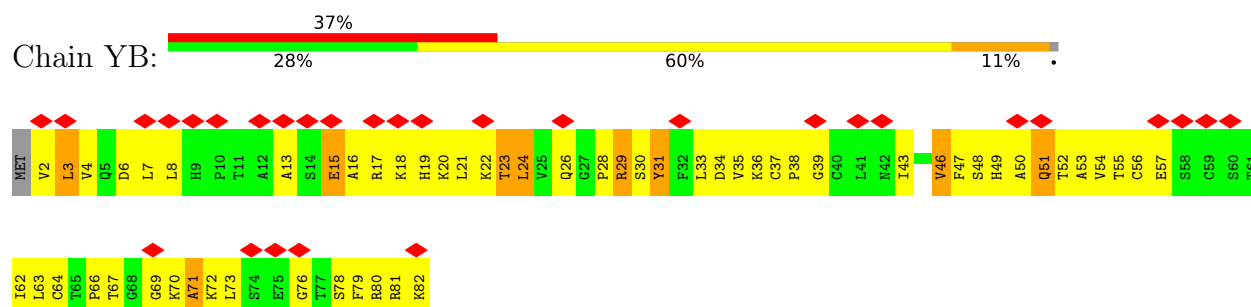
- Molecule 75: eS25 (yeast S25)



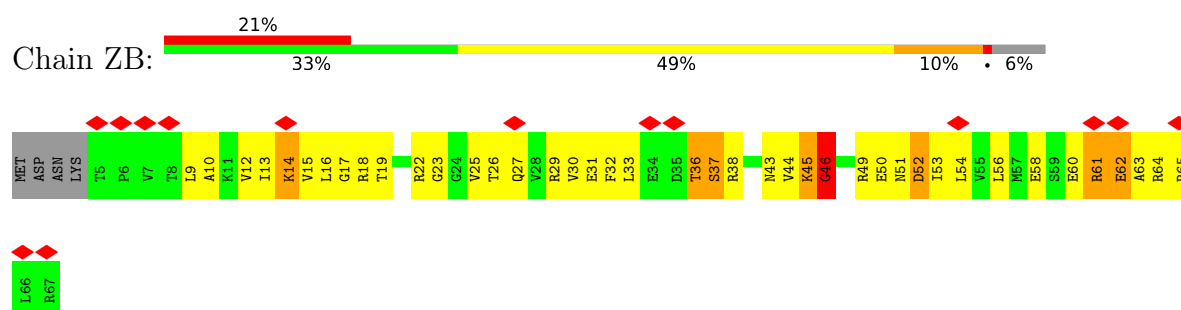
- Molecule 76: eS26 (yeast S26)



- Molecule 77: eS27 (yeast S27)



- Molecule 78: eS28 (yeast S28)

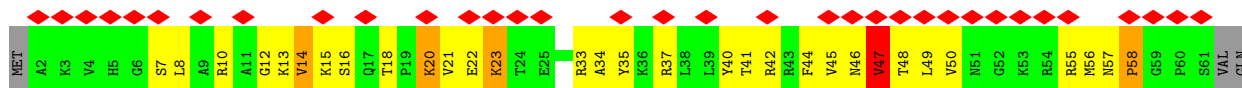


- Molecule 79: uS14 (yeast S29)

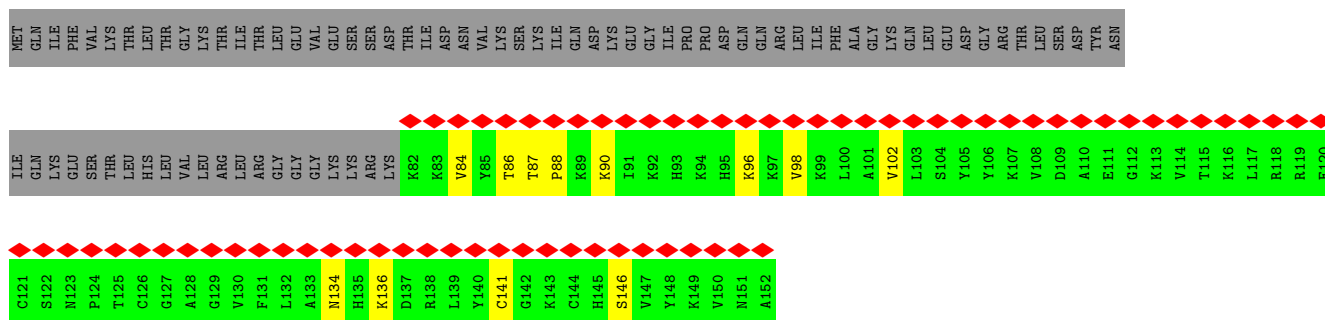
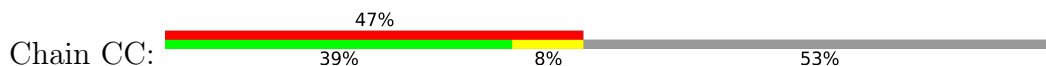




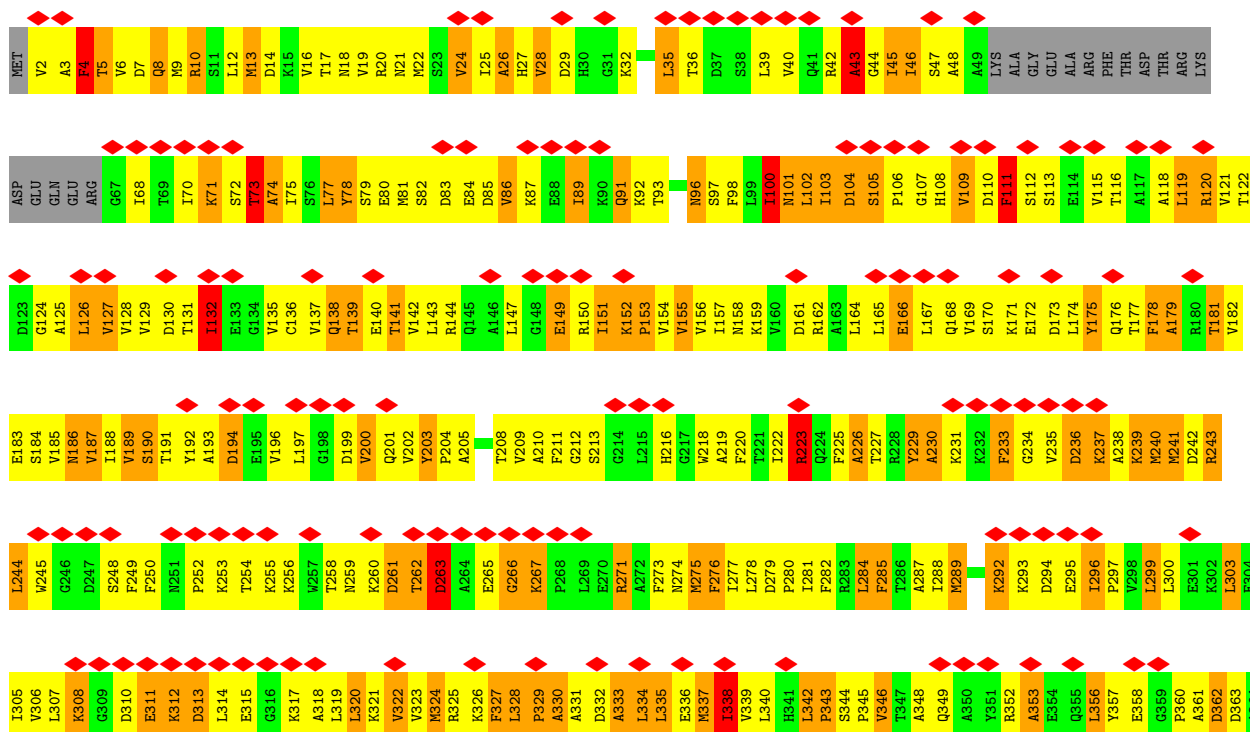
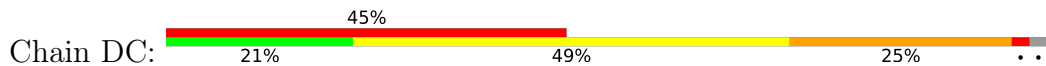
• Molecule 80: eS30 (yeast S30)

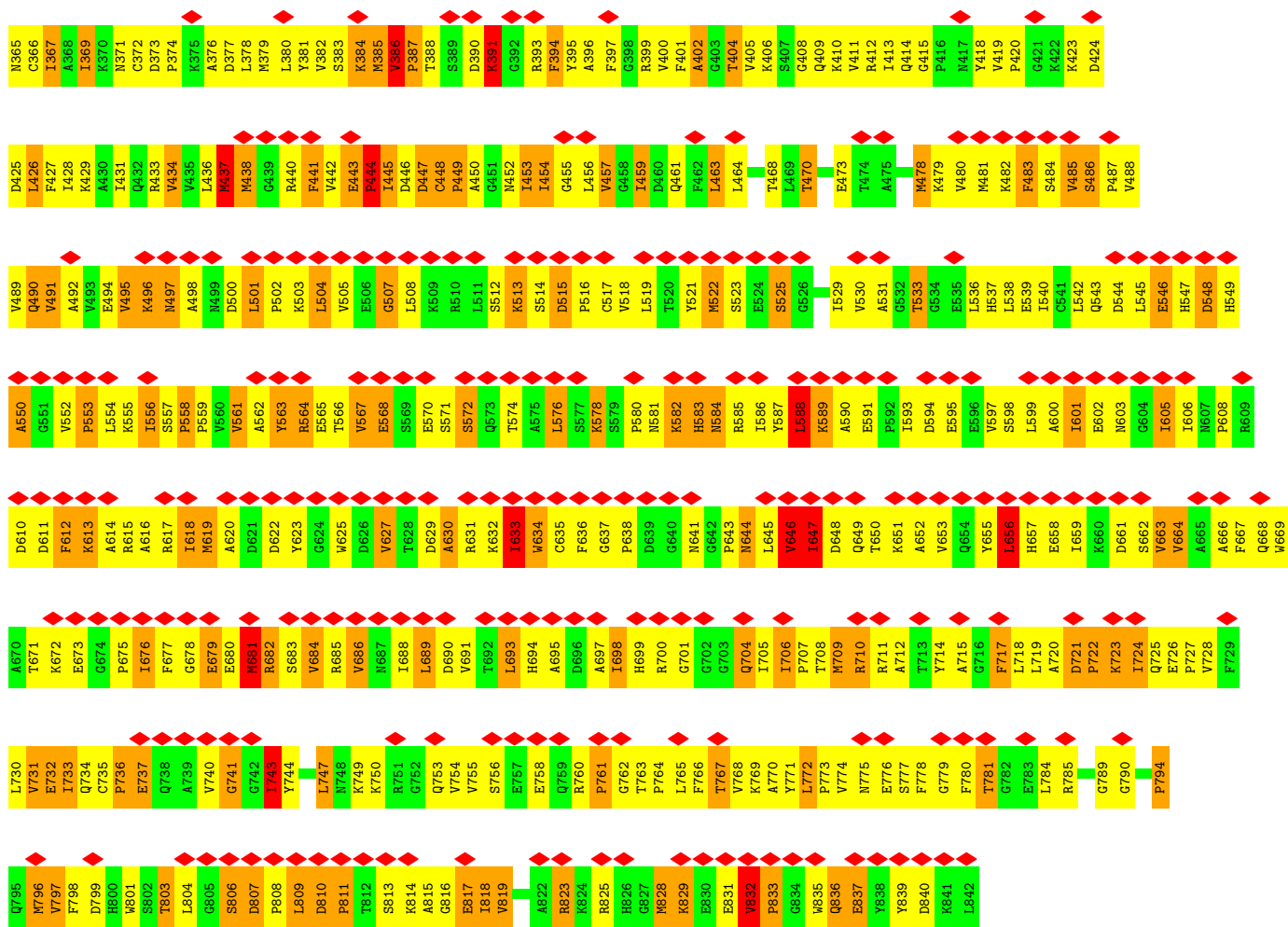


• Molecule 81: eS31 (yeast S31)

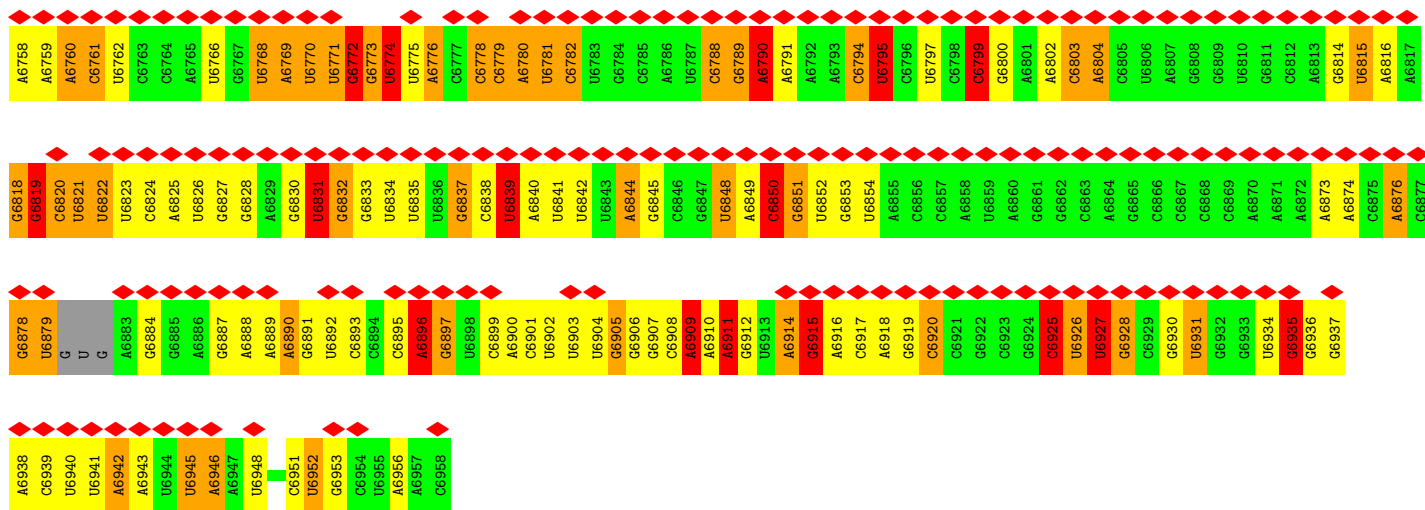
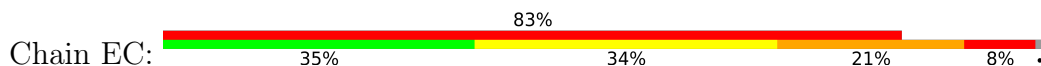


• Molecule 82: yeast eEF2





• Molecule 83: IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35045	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.067	Depositor
Minimum map value	-0.025	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	419.84, 419.84, 419.84	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.68	0/42096	0.65	36/65570 (0.1%)
2	B	0.84	0/78587	0.69	62/122484 (0.1%)
3	C	0.85	0/3747	0.68	2/5832 (0.0%)
4	D	0.81	0/2884	0.65	1/4491 (0.0%)
5	E	2.87	143/1377 (10.4%)	1.25	12/1844 (0.7%)
6	F	1.54	20/1952 (1.0%)	1.00	12/2622 (0.5%)
7	G	1.41	6/3153 (0.2%)	0.94	9/4239 (0.2%)
8	H	1.62	25/2802 (0.9%)	1.10	24/3792 (0.6%)
9	I	1.29	3/2426 (0.1%)	1.02	14/3271 (0.4%)
10	J	1.57	13/1425 (0.9%)	1.08	9/1912 (0.5%)
11	K	1.53	8/1822 (0.4%)	1.05	8/2451 (0.3%)
12	L	1.40	8/1850 (0.4%)	1.07	13/2495 (0.5%)
13	M	1.55	8/1540 (0.5%)	0.97	4/2073 (0.2%)
14	N	1.49	7/1754 (0.4%)	0.97	8/2350 (0.3%)
15	O	1.26	0/1375	0.97	3/1842 (0.2%)
16	P	2.87	81/728 (11.1%)	1.27	8/975 (0.8%)
17	Q	1.45	7/1568 (0.4%)	1.16	15/2106 (0.7%)
18	R	1.71	10/1069 (0.9%)	1.09	5/1438 (0.3%)
19	S	1.52	12/1758 (0.7%)	1.08	14/2354 (0.6%)
20	T	1.55	14/1586 (0.9%)	1.06	7/2128 (0.3%)
21	U	1.57	9/1466 (0.6%)	1.05	10/1968 (0.5%)
22	V	1.57	9/1466 (0.6%)	1.02	6/1965 (0.3%)
23	W	1.33	1/1539 (0.1%)	1.13	11/2050 (0.5%)
24	X	1.64	13/1482 (0.9%)	1.02	5/1990 (0.3%)
25	Y	1.66	11/1301 (0.8%)	1.00	4/1743 (0.2%)
26	Z	1.17	0/812	0.93	5/1099 (0.5%)
27	AA	1.51	5/1019 (0.5%)	0.99	3/1369 (0.2%)
28	BA	1.55	3/521 (0.6%)	1.03	3/691 (0.4%)
29	CA	1.53	2/984 (0.2%)	1.00	5/1325 (0.4%)
30	DA	1.60	8/1005 (0.8%)	1.06	8/1341 (0.6%)
31	EA	1.21	1/1119 (0.1%)	0.90	1/1497 (0.1%)
32	FA	1.46	8/1205 (0.7%)	1.00	6/1612 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	GA	1.49	3/474 (0.6%)	1.10	3/629 (0.5%)
34	HA	1.23	0/751	1.00	2/1008 (0.2%)
35	IA	1.35	2/904 (0.2%)	0.90	2/1213 (0.2%)
36	JA	1.66	11/1041 (1.1%)	0.95	1/1394 (0.1%)
37	KA	1.50	7/869 (0.8%)	1.02	3/1168 (0.3%)
38	LA	1.44	4/891 (0.4%)	1.01	3/1191 (0.3%)
39	MA	1.50	8/979 (0.8%)	1.05	3/1301 (0.2%)
40	NA	1.38	1/779 (0.1%)	1.12	5/1034 (0.5%)
41	OA	1.68	8/697 (1.1%)	0.97	0/923
42	PA	1.47	3/619 (0.5%)	0.94	3/826 (0.4%)
43	QA	1.68	7/444 (1.6%)	1.17	5/588 (0.9%)
44	RA	1.65	3/424 (0.7%)	0.99	2/562 (0.4%)
45	SA	1.38	0/235	1.02	1/300 (0.3%)
46	TA	1.46	5/861 (0.6%)	0.90	3/1136 (0.3%)
47	UA	1.47	3/702 (0.4%)	0.97	1/934 (0.1%)
48	VA	2.47	110/1498 (7.3%)	1.31	20/2025 (1.0%)
49	WA	1.30	3/2498 (0.1%)	0.82	6/3398 (0.2%)
50	XA	1.02	1/1653 (0.1%)	1.03	10/2261 (0.4%)
51	YA	1.12	1/1735 (0.1%)	0.87	2/2335 (0.1%)
52	ZA	1.14	1/1665 (0.1%)	0.92	2/2263 (0.1%)
53	AB	1.28	3/1759 (0.2%)	0.92	2/2368 (0.1%)
54	BB	1.09	1/2110 (0.0%)	0.95	10/2839 (0.4%)
55	CB	1.15	0/1630	1.04	13/2202 (0.6%)
56	DB	1.12	0/1844	1.01	12/2464 (0.5%)
57	EB	1.24	1/1506 (0.1%)	0.98	4/2028 (0.2%)
58	FB	1.25	2/1515 (0.1%)	0.92	3/2021 (0.1%)
59	GB	1.02	0/1519	0.99	4/2035 (0.2%)
60	HB	1.39	1/837 (0.1%)	0.93	2/1131 (0.2%)
61	IB	1.35	3/1273 (0.2%)	0.90	2/1712 (0.1%)
62	JB	2.09	4/495 (0.8%)	1.16	1/617 (0.2%)
63	KB	1.21	3/1216 (0.2%)	1.09	5/1638 (0.3%)
64	LB	1.01	0/953	0.91	1/1279 (0.1%)
65	MB	1.59	9/996 (0.9%)	0.99	7/1335 (0.5%)
66	NB	1.21	1/1126 (0.1%)	0.97	5/1510 (0.3%)
67	OB	1.16	0/844	1.16	6/1120 (0.5%)
68	PB	1.31	2/1212 (0.2%)	0.98	5/1628 (0.3%)
69	QB	1.20	0/1131	0.99	3/1517 (0.2%)
70	RB	1.40	3/866 (0.3%)	0.91	3/1169 (0.3%)
71	SB	1.08	0/694	0.86	2/935 (0.2%)
72	TB	1.08	0/1039	0.93	4/1395 (0.3%)
73	UB	1.26	1/1140 (0.1%)	0.97	6/1518 (0.4%)
74	VB	1.06	0/1088	0.99	7/1449 (0.5%)
75	WB	1.29	2/571 (0.4%)	0.99	5/768 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	XB	1.12	1/782 (0.1%)	0.98	7/1047 (0.7%)
77	YB	1.15	0/621	0.90	3/838 (0.4%)
78	ZB	1.22	1/500 (0.2%)	0.81	2/670 (0.3%)
79	AC	1.32	0/454	0.82	0/602
80	BC	1.30	0/483	0.82	0/643
81	CC	1.97	1/283 (0.4%)	1.15	0/352
82	DC	2.04	204/6521 (3.1%)	1.10	49/8830 (0.6%)
83	EC	1.48	0/4413	0.97	29/6849 (0.4%)
All	All	1.17	859/230558 (0.4%)	0.83	612/337917 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	19
2	B	0	65
3	C	0	4
4	D	0	1
83	EC	0	8
All	All	0	97

The worst 5 of 859 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	123	LEU	CA-C	21.89	1.64	1.52
5	E	70	ASP	CA-C	18.87	1.61	1.52
16	P	74	VAL	CA-C	11.37	1.61	1.53
5	E	26	ARG	CA-C	11.12	1.59	1.53
16	P	74	VAL	CA-CB	10.84	1.64	1.53

The worst 5 of 612 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	XA	201	LEU	N-CA-C	-12.10	97.88	112.89
56	DB	61	PHE	CA-C-N	11.92	132.06	119.78
56	DB	61	PHE	C-N-CA	11.92	132.06	119.78
48	VA	104	ARG	N-CA-C	10.59	122.91	110.41
1	A	103	A	C2'-C3'-O3'	10.03	124.55	109.50

There are no chirality outliers.

5 of 97 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	313	U	Sidechain
1	A	322	G	Sidechain
1	A	324	U	Sidechain
1	A	330	G	Sidechain
1	A	396	G	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	37658	0	18908	1742	0
2	B	70248	0	35241	3746	0
3	C	3354	0	1695	183	0
4	D	2580	0	1304	123	0
5	E	1359	0	1425	119	0
6	F	1918	0	1987	286	0
7	G	3082	0	3165	377	0
8	H	2750	0	2863	364	0
9	I	2376	0	2325	276	0
10	J	1401	0	1501	162	0
11	K	1785	0	1862	241	0
12	L	1818	0	1908	209	0
13	M	1519	0	1587	163	0
14	N	1718	0	1754	173	0
15	O	1354	0	1383	188	0
16	P	723	0	774	107	0
17	Q	1543	0	1608	192	0
18	R	1054	0	1149	176	0
19	S	1721	0	1779	251	0
20	T	1556	0	1659	156	0
21	U	1443	0	1485	171	0
22	V	1442	0	1543	209	0
23	W	1522	0	1617	167	0
24	X	1446	0	1487	183	0
25	Y	1277	0	1323	158	0
26	Z	796	0	812	63	0
27	AA	1004	0	1048	123	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	BA	509	0	537	54	0
29	CA	969	0	1036	138	0
30	DA	994	0	1081	130	0
31	EA	1093	0	1155	141	0
32	FA	1174	0	1215	134	0
33	GA	463	0	491	42	0
34	HA	743	0	797	92	0
35	IA	890	0	938	88	0
36	JA	1020	0	1090	96	0
37	KA	851	0	880	123	0
38	LA	881	0	949	132	0
39	MA	970	0	1078	121	0
40	NA	772	0	849	110	0
41	OA	682	0	687	85	0
42	PA	613	0	682	53	0
43	QA	437	0	475	71	0
44	RA	418	0	459	42	0
45	SA	234	0	284	21	0
46	TA	848	0	918	72	0
47	UA	695	0	738	89	0
48	VA	1473	0	1514	183	0
49	WA	2445	0	2401	202	0
50	XA	1612	0	1623	183	0
51	YA	1709	0	1784	222	0
52	ZA	1635	0	1723	213	0
53	AB	1734	0	1817	172	0
54	BB	2069	0	2154	264	0
55	CB	1610	0	1675	189	0
56	DB	1820	0	1918	163	0
57	EB	1481	0	1572	156	0
58	FB	1490	0	1525	160	0
59	GB	1494	0	1573	185	0
60	HB	817	0	804	78	0
61	IB	1245	0	1314	128	0
62	JB	496	0	141	1	0
63	KB	1193	0	1255	127	0
64	LB	942	0	979	151	0
65	MB	975	0	1017	91	0
66	NB	1106	0	1166	147	0
67	OB	836	0	827	78	0
68	PB	1193	0	1222	103	0
69	QB	1113	0	1124	145	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	RB	856	0	917	99	0
71	SB	685	0	672	109	0
72	TB	1022	0	1060	137	0
73	UB	1122	0	1196	125	0
74	VB	1074	0	1132	123	0
75	WB	563	0	603	87	0
76	XB	769	0	818	111	0
77	YB	611	0	633	77	0
78	ZB	498	0	535	56	0
79	AC	444	0	436	63	0
80	BC	475	0	525	39	0
81	CC	284	0	76	0	0
82	DC	6419	0	6493	750	0
83	EC	3968	0	1973	103	0
84	DC	28	0	12	2	0
85	DC	1	0	0	0	0
86	DC	35	0	40	6	0
All	All	215045	0	159780	15109	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 40.

The worst 5 of 15109 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:509:U:H2'	2:B:510:G:H5''	1.22	1.20
56:DB:64:LYS:HE3	56:DB:81:VAL:HG21	1.24	1.19
2:B:1948:G:H5'	23:W:101:VAL:HG11	1.25	1.17
19:S:73:ARG:HE	19:S:92:LEU:HD21	1.11	1.15
18:R:21:VAL:HG12	18:R:65:LEU:HA	1.27	1.15

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	165/217 (76%)	114 (69%)	40 (24%)	11 (7%)	1	15
6	F	250/254 (98%)	165 (66%)	71 (28%)	14 (6%)	1	17
7	G	384/387 (99%)	277 (72%)	79 (21%)	28 (7%)	1	13
8	H	359/362 (99%)	253 (70%)	76 (21%)	30 (8%)	0	11
9	I	294/297 (99%)	221 (75%)	57 (19%)	16 (5%)	1	18
10	J	173/176 (98%)	117 (68%)	40 (23%)	16 (9%)	0	10
11	K	220/244 (90%)	173 (79%)	30 (14%)	17 (8%)	1	12
12	L	231/256 (90%)	165 (71%)	43 (19%)	23 (10%)	0	8
13	M	189/191 (99%)	146 (77%)	37 (20%)	6 (3%)	3	25
14	N	207/221 (94%)	157 (76%)	42 (20%)	8 (4%)	2	22
15	O	167/174 (96%)	125 (75%)	28 (17%)	14 (8%)	0	11
16	P	92/165 (56%)	63 (68%)	18 (20%)	11 (12%)	0	5
17	Q	191/199 (96%)	140 (73%)	38 (20%)	13 (7%)	1	14
18	R	134/138 (97%)	101 (75%)	24 (18%)	9 (7%)	1	15
19	S	201/204 (98%)	155 (77%)	33 (16%)	13 (6%)	1	15
20	T	195/199 (98%)	158 (81%)	30 (15%)	7 (4%)	2	23
21	U	181/184 (98%)	135 (75%)	35 (19%)	11 (6%)	1	15
22	V	183/186 (98%)	135 (74%)	34 (19%)	14 (8%)	1	12
23	W	186/189 (98%)	151 (81%)	30 (16%)	5 (3%)	4	28
24	X	170/172 (99%)	126 (74%)	25 (15%)	19 (11%)	0	6
25	Y	157/160 (98%)	102 (65%)	41 (26%)	14 (9%)	0	10
26	Z	98/121 (81%)	68 (69%)	22 (22%)	8 (8%)	0	11
27	AA	134/137 (98%)	95 (71%)	32 (24%)	7 (5%)	1	18
28	BA	59/155 (38%)	44 (75%)	8 (14%)	7 (12%)	0	5
29	CA	119/142 (84%)	90 (76%)	18 (15%)	11 (9%)	0	10
30	DA	124/127 (98%)	93 (75%)	21 (17%)	10 (8%)	1	11
31	EA	133/136 (98%)	93 (70%)	28 (21%)	12 (9%)	0	10
32	FA	146/149 (98%)	108 (74%)	31 (21%)	7 (5%)	2	19
33	GA	56/59 (95%)	45 (80%)	9 (16%)	2 (4%)	2	23
34	HA	95/105 (90%)	74 (78%)	16 (17%)	5 (5%)	1	18

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	NB	139/143 (97%)	104 (75%)	26 (19%)	9 (6%)	1	15
67	OB	115/136 (85%)	84 (73%)	21 (18%)	10 (9%)	0	10
68	PB	143/146 (98%)	109 (76%)	20 (14%)	14 (10%)	0	9
69	QB	141/144 (98%)	104 (74%)	23 (16%)	14 (10%)	0	8
70	RB	105/121 (87%)	73 (70%)	28 (27%)	4 (4%)	2	22
71	SB	85/87 (98%)	61 (72%)	14 (16%)	10 (12%)	0	5
72	TB	127/130 (98%)	93 (73%)	27 (21%)	7 (6%)	1	18
73	UB	142/145 (98%)	97 (68%)	36 (25%)	9 (6%)	1	15
74	VB	132/135 (98%)	94 (71%)	26 (20%)	12 (9%)	0	10
75	WB	68/108 (63%)	41 (60%)	21 (31%)	6 (9%)	0	10
76	XB	95/119 (80%)	52 (55%)	26 (27%)	17 (18%)	0	2
77	YB	79/82 (96%)	53 (67%)	21 (27%)	5 (6%)	1	15
78	ZB	61/67 (91%)	46 (75%)	10 (16%)	5 (8%)	0	11
79	AC	51/56 (91%)	37 (72%)	12 (24%)	2 (4%)	2	22
80	BC	58/63 (92%)	38 (66%)	15 (26%)	5 (9%)	0	10
81	CC	69/152 (45%)	41 (59%)	17 (25%)	11 (16%)	0	3
82	DC	819/842 (97%)	620 (76%)	154 (19%)	45 (6%)	1	18
All	All	12207/13416 (91%)	8881 (73%)	2429 (20%)	897 (7%)	1	13

5 of 897 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	157/198 (79%)	130 (83%)	27 (17%)	2	13
6	F	194/196 (99%)	163 (84%)	31 (16%)	2	14
7	G	322/323 (100%)	285 (88%)	37 (12%)	5	22
8	H	288/289 (100%)	260 (90%)	28 (10%)	8	27
9	I	244/245 (100%)	220 (90%)	24 (10%)	7	27
10	J	152/153 (99%)	133 (88%)	19 (12%)	4	20
11	K	186/205 (91%)	164 (88%)	22 (12%)	5	21
12	L	191/208 (92%)	172 (90%)	19 (10%)	7	27
13	M	171/171 (100%)	157 (92%)	14 (8%)	10	34
14	N	180/187 (96%)	158 (88%)	22 (12%)	5	21
15	O	147/150 (98%)	122 (83%)	25 (17%)	2	13
16	P	81/136 (60%)	66 (82%)	15 (18%)	1	11
17	Q	154/159 (97%)	132 (86%)	22 (14%)	3	17
18	R	107/109 (98%)	90 (84%)	17 (16%)	2	15
19	S	175/176 (99%)	154 (88%)	21 (12%)	5	21
20	T	160/162 (99%)	146 (91%)	14 (9%)	9	32
21	U	145/146 (99%)	124 (86%)	21 (14%)	3	16
22	V	150/151 (99%)	137 (91%)	13 (9%)	9	32
23	W	153/154 (99%)	135 (88%)	18 (12%)	5	21
24	X	156/156 (100%)	136 (87%)	20 (13%)	4	20
25	Y	136/137 (99%)	109 (80%)	27 (20%)	1	9
26	Z	87/107 (81%)	82 (94%)	5 (6%)	18	43
27	AA	104/105 (99%)	89 (86%)	15 (14%)	3	17
28	BA	54/129 (42%)	49 (91%)	5 (9%)	8	29
29	CA	105/118 (89%)	89 (85%)	16 (15%)	3	15
30	DA	109/110 (99%)	95 (87%)	14 (13%)	4	20
31	EA	115/116 (99%)	102 (89%)	13 (11%)	5	22
32	FA	118/119 (99%)	109 (92%)	9 (8%)	12	36
33	GA	46/47 (98%)	39 (85%)	7 (15%)	3	15
34	HA	81/88 (92%)	70 (86%)	11 (14%)	3	18
35	IA	96/97 (99%)	88 (92%)	8 (8%)	10	33
36	JA	109/111 (98%)	97 (89%)	12 (11%)	6	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	KA	90/91 (99%)	78 (87%)	12 (13%)	4	18
38	LA	95/103 (92%)	87 (92%)	8 (8%)	10	33
39	MA	104/105 (99%)	92 (88%)	12 (12%)	5	22
40	NA	81/82 (99%)	67 (83%)	14 (17%)	2	13
41	OA	70/71 (99%)	64 (91%)	6 (9%)	10	33
42	PA	68/69 (99%)	61 (90%)	7 (10%)	7	25
43	QA	45/46 (98%)	36 (80%)	9 (20%)	1	9
44	RA	47/116 (40%)	44 (94%)	3 (6%)	16	40
45	SA	23/23 (100%)	19 (83%)	4 (17%)	2	13
46	TA	90/91 (99%)	79 (88%)	11 (12%)	5	21
47	UA	71/72 (99%)	63 (89%)	8 (11%)	5	22
48	VA	160/254 (63%)	144 (90%)	16 (10%)	7	26
49	WA	261/262 (100%)	236 (90%)	25 (10%)	8	28
50	XA	173/210 (82%)	157 (91%)	16 (9%)	8	30
51	YA	191/224 (85%)	173 (91%)	18 (9%)	8	29
52	ZA	176/205 (86%)	163 (93%)	13 (7%)	13	36
53	AB	182/195 (93%)	162 (89%)	20 (11%)	6	23
54	BB	221/222 (100%)	193 (87%)	28 (13%)	4	20
55	CB	173/191 (91%)	161 (93%)	12 (7%)	14	39
56	DB	193/201 (96%)	178 (92%)	15 (8%)	11	35
57	EB	165/170 (97%)	157 (95%)	8 (5%)	23	46
58	FB	150/161 (93%)	139 (93%)	11 (7%)	13	37
59	GB	158/166 (95%)	142 (90%)	16 (10%)	7	26
60	HB	89/98 (91%)	81 (91%)	8 (9%)	9	31
61	IB	136/137 (99%)	122 (90%)	14 (10%)	7	25
63	KB	127/128 (99%)	116 (91%)	11 (9%)	9	32
64	LB	96/105 (91%)	81 (84%)	15 (16%)	2	15
65	MB	103/118 (87%)	96 (93%)	7 (7%)	14	39
66	NB	117/119 (98%)	110 (94%)	7 (6%)	17	42
67	OB	82/124 (66%)	67 (82%)	15 (18%)	2	12
68	PB	128/129 (99%)	113 (88%)	15 (12%)	5	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	QB	115/116 (99%)	102 (89%)	13 (11%)	5	22
70	RB	100/114 (88%)	89 (89%)	11 (11%)	6	23
71	SB	74/74 (100%)	66 (89%)	8 (11%)	6	24
72	TB	110/111 (99%)	95 (86%)	15 (14%)	3	18
73	UB	119/120 (99%)	108 (91%)	11 (9%)	8	30
74	VB	112/113 (99%)	106 (95%)	6 (5%)	20	44
75	WB	61/89 (68%)	57 (93%)	4 (7%)	15	40
76	XB	83/101 (82%)	75 (90%)	8 (10%)	8	28
77	YB	70/71 (99%)	65 (93%)	5 (7%)	13	38
78	ZB	56/60 (93%)	53 (95%)	3 (5%)	20	44
79	AC	47/49 (96%)	43 (92%)	4 (8%)	10	33
80	BC	51/54 (94%)	48 (94%)	3 (6%)	18	42
82	DC	699/714 (98%)	606 (87%)	93 (13%)	4	18
All	All	10235/11032 (93%)	9096 (89%)	1139 (11%)	8	23

5 of 1139 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
67	OB	23	LYS
68	PB	131	LEU
67	OB	16	LEU
79	AC	11	PRO
22	V	138	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 376 such sidechains are listed below:

Mol	Chain	Res	Type
52	ZA	189	GLN
66	NB	74	HIS
53	AB	159	HIS
57	EB	29	ASN
68	PB	104	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1753/1798 (97%)	358 (20%)	19 (1%)
2	B	3263/3396 (96%)	571 (17%)	29 (0%)
3	C	157/158 (99%)	25 (15%)	2 (1%)
4	D	120/121 (99%)	17 (14%)	0
83	EC	174/201 (86%)	69 (39%)	4 (2%)
All	All	5467/5674 (96%)	1040 (19%)	54 (0%)

5 of 1040 RNA backbone outliers are listed below:

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

5 of 54 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	1329	U
2	B	2501	U
3	C	85	G
2	B	1352	A
2	B	1816	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
82	DDE	DC	699	82	18,20,21	2.44	6 (33%)	17,28,30	2.47	6 (35%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	DDE	DC	699	82	-	3/20/21/23	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	7.41	1.51	1.36
82	DC	699	DDE	CBW-CBI	3.89	1.59	1.53
82	DC	699	DDE	CBW-NCB	3.18	1.60	1.54
82	DC	699	DDE	CB-CG	2.63	1.56	1.49
82	DC	699	DDE	CAT-CE1	2.43	1.53	1.49

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	DC	699	DDE	CAU-CAT-CE1	6.89	140.08	114.38
82	DC	699	DDE	CAU-CBW-CBI	-4.82	101.78	111.22
82	DC	699	DDE	CD2-NE2-CE1	2.93	110.00	107.55
82	DC	699	DDE	OAG-CBI-NAD	2.38	127.25	123.04
82	DC	699	DDE	CAC-NCB-CBW	2.32	116.07	110.52

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
82	DC	699	DDE	OAG-CBI-CBW-NCB
82	DC	699	DDE	OAG-CBI-CBW-CAU
82	DC	699	DDE	NAD-CBI-CBW-CAU

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	$\# Z > 2$
84	GDP	DC	901	85	29,30,30	2.09	6 (20%)	45,47,47	1.75	9 (20%)
86	SO1	DC	903	-	34,39,39	2.44	17 (50%)	38,64,64	2.16	11 (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
84	GDP	DC	901	85	-	0/16/32/32	0/3/3/3
86	SO1	DC	903	-	-	4/21/104/104	0/7/5/5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	DC	901	GDP	PA-O3A	6.93	1.67	1.59
86	DC	903	SO1	O56-C52	-4.37	1.30	1.41
84	DC	901	GDP	PB-O1B	4.18	1.63	1.50
86	DC	903	SO1	O17-C52	4.12	1.47	1.40
86	DC	903	SO1	C10-C6	3.89	1.61	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	DC	903	SO1	C12-C6-C10	-7.31	102.20	107.92
84	DC	901	GDP	C2-N3-C4	5.65	122.03	112.30
86	DC	903	SO1	C25-C22-C24	5.30	130.48	113.64
84	DC	901	GDP	C5-C4-N3	-4.42	121.36	128.39
86	DC	903	SO1	C10-C6-C2	4.04	108.91	104.12

There are no chirality outliers.

All (4) torsion outliers are listed below:

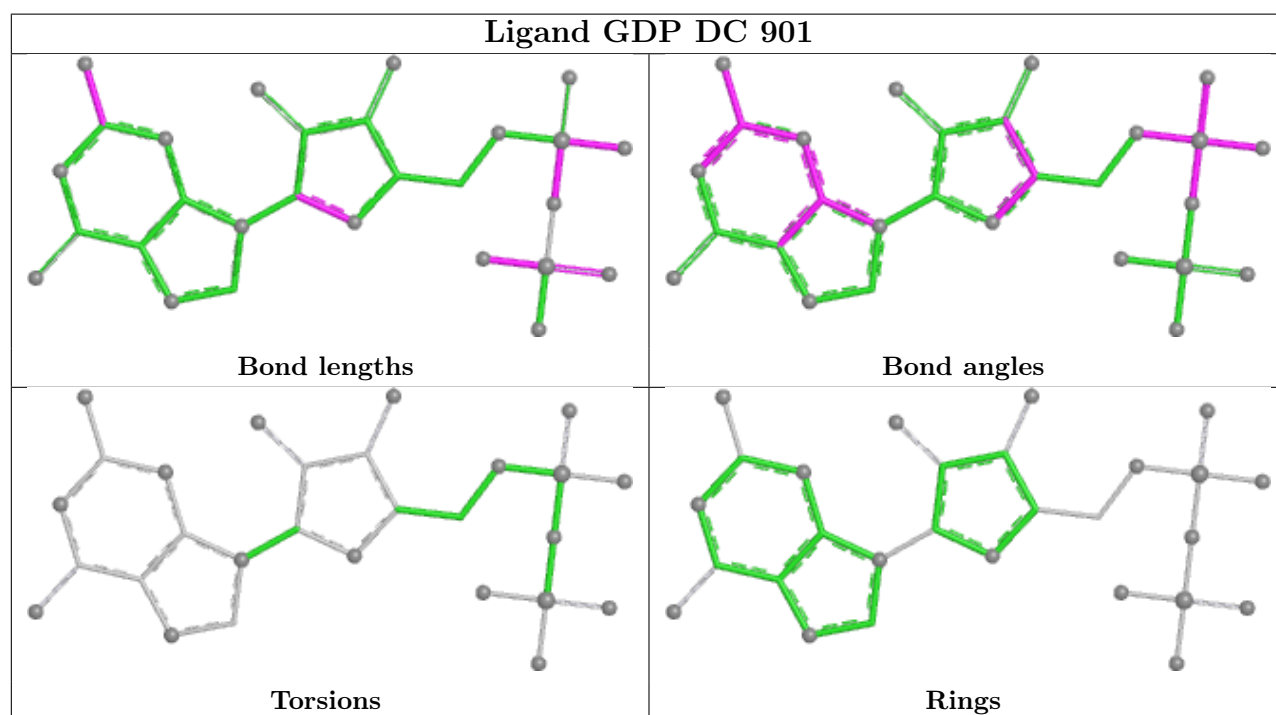
Mol	Chain	Res	Type	Atoms
86	DC	903	SO1	C3-C1-C5-O14
86	DC	903	SO1	C3-C1-C5-O15
86	DC	903	SO1	O19-C11-C3-C10
86	DC	903	SO1	O19-C11-C3-C9

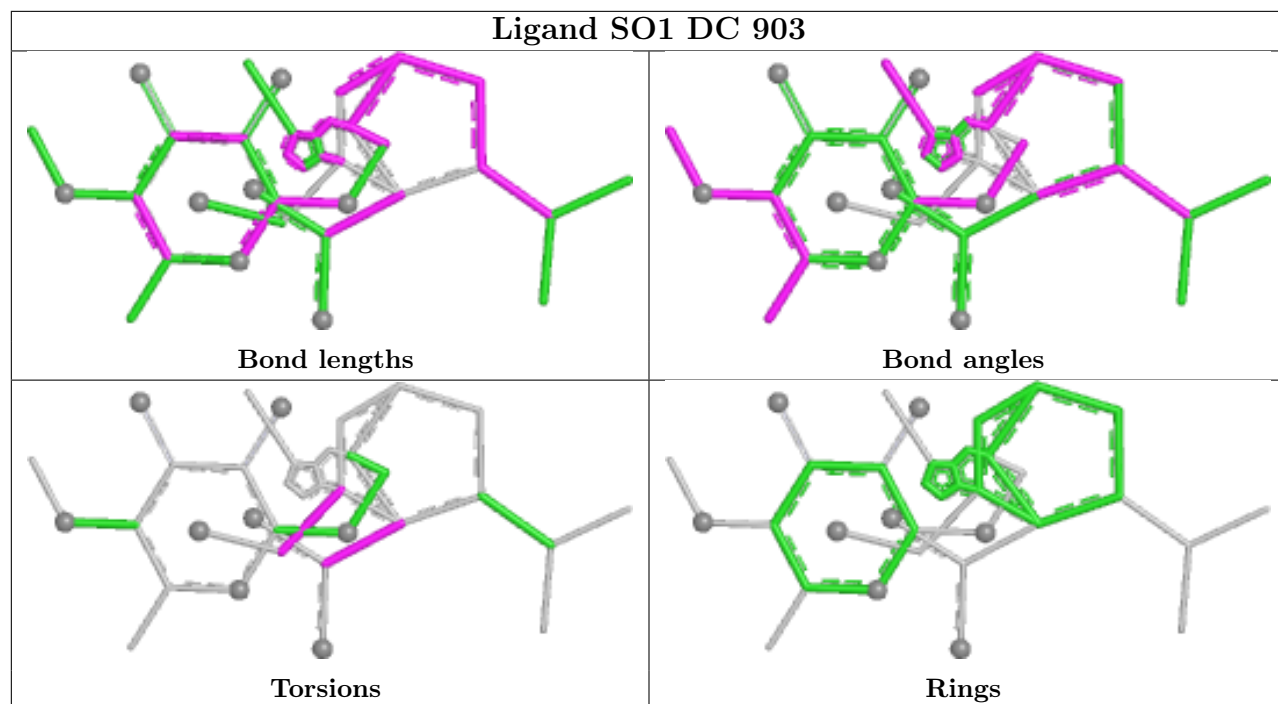
There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	DC	901	GDP	2	0
86	DC	903	SO1	6	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.

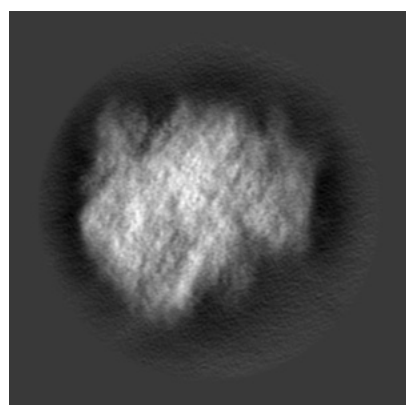
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6647. These allow visual inspection of the internal detail of the map and identification of artifacts.

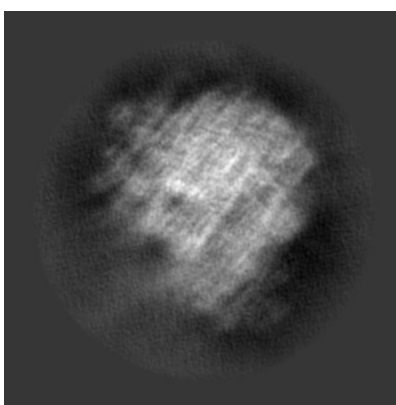
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

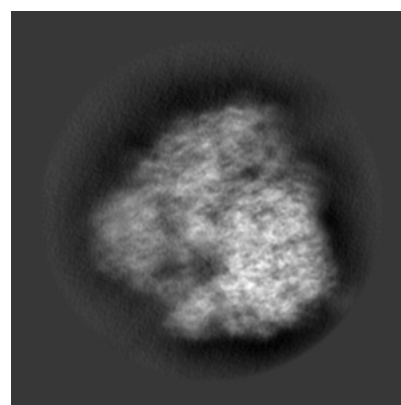
6.1.1 Primary map



X



Y

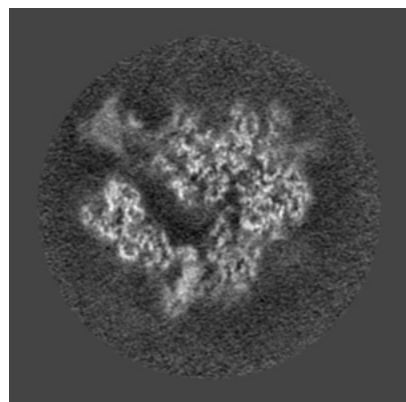


Z

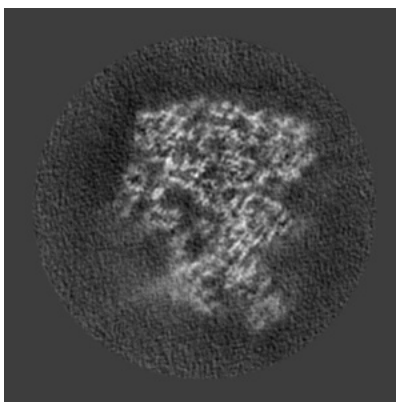
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

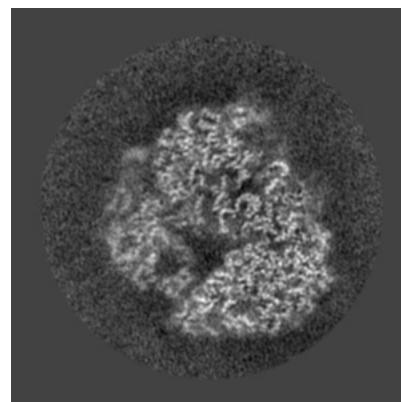
6.2.1 Primary map



X Index: 256



Y Index: 256

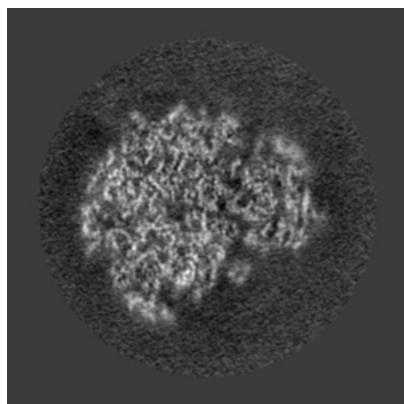


Z Index: 256

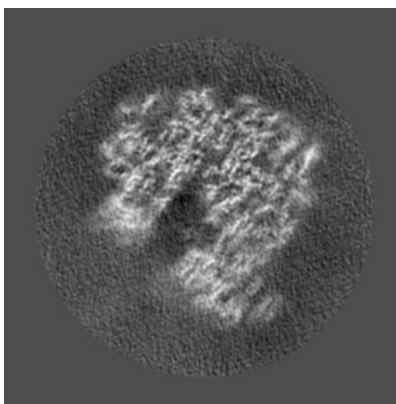
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

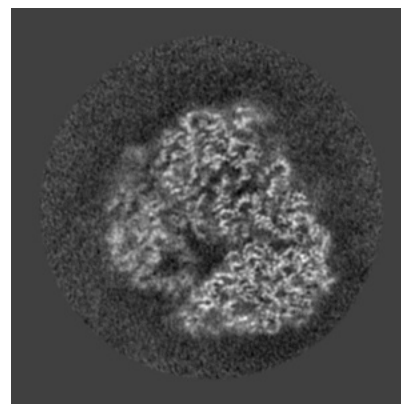
6.3.1 Primary map



X Index: 291



Y Index: 222

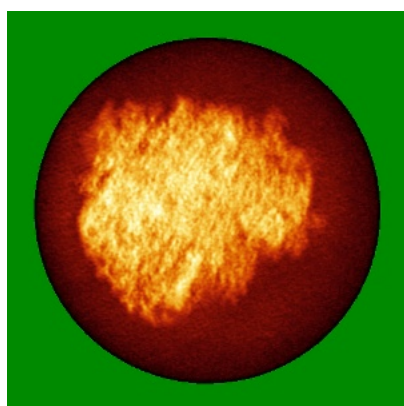


Z Index: 259

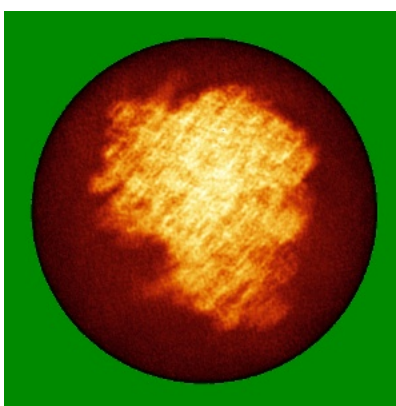
The images above show the largest variance slices of the map in three orthogonal directions.

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

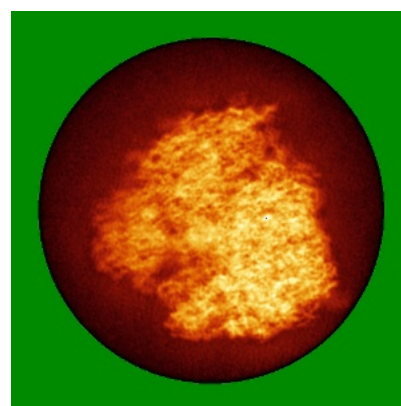
6.4.1 Primary map



X



Y

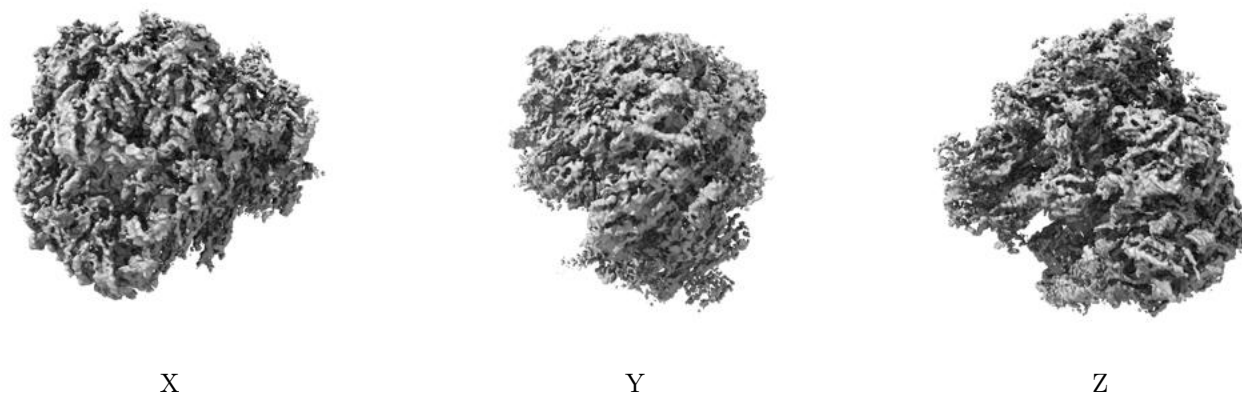


Z

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 0.017. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

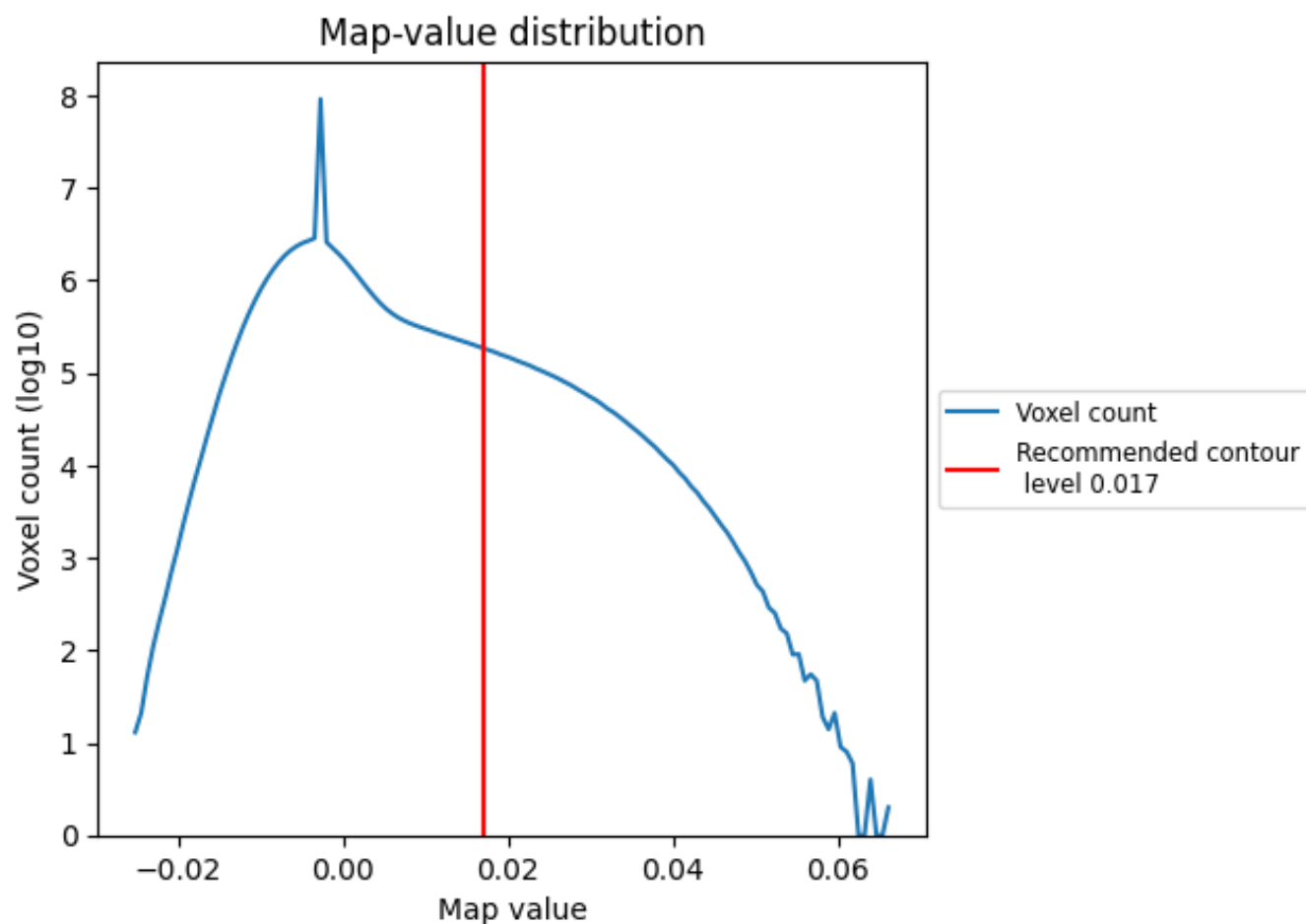
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

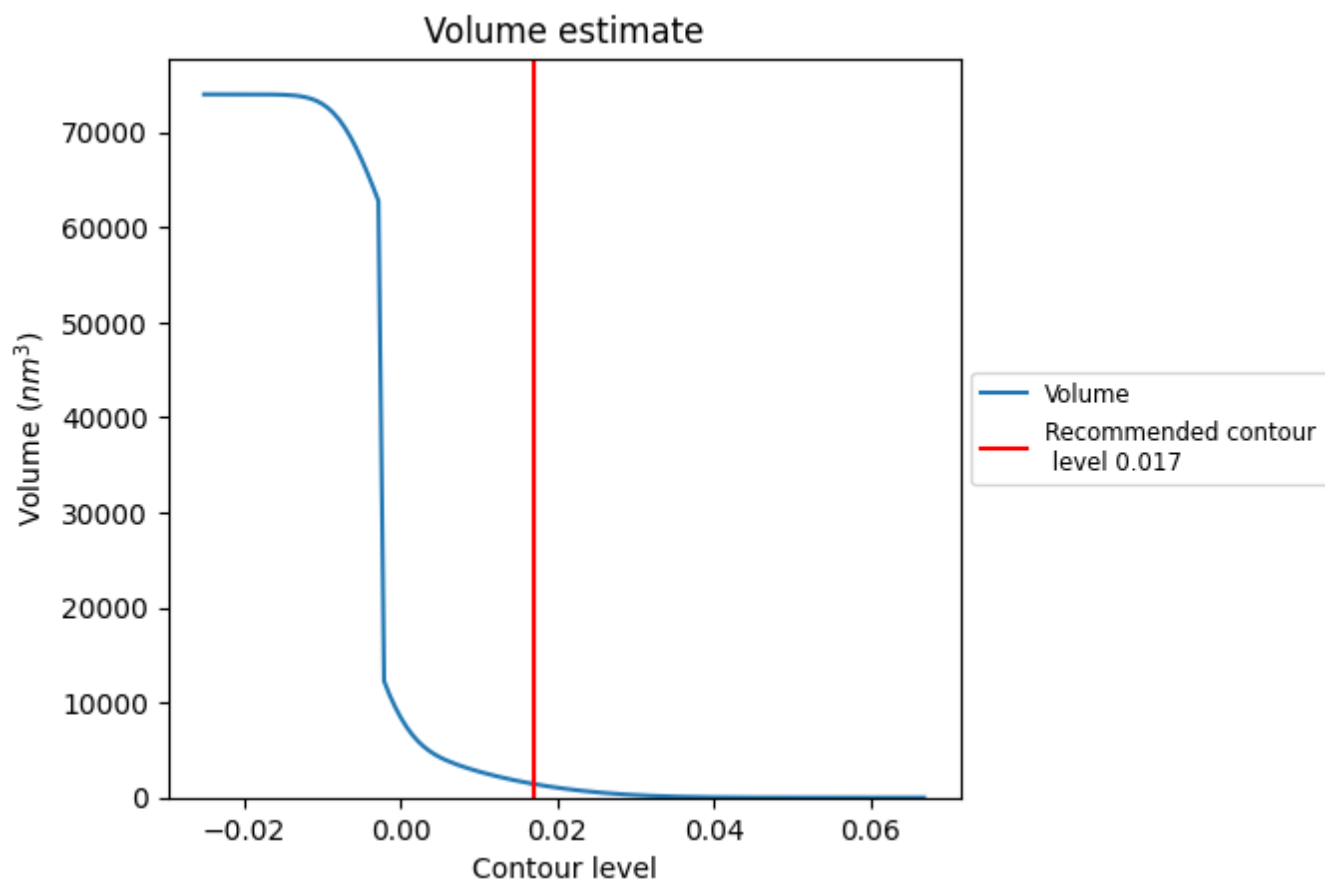
This section contains the results of statistical analysis of the map.

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.

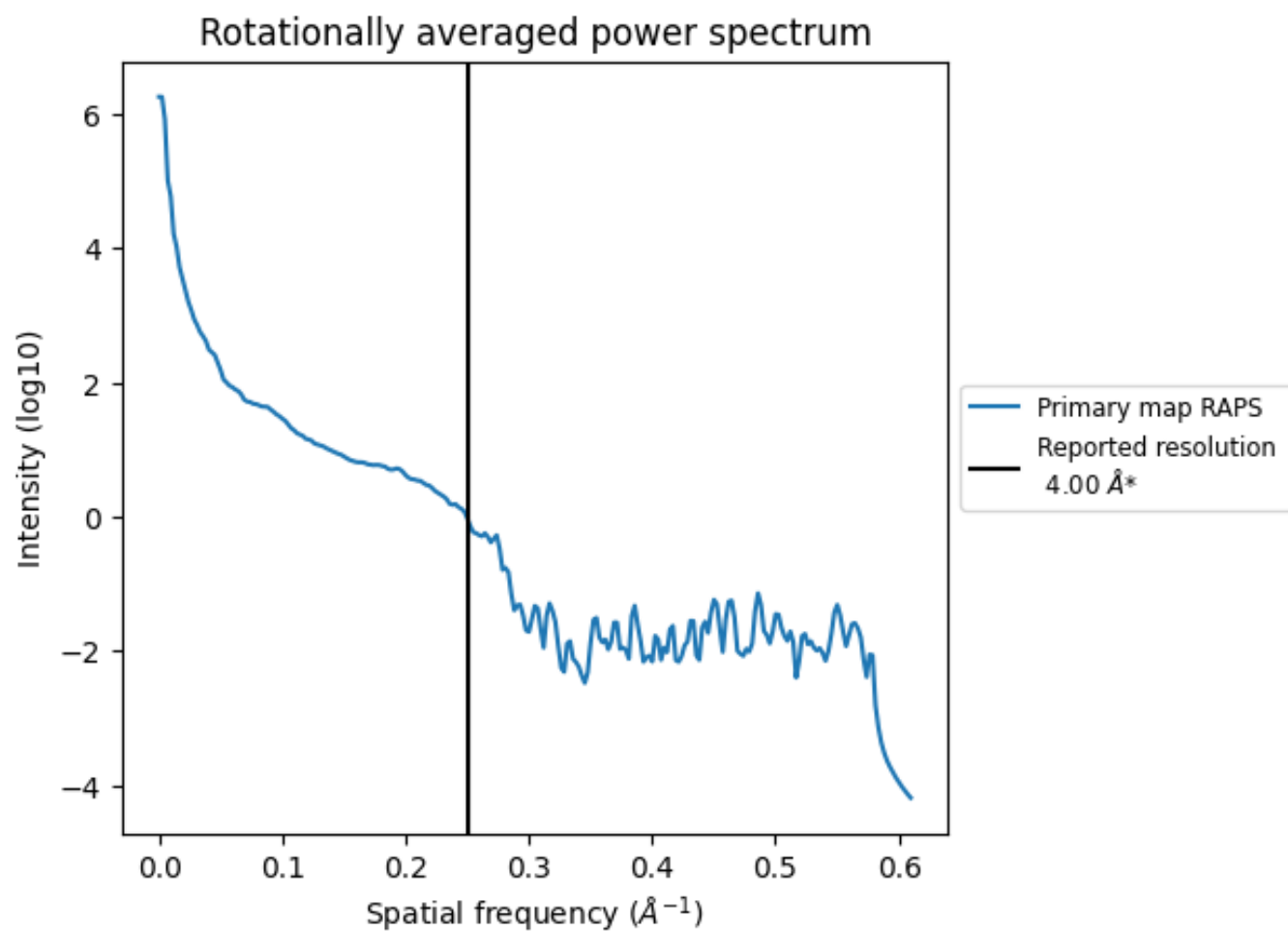
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1426 nm³; this corresponds to an approximate mass of 1288 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



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

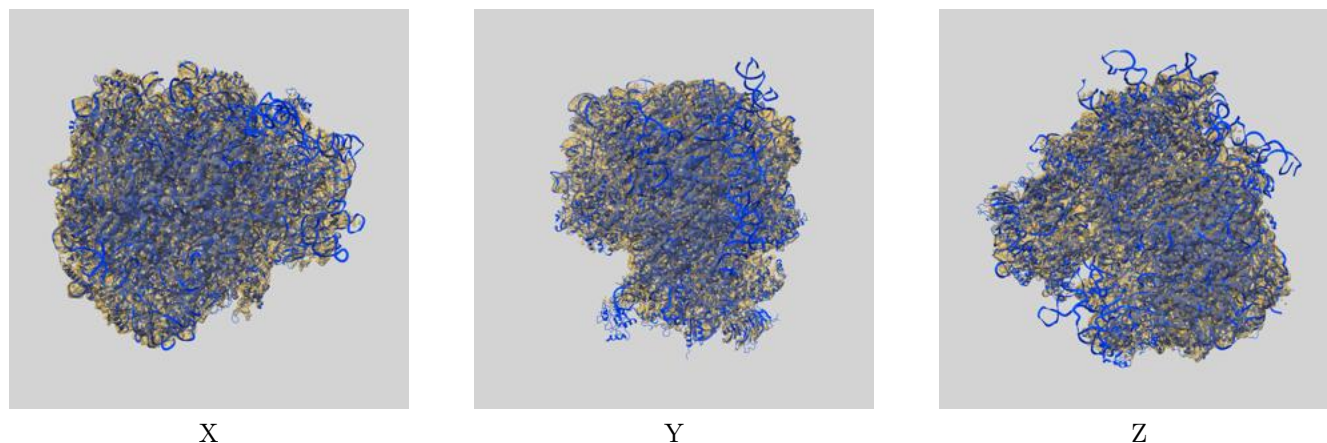
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

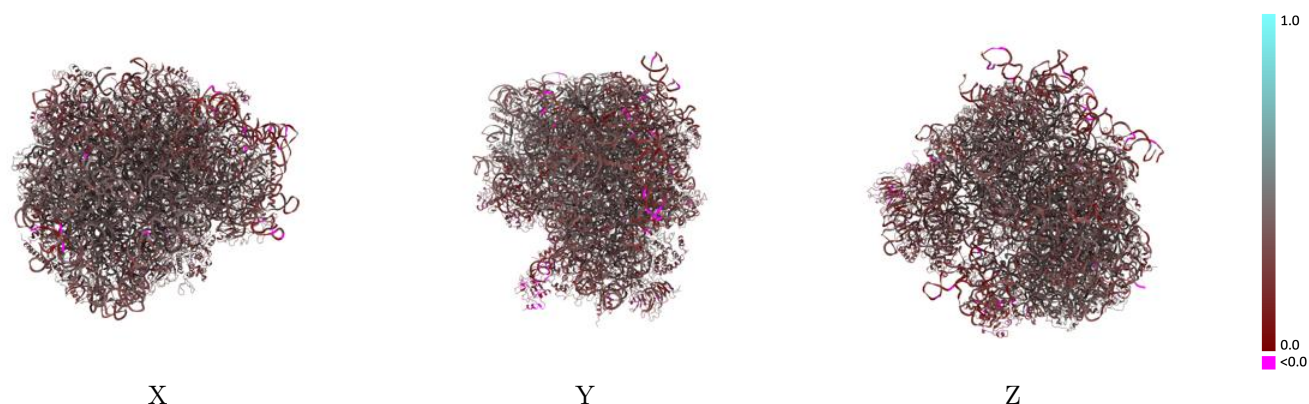
This section contains information regarding the fit between EMDB map EMD-6647 and PDB model 5JUU. Per-residue inclusion information can be found in [section 3](#) on [page 21](#).

9.1 Map-model overlay [i](#)



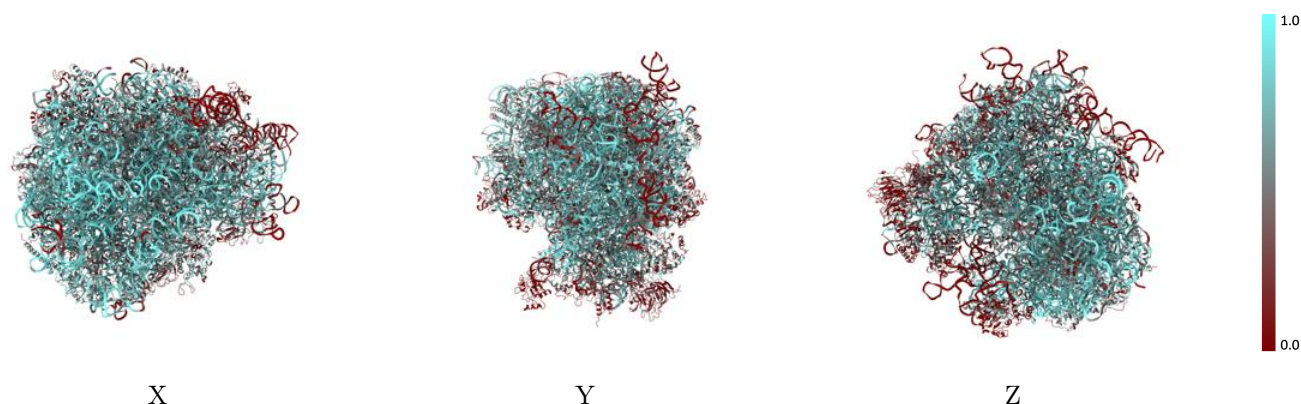
The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



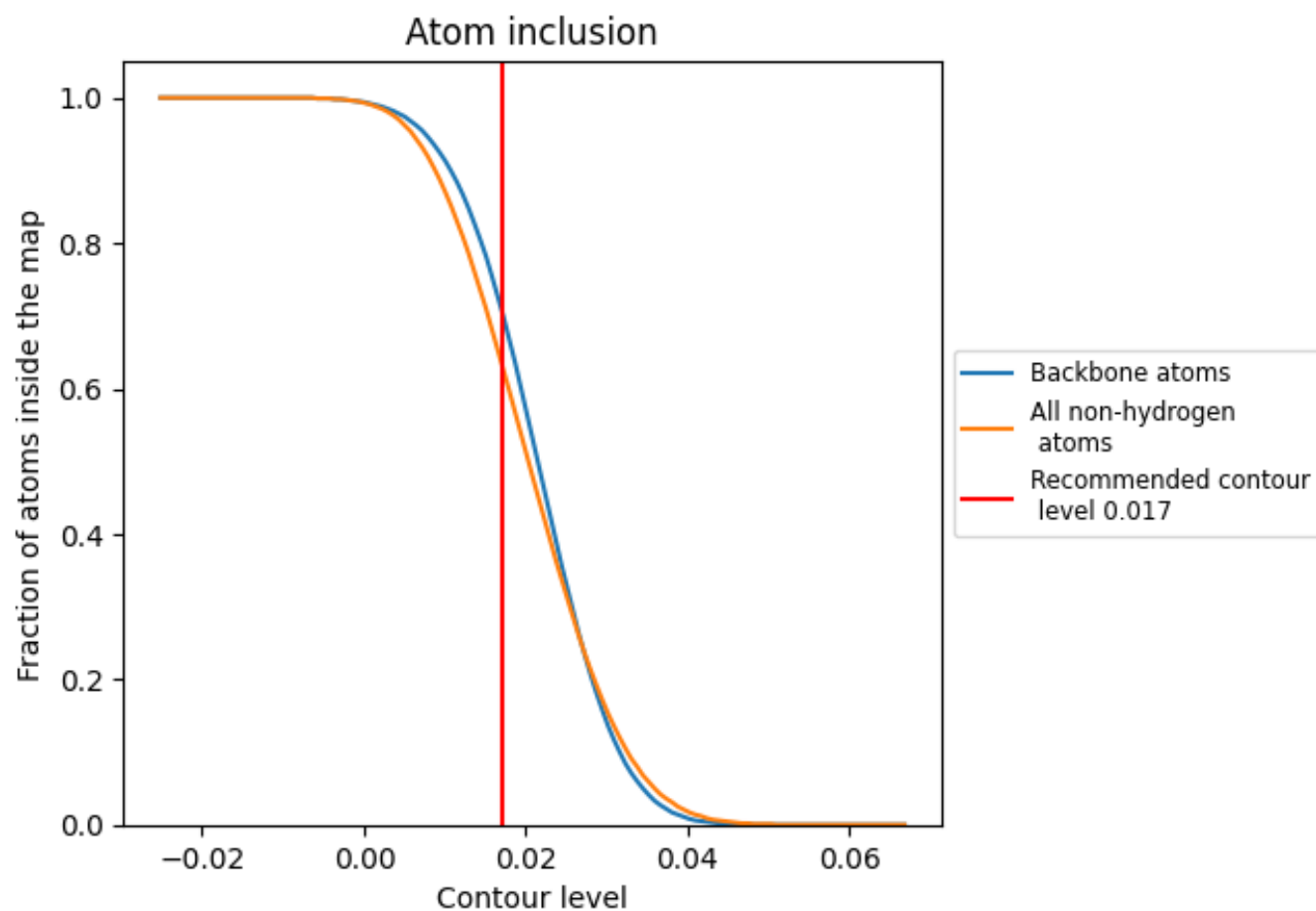
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.017).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 64% 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 (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6360	 0.3360
A	 0.7160	 0.3230
AA	 0.4740	 0.4030
AB	 0.2920	 0.3120
AC	 0.4960	 0.2960
B	 0.8050	 0.3510
BA	 0.5740	 0.3780
BB	 0.6930	 0.3600
BC	 0.3460	 0.3430
C	 0.8210	 0.3550
CA	 0.4000	 0.3380
CB	 0.3640	 0.2970
CC	 0.0000	 0.1350
D	 0.9170	 0.3450
DA	 0.6280	 0.3340
DB	 0.3820	 0.3180
DC	 0.4330	 0.3180
E	 0.0770	 0.2210
EA	 0.5240	 0.3110
EB	 0.2610	 0.3130
EC	 0.1710	 0.2200
F	 0.6090	 0.3740
FA	 0.6560	 0.3880
FB	 0.4430	 0.3540
G	 0.5670	 0.3870
GA	 0.5810	 0.3590
GB	 0.6170	 0.3280
H	 0.6460	 0.3790
HA	 0.6910	 0.3470
HB	 0.3190	 0.2490
I	 0.6540	 0.3290
IA	 0.6220	 0.3790
IB	 0.3890	 0.3580
J	 0.4860	 0.3330
JA	 0.6720	 0.4080



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Chain	Atom inclusion	Q-score
JB	 0.0060	 0.1190
K	 0.6270	 0.3600
KA	 0.5130	 0.3790
KB	 0.5470	 0.3460
L	 0.4480	 0.3250
LA	 0.5450	 0.3390
LB	 0.6620	 0.3700
M	 0.5150	 0.3660
MA	 0.5120	 0.3320
MB	 0.0870	 0.2300
N	 0.5950	 0.3470
NA	 0.6340	 0.3540
NB	 0.2990	 0.3010
O	 0.5620	 0.2960
OA	 0.6400	 0.3630
OB	 0.3350	 0.2860
P	 0.1760	 0.2120
PA	 0.1100	 0.2930
PB	 0.2680	 0.2590
Q	 0.6800	 0.3750
QA	 0.5910	 0.3550
QB	 0.4050	 0.2770
R	 0.5930	 0.3420
RA	 0.6560	 0.3610
RB	 0.2200	 0.2840
S	 0.5540	 0.3510
SA	 0.3760	 0.3720
SB	 0.4650	 0.3580
T	 0.5540	 0.3720
TA	 0.7530	 0.3850
TB	 0.5050	 0.3630
U	 0.6200	 0.3810
UA	 0.5930	 0.3510
UB	 0.4350	 0.3710
V	 0.7030	 0.3880
VA	 0.1980	 0.2520
VB	 0.4450	 0.3350
W	 0.4770	 0.3330
WA	 0.1360	 0.2710
WB	 0.1750	 0.2650
X	 0.5820	 0.3590
XA	 0.3330	 0.3290

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Chain	Atom inclusion	Q-score
XB	 0.6390	 0.3690
Y	 0.6390	 0.3860
YA	 0.5030	 0.3440
YB	 0.5410	 0.3370
Z	 0.4160	 0.3260
ZA	 0.6260	 0.3780
ZB	 0.6050	 0.3290