



wwPDB EM Map/Model Validation Report ⓘ

Sep 29, 2016 – 09:09 PM EDT

PDB ID : 5JUJ
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 Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

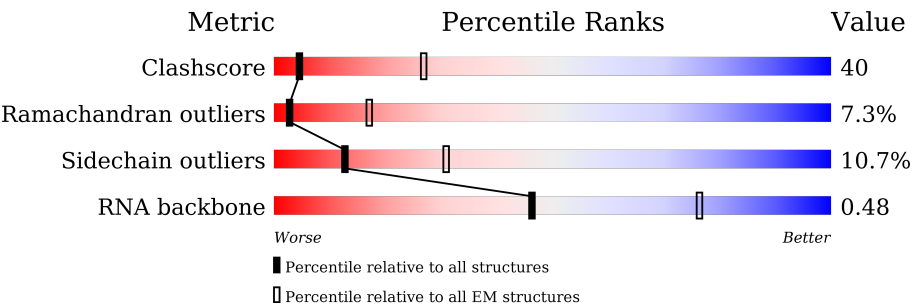
MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027939

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.



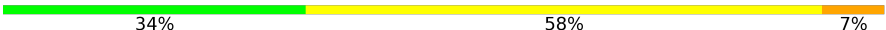

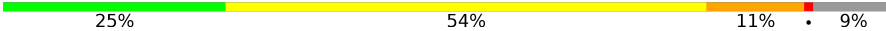








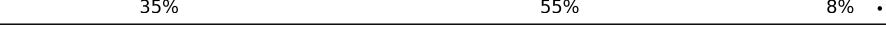







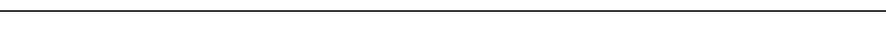

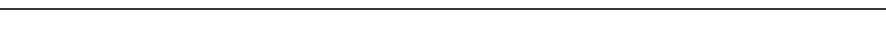
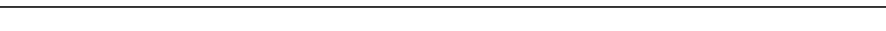


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	1798	<div><div>22%</div><div>62%</div><div>15%</div><div>..</div></div>
2	B	3396	<div><div>20%</div><div>62%</div><div>14%</div><div>..</div></div>
3	C	158	<div><div>20%</div><div>64%</div><div>13%</div><div>.</div></div>
4	D	121	<div><div>17%</div><div>73%</div><div>11%</div><div></div></div>
5	E	217	<div><div>30%</div><div>38%</div><div>9%</div><div>.</div><div>21%</div></div>
6	F	254	<div><div>29%</div><div>59%</div><div>11%</div><div>.</div></div>
7	G	387	<div><div>29%</div><div>58%</div><div>12%</div><div>.</div></div>
8	H	362	<div><div>33%</div><div>56%</div><div>11%</div><div></div></div>


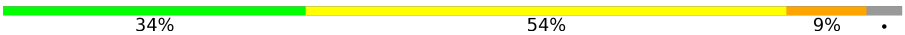
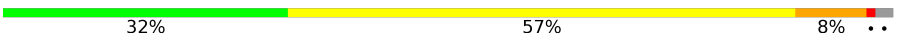



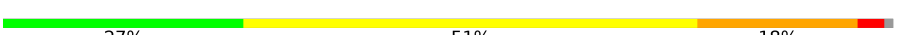
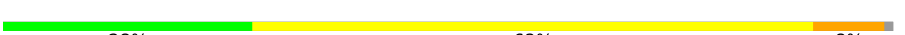



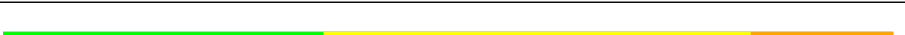

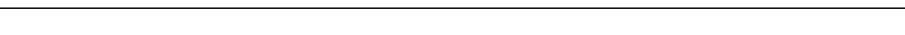
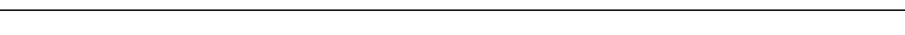
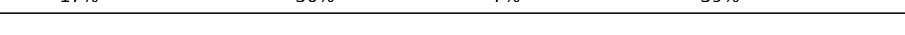

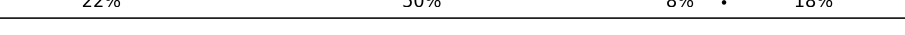
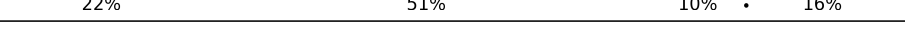
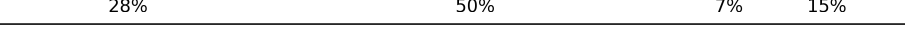





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Mol	Chain	Length	Quality of chain
9	I	297	
10	J	176	
11	K	244	
12	L	256	
13	M	191	
14	N	221	
15	O	174	
16	P	165	
17	Q	199	
18	R	138	
19	S	204	
20	T	199	
21	U	184	
22	V	186	
23	W	189	
24	X	172	
25	Y	160	
26	Z	121	
27	AA	137	
28	BA	155	
29	CA	142	
30	DA	127	
31	EA	136	
32	FA	149	
33	GA	59	

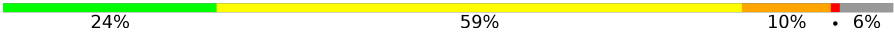
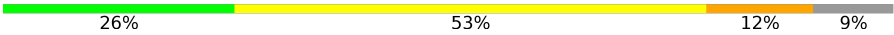


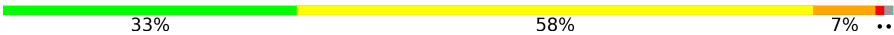
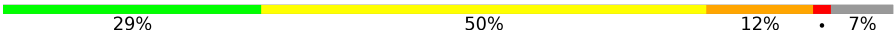
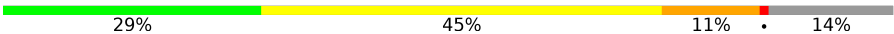
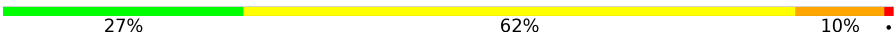
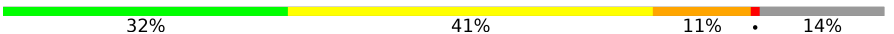
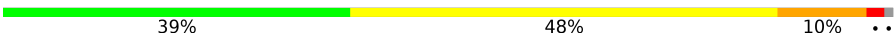
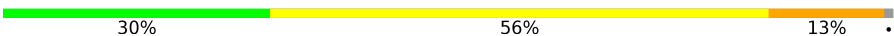
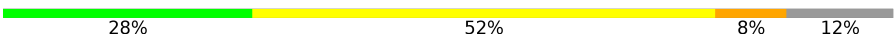
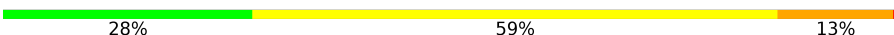
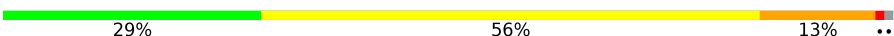



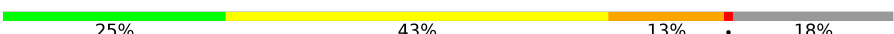







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Mol	Chain	Length	Quality of chain
34	HA	105	
35	IA	113	
36	JA	130	
37	KA	107	
38	LA	121	
39	MA	120	
40	NA	100	
41	OA	88	
42	PA	78	
43	QA	51	
44	RA	128	
45	SA	25	
46	TA	106	
47	UA	92	
48	VA	312	
49	WA	319	
50	XA	252	
51	YA	255	
52	ZA	254	
53	AB	240	
54	BB	261	
55	CB	225	
56	DB	236	
57	EB	190	
58	FB	200	

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Mol	Chain	Length	Quality of chain
59	GB	197	
60	HB	105	
61	IB	156	
62	JB	143	
63	KB	151	
64	LB	137	
65	MB	142	
66	NB	143	
67	OB	136	
68	PB	146	
69	QB	144	
70	RB	121	
71	SB	87	
72	TB	130	
73	UB	145	
74	VB	135	
75	WB	108	
76	XB	119	
77	YB	82	
78	ZB	67	
79	AC	56	
80	BC	63	
81	CC	152	
82	DC	842	
83	EC	201	

2 Entry composition [i](#)

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	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	S	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	S	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		

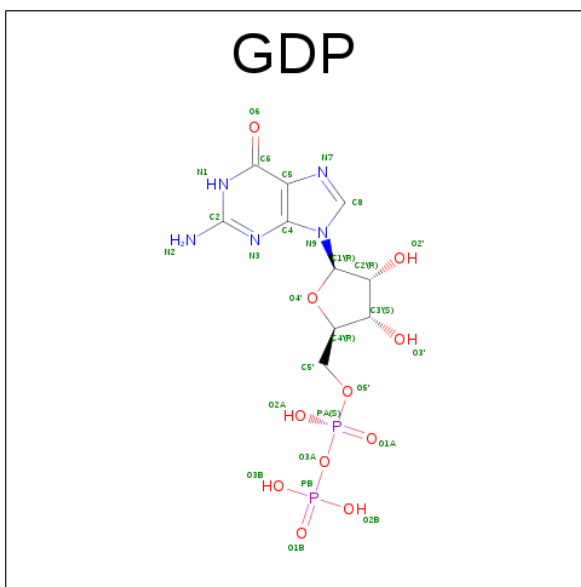
- Molecule 82 is a protein called yeast eEF2.

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 (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

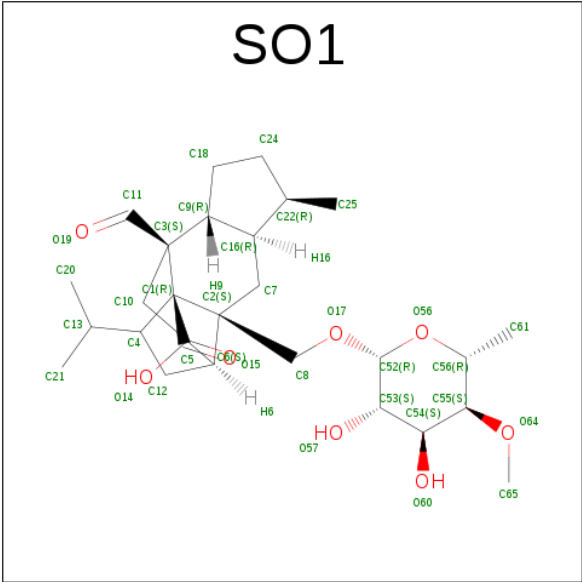


Mol	Chain	Residues	Atoms					AltConf
84	DC	1	Total	C	N	O	P	0
			28	10	5	11	2	

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

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

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

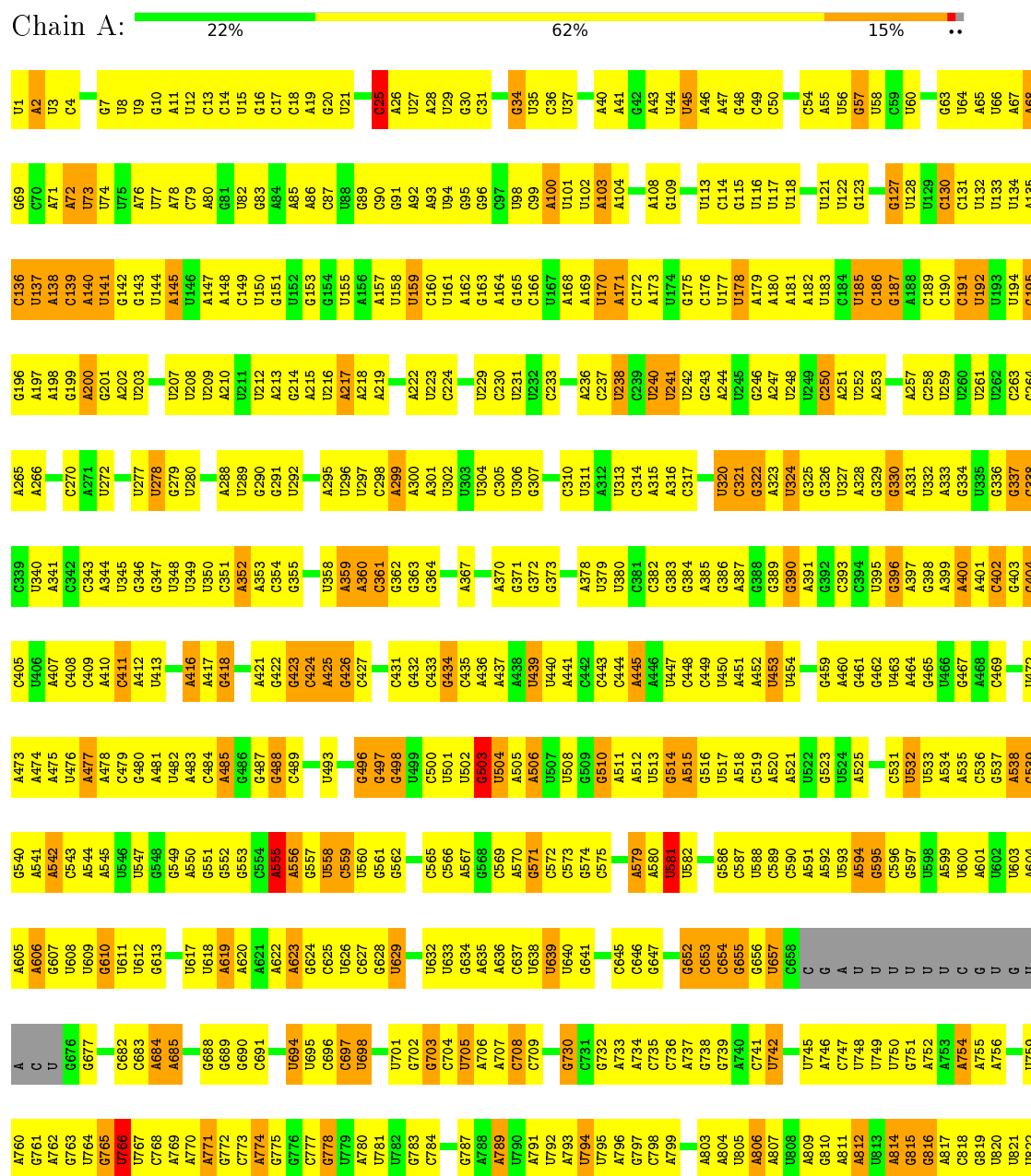


Mol	Chain	Residues	Atoms			AltConf
86	DC	1	Total	C	O	0
			35	27	8	

3 Residue-property plots

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



U1775	A1714	G1643	U1582	U1398	C1338	U1276	C1210	A1147	A1081	G1016	G954	A887	G823
A1776	G1715	U1643	A1583	C1399	C1339	G1277	U1214	C1143	C1082	U1017	A955	U888	G824
G1777	G1644	G1644	G1584	A1524	A1340	G1278	U1215	G1149	G1083	A1020	C956	U889	U825
G1778	G1645	G1645	A1585	A1525	A1401	C1279	C1216	G1150	A1084	G1021	G957	C890	
U1779	G1716	G1646	A1586	A1526	C1342	G1280	G1217	A1151	G1085	C1022	U958	U853	U828
G1780	A1719	C1647	A1587	U1407	C1343	G1281	G1218	A1152	A1086	U1025	U959	U834	A829
A1781	G1720	U1468	U1468	G1408	A1344	U1282	G1219	A1157	A1087	U1026	U960	U830	U830
A1782	C1721	A1469	A1469	G1409	A1345	U1283		C1158	A1088	A1027	U961	U831	U831
G1783	U1722	G1590	C1529	A1408	A1346	U1284	U1225	C1159		A1026	C962	U896	U832
C1784	U1723	G1531	C1531	A1471	U1347	U1285	A1226	A1160	A1092	A1028	A963	U897	U833
U1785	U1724	G1652	A1592	C1472	A1348	U1286	U1227	C1161	G1094	G1032	U965	A898	A834
G1786	U1725	C1653	A1593	U1413	U1349	A1287	A1228	C1162	U1095	U1031	A966	U836	U835
C1787	G1726	G1654	G1594	A1474	U1350	G1288	G1229	A1163	C1096	G1033	A967	U837	U837
G1788	G1727	A1655	U1595	U1415	G1351	U1289	U1230	G1164	U1097	G1034	U968	U838	U838
G1789	A1728	C1596	G1536	A1416	U1352	G1290	G1231	G1165	U1098	A970	C969	U903	U839
A1790	U1729	A1597	C1537	A1417	G1353	G1291	U1232	A1166	U1099	G1035	U971	A905	U840
G1791	U1730	G1658	U1538	G1478	G1354	G1292	G1233	G1167	G1100	A1036	G972	A906	U841
A1791	A1731	A1659	G1539	G1419	U1355	U1293	U1234	U1168	G1101	C1037	A973	U843	C842
G1793	G1732	A1660	A1600	C1420	U1356		U1235	G1169	G1102	U1038	A974	U844	U844
A1794	C1733	U1661	G1601	A1421	A1357	G1297	A1236	G1170	U1103	G1039	C975	G914	G845
U1795	U1734	G1662	C1602	A1422	G1358	U1298	G1237	A1171	U1104	G1040	G976	A915	U846
C1796	U1735		U1603	U1423	C1359	U1299	U1238	G1172	C1105	G1041	A977	U916	U847
A1797	G1736	A1667	U1604	A1424	A1360	G1299	A1239	G1173	U1106	G1042	A978	U917	C848
G1798		G1668	U1605	A1425	U1361	A1300	U1240	C1174	G1107	A1043	A979	U918	
C1799	A1740	U1669	G1606	C1426	U1362	U1301		U1175	G1108		G980	A919	U851
U1799	G1741	G1670	G1607	A1427	U1363	U1302	G1241	G1176	G1109	G1046	U981	A920	C852
	U1742	A1671	U1608	G1428	G1364	U1303	G1242	G1177	U1110	G1047	U982	U921	G853
G1743	U1743	G1672	U1609	A1429	C1365	U1304	G1243	G1178	G1111	G1048		G922	U854
A1744	G1744	C1673	G1610	U1430	U1366	U1305	A1244	G1179	G1112	U1049	G886	A923	A855
G1745	U1745	A1681	U1611	C1431	G1367	C1306	G1245	C1180	G1113		G987	A924	A856
A1746	G1746	G1675	G1612	U1432	U1368	U1307	G1246	U1181		G1053	A988	G925	U857
U1747	U1747	U1676	U1613	G1433	U1369	G1308	U1247	U1182	U1116	U1054	U989	A926	G858
C1748	A1748	A1678	G1615	U1434	A1371	U1310	C1248	A1183	U1117	U1055	C990	C927	A859
G1749	G1749	G1679	A1616	G1435	U1372	U1311	U1249	A1184	G1118	U1056	G991		U860
A1750	U1750	U1680	U1617	A1436	C1373	A1312	U1250	U1185	U1119	U1057	A992	A930	A863
G1751	C1751	A1681	C1618	U1437	C1374	A1313	U1251	U1186	U1120	U1058	A993	C931	U864
U1752	U1752	U1682	C1619	G1438	A1375	U1314	C1252	U1187	C1121	U1059	A994	A932	A865
A1753	C1753	C1683	C1620	U1439	U1376	U1315	U1253	G1188	G1122	U1060	A995	A933	G866
A1754	U1754	U1684	U1621	C1440	U1377	G1316	G1254	A1189	A1124	A1061	U996	U935	G867
A1755	G1755	G1685	G1622	U1442	U1378	C1317	G1255	U1191	A1125	A1062	G997	G936	G868
A1756	C1756	C1686	C1623	U1443	C1379	U1318	G1256	C1192	G1126	U1063	U999	C937	A869
G1757	U1757	U1687	U1624	A1444	U1380	G1318	U1257	U1193	C1127	G1064	C1000	G938	C870
U1758			C1625	G1445	U1381		U1258	A1194	C1128	A1065	A1001	A939	G871
C1759	G1759	G1690	U1626	A1446	A1382	A1321	U1259	U1195	U1129	C1066	G1002	A940	G872
U1760	U1760	A1691	U1627	C1447	G1383	C1323	U1260	C1196	G1130	C1067	U1003	A941	U873
U1761	G1761	G1692	U1628	G1448	A1384	G1324	G1261	A1196	G1131	C1068	U1004	G942	C874
A1762	U1762	A1693	G1629	U1449	G1385	A1325	U1262	C1197	A1132	A1069	A1005	C943	G875
G1763	C1763		U1630	U1450	G1386	A1326	G1263	G1198	A1133	C1070	C1006	A944	G876
A1764	U1764	G1696	A1631	C1451	U1387	C1327	G1264	G1199	U1133	U1071	U1007	U945	G877
U1765	G1765	G1697	C1632	U1452	A1388	G1328	G1265	G1200	C1134	G1072	C1007	U946	C880
A1766	A1766		A1633	G1453	C1389	A1329	U1266	G1201	U1135	G1073	U1008	U947	
G1767	C1767	C1706	C1634	G1454	U1390	A1331	G1267	A1202	G1074	U1009	U1009	U948	G881
U1768	U1768	A1707	A1635	G1455	A1391	A1332	G1270	A1203	G1141	C1075	G1010	G949	U882
U1769	C1769	U1708	C1636	G1456	U1392	C1332	U1271	A1204	A1142	A1076	C1011	C949	C883
U1770	U1770	U1709	C1637	G1457	C1393	C1333	G1272	C1205	A1143	C1077	U1012	C950	U884
U1771	U1771	U1710	G1638	G1458	G1394	U1334	U1273	U1206	A1144	C1078	U1013	A951	G885
C1772	G1772	C1711	C1639	G1459	U1395	U1335	G1274	C1207	U1145	U1079	G1014	A952	
C1773	G1773	A1712	U1520	A1460	U1396	A1336	A1275	A1208	G1146	U1080	U1015	G953	U886

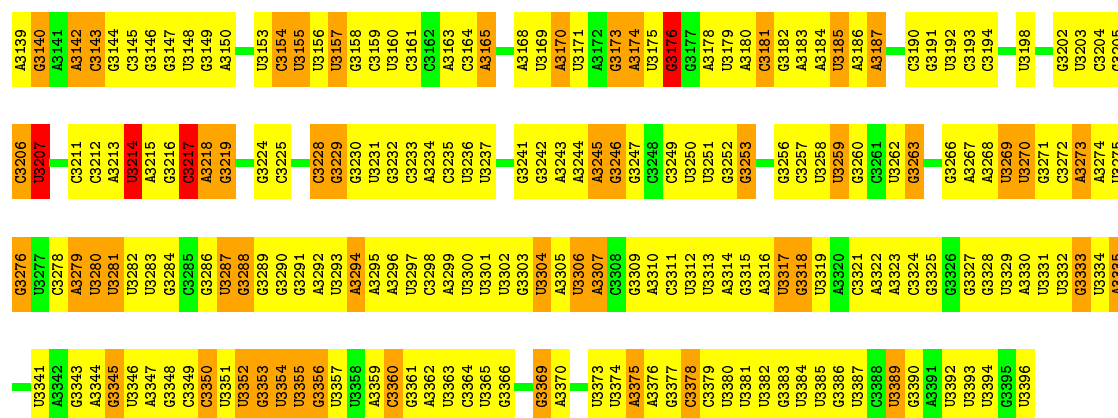
● Molecule 2: 25S ribosomal RNA

Chain B:  20% 62% 14%

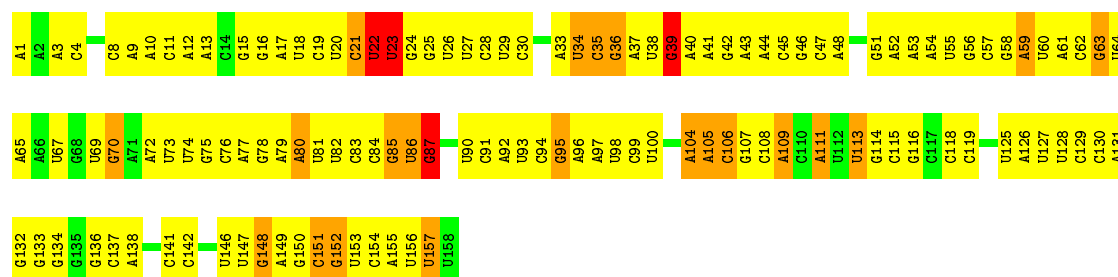
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U	G1936	G1748	G1681	U1621	A1558	A1490	C1426	A1363	G1237	A1170	U1109	A1047
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G	A1873	G1751	G1684	G1623	G1561	G1493	G1429	A1366	A1240	G1175	U1050	U1050
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U	U1821	G1758	U1691	U1630	U1568	G1500	U1436	A1373	U1247	U1181	A1120	
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C	G1761	U1694	U1694	C1633	A1571	A1503	U1439	G1379	G1250	A1184	U1123	A1061
A	U1762	U1695	G1572	G1634	U1573	A1504	G1440	G1380	C1251	C1185	U1124	A1062
U	U1763	A1696	G1573	G1635	C1574	A1506	G1441	G1381	G1254	C1187	G1126	A1064
C	U1764	A1697	C1574	U1636	A1575	C1507	U1442	G1382	C1255	U1188	G1127	A1065
U	U1765	U1637	A1575	A1637	G1576	C1508	G1443	G1383	G1256	C1189	U1128	G1066
U	G1766	A1638	G1577	U1638	C1577	A1509	U1444	U1384	C1257	A1190	A1129	U1067
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C	C1771	C1706	C1579	U1641	C1579	U1511	G1447	A1386	A1259	C1192	G1131	C1069
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C	G1775	C1710	A1583	G1645	A1583	G1517	C1451	A1390	A1263	C1196	A1135	G1073
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U	G1780	A1714	U1587	U1649	A1587	G1522	A1456	U1331	G1268	A1203	G1139	U1077
C	C1781	A1715	A1588	G1650	C1588	U1521	U1457	A1332	U1269	A1204	G1140	U1078
G	U1782	U1716	A1589	G1651	A1589	U1523	U1458	C1333	A1270	A1205	C1141	A1079
U	U1783	U1717	G1590	G1652	C1590	A1524	C1459	U1334	A1271	G1206	G1142	A1080
C	G1784	G1718	G1591	G1653	G1591	U1525	A1460	C1335	C1272	G1207	A1143	U1081
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G	U1795	G1730	G1604	C1665	G1604	G1538	U1473	U1410	C1283	A1217	A1154	A1093
C	A1796	A1731	G1605	G1666	G1605	A1539	A1474	U1347	C1284	C1217	C1155	U1094
U	U1797	U1732	A1606	G1667	A1606	U1540	A1475	U1348	G1285	U1221	G1156	U1095
C	A1798	G1733	U1606	A1667	U1606	G1541	A1475	A1350	A1286	G1222	G1157	U1096
U	A1799	G1668	U1607	G1668	U1607	U1546	U1475	U1351	A1287	A1223	A1158	G1097
G	U1799	G1669	C1608	C1669	C1608	A1546	C1478	U1415	U1288	C1224	A1159	A1098
A	A1800	U1737	U1609	U1670	C1609	U1549	U1479	U1416	G1289	A1225	C1160	A1099
U	C1802	C1738	G1610	C1671	G1610	U1549	G1480	G1417	A1290	G1229	G1161	U1100
G	A1803	U1739	G1611	G1672	G1611	C1550	A1481	A1418	A1291	G1230	U1162	G1101
C	A1804	U1740	A1612	G1673	A1612	C1551	A1482	A1419	A1292	A1231	A1163	A1102
U	A1805	A1741	A1613	G1674	A1613	G1552	G1483	C1420	U1293	G1232	G1164	A1103
C	A1806	U1742	C1614	A1675	U1553	U1553	U1484	G1421	A1294	C1232	A1165	G1104
U	G1743	A1676	C1615	A1676	U1554	U1555	U1487	C1422	G1295	G1233	G1166	A1105
C	G1808		U1616		U1555			C1423	C1296	G1234	U1167	G1106

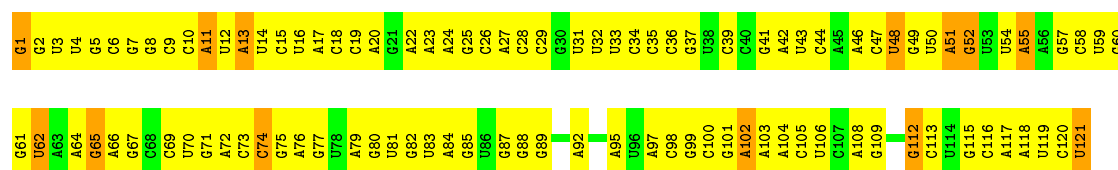


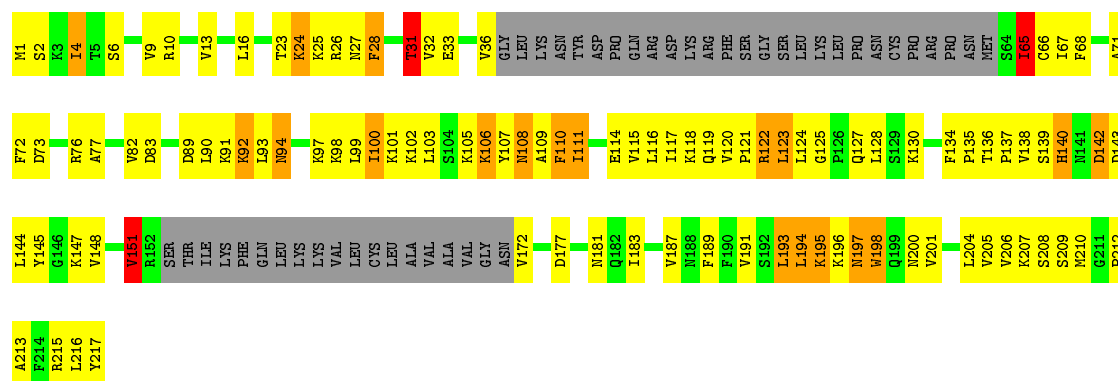
• Molecule 3: 5.8S ribosomal RNA



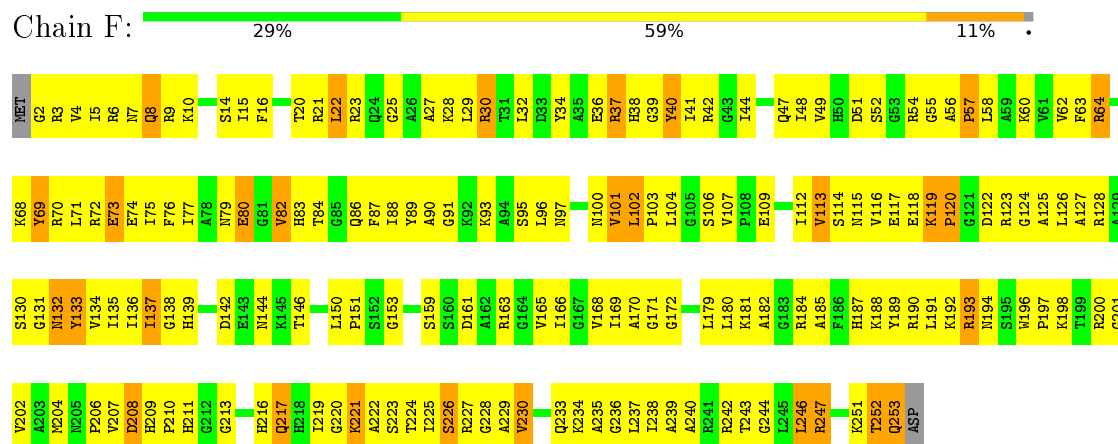
• Molecule 4: 5S ribosomal RNA



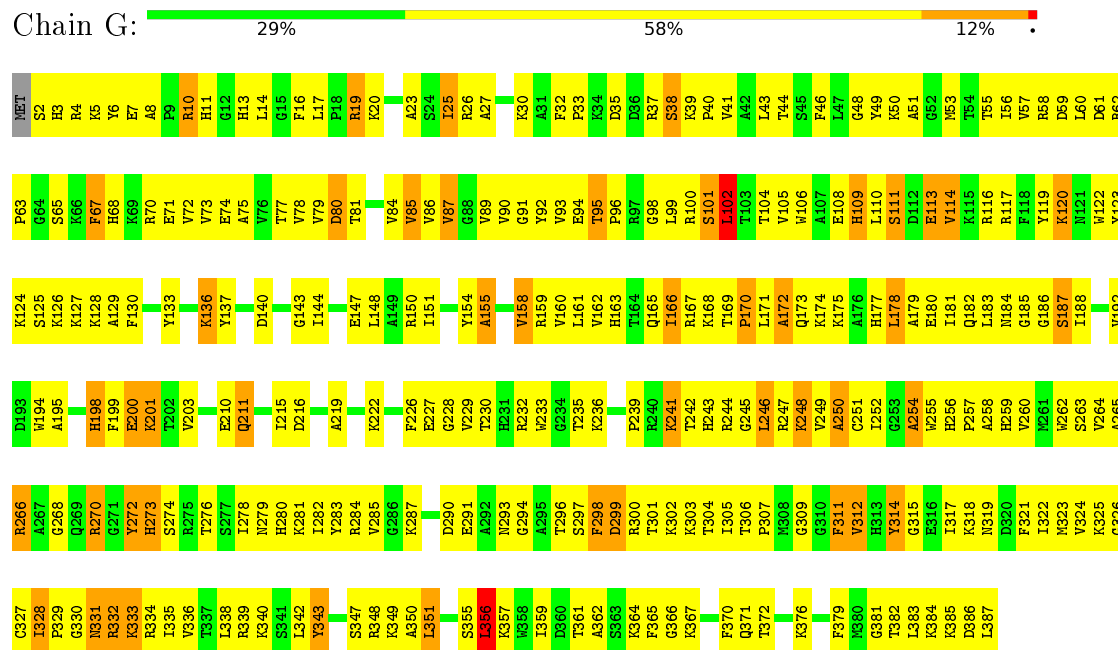
• Molecule 5: uL1 (yeast L1)



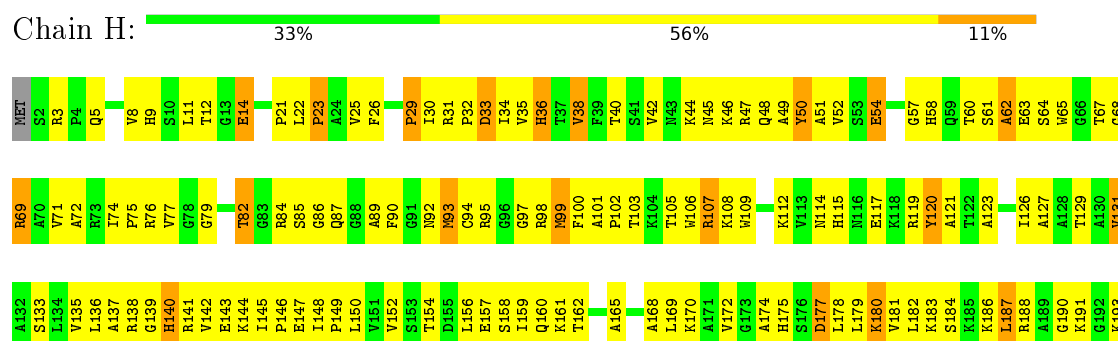
- Molecule 6: uL2 (yeast L2)

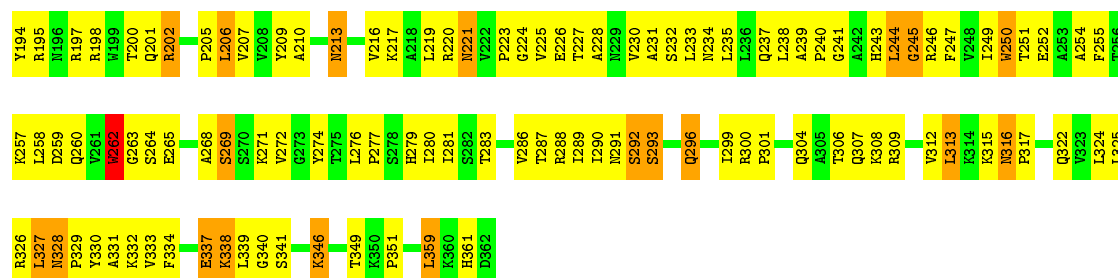


- Molecule 7: uL3 (yeast L3)

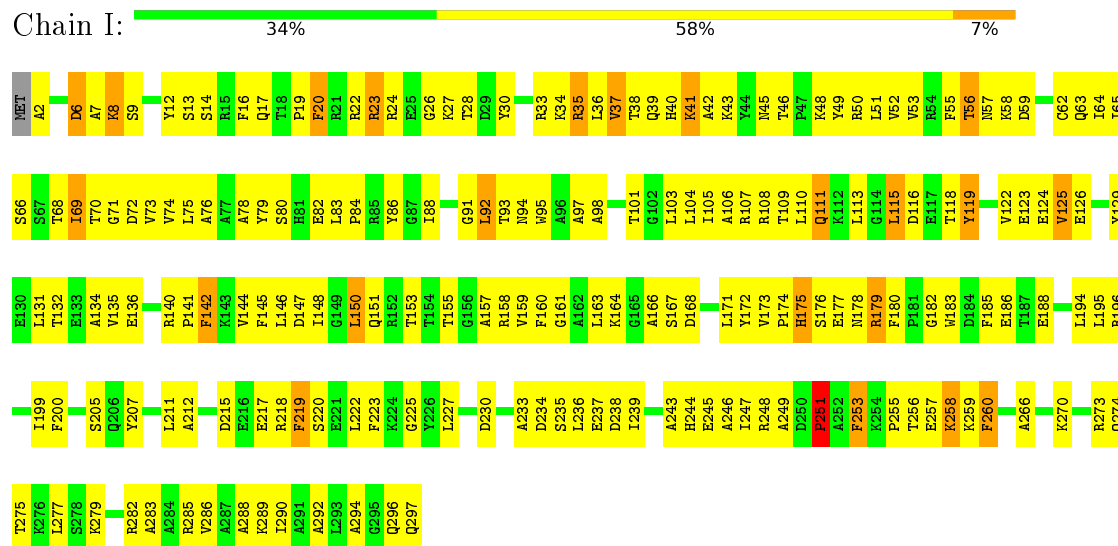


- Molecule 8: uL4 (yeast L4)

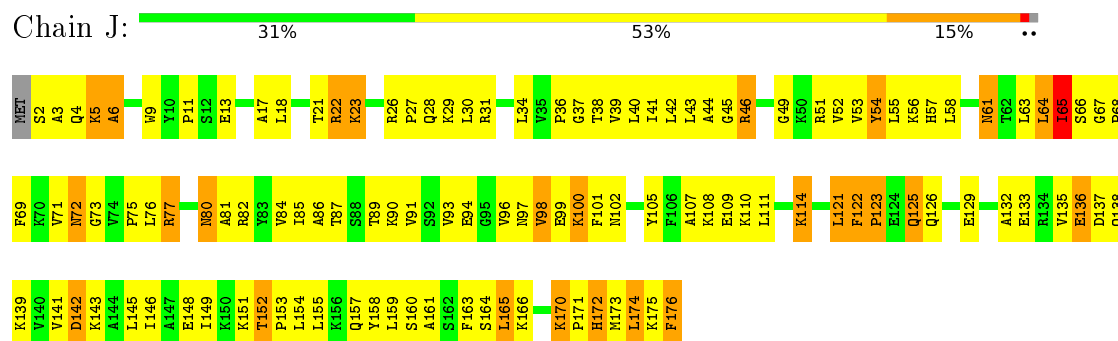




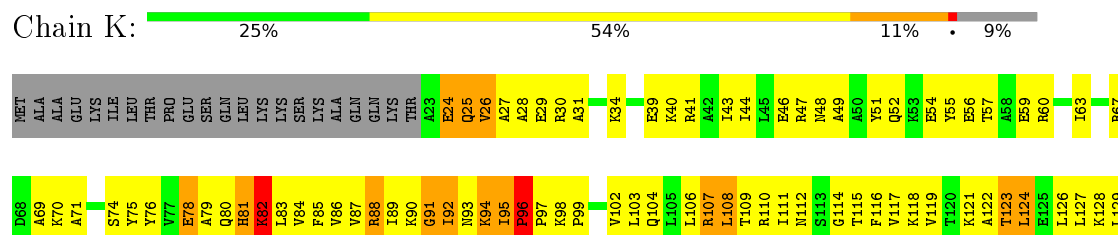
• Molecule 9: uL18 (yeast L5)

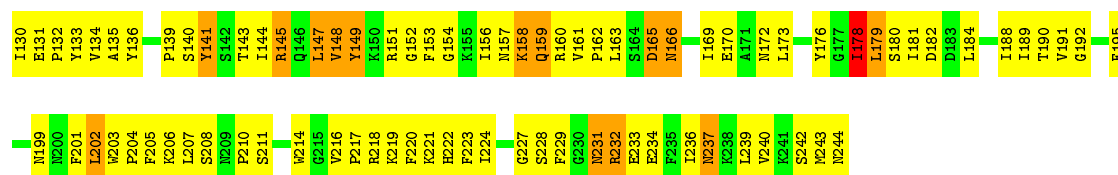


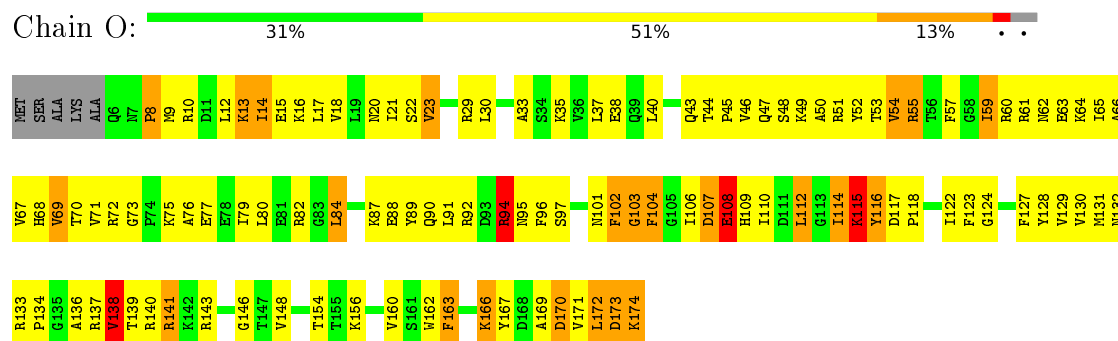
• Molecule 10: eL6 (yeast L6)



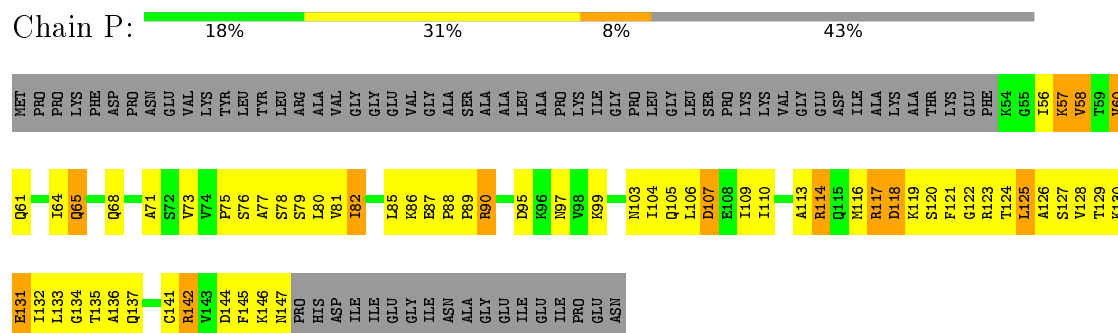
• Molecule 11: uL30 (yeast L7)



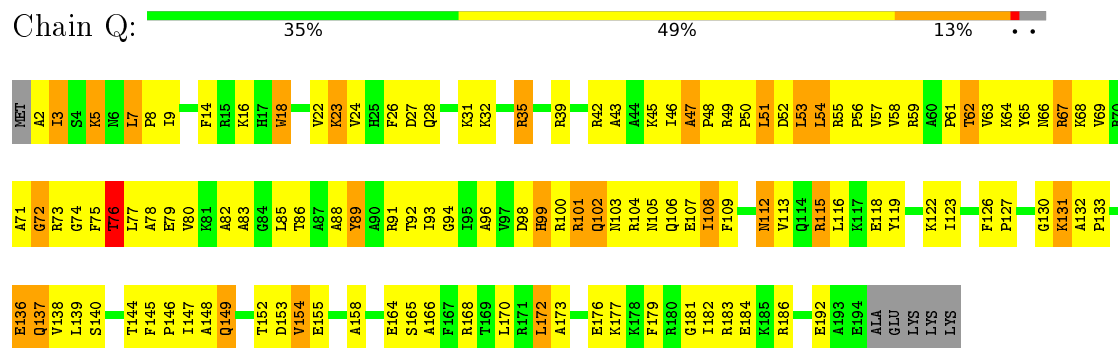




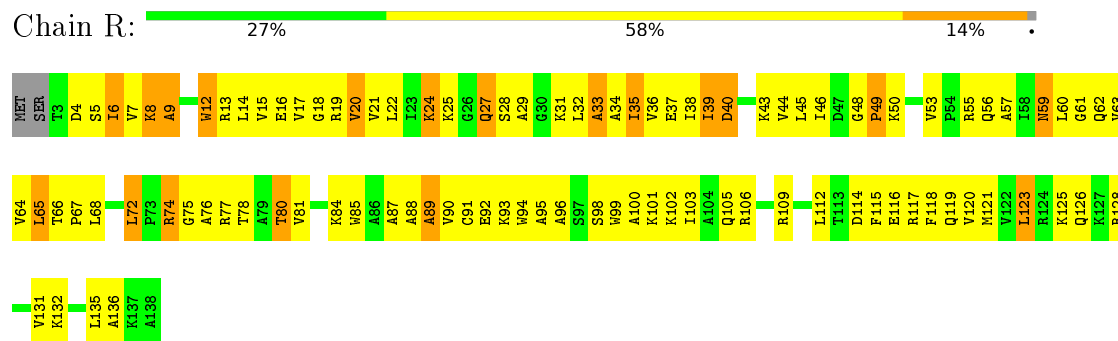
• Molecule 16: uL11 (yeast L12)



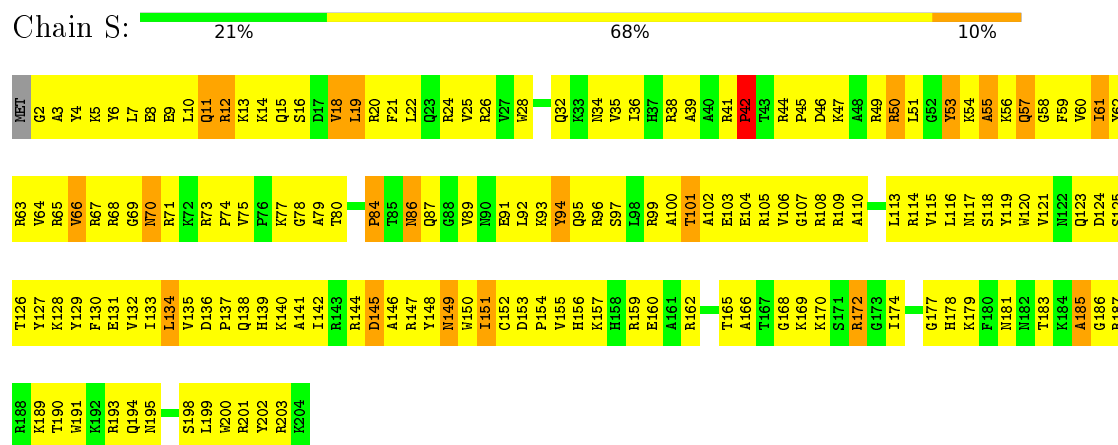
• Molecule 17: eL13 (yeast L13)



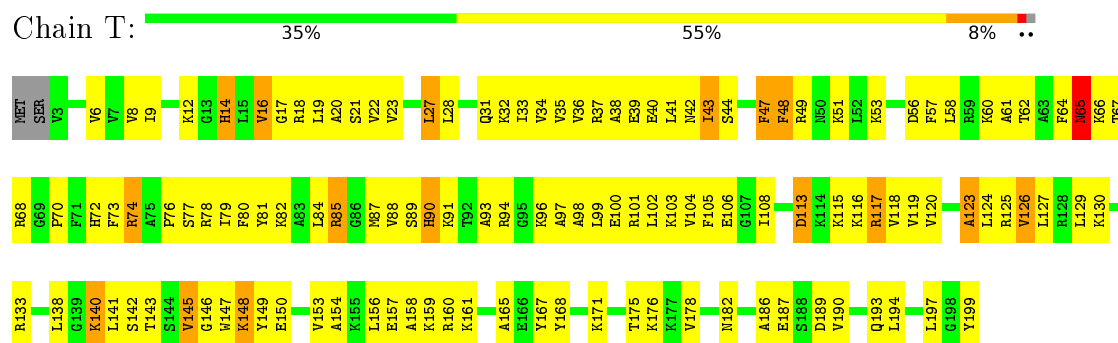
• Molecule 18: eL14 (yeast L14)



• Molecule 19: eL15 (yeast L15)



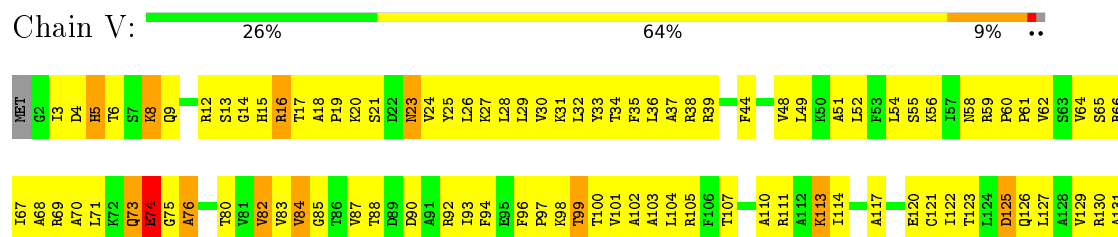
• Molecule 20: uL13 (yeast L16)



• Molecule 21: uL22 (yeast L17)



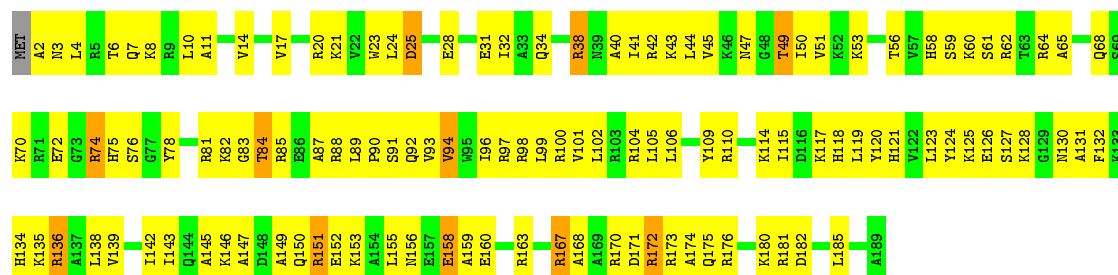
• Molecule 22: eL18 (yeast L18)





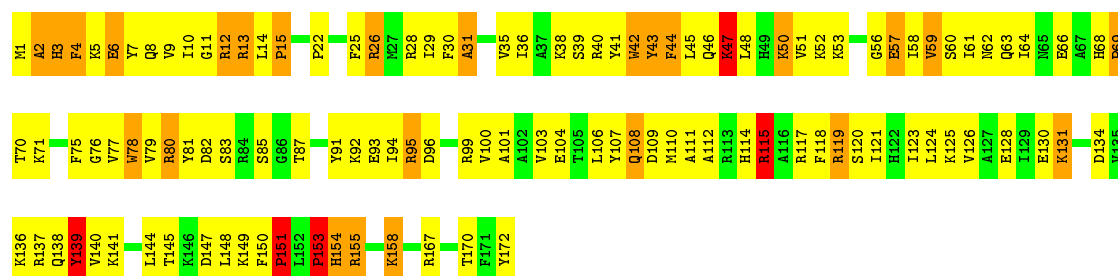
• Molecule 23: eL19 (yeast L19)

Chain W: 35% 58% 6%



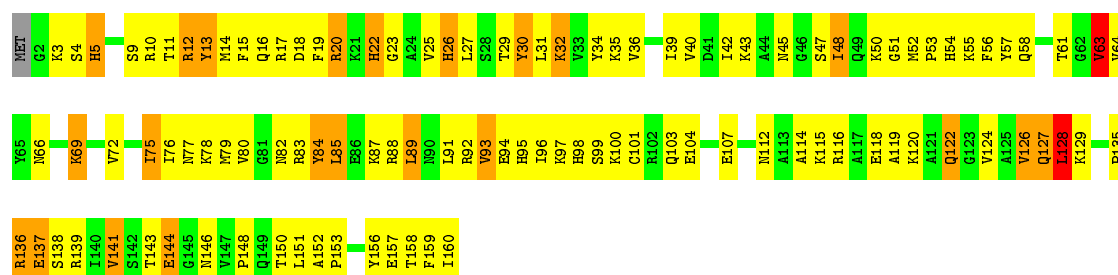
• Molecule 24: eL20 (yeast L20)

Chain X: 32% 51% 15%



• Molecule 25: eL21 (yeast L21)

Chain Y: 32% 53% 14%

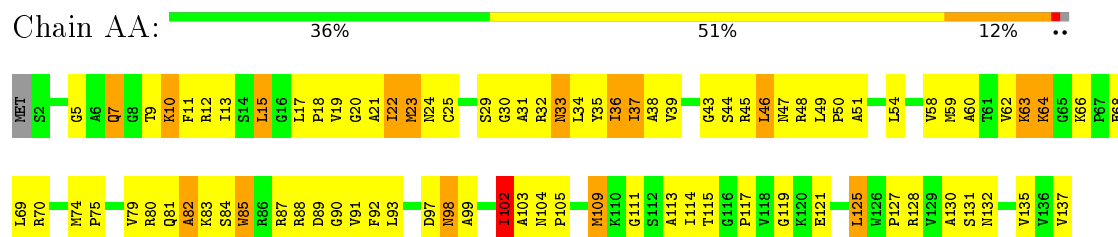


• Molecule 26: eL22 (yeast L22)

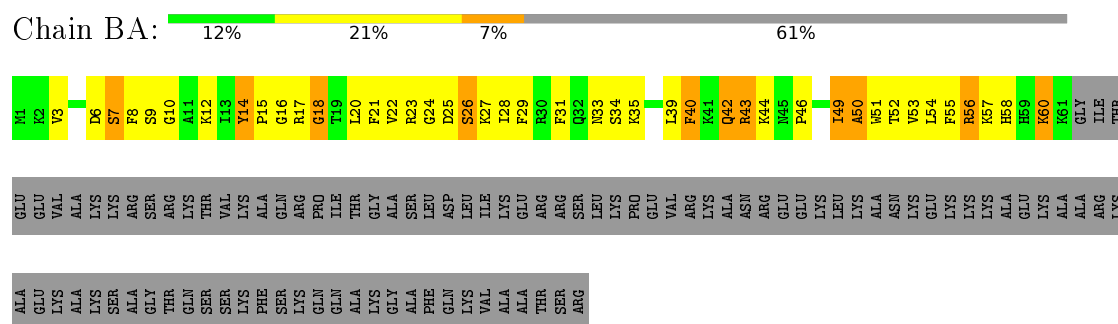
Chain Z: 36% 41% 6% 17%



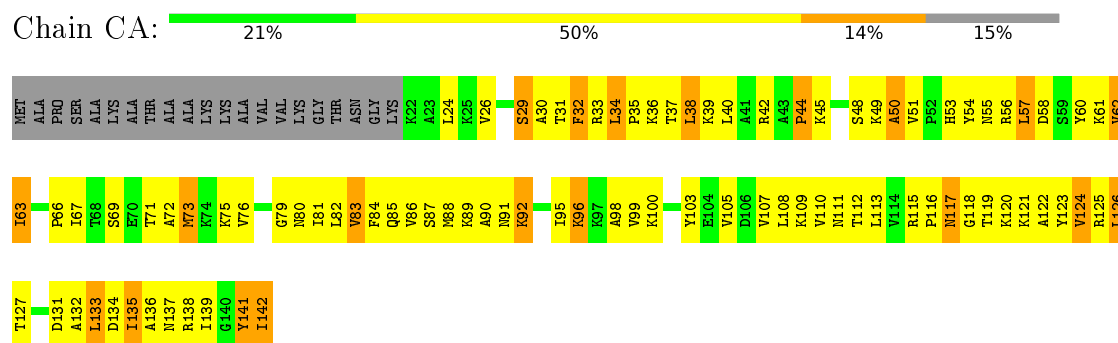
- Molecule 27: uL14 (yeast L23)



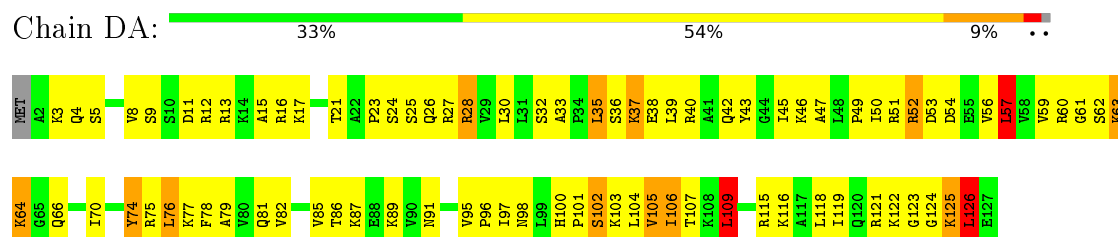
- Molecule 28: eL24 (yeast L24)



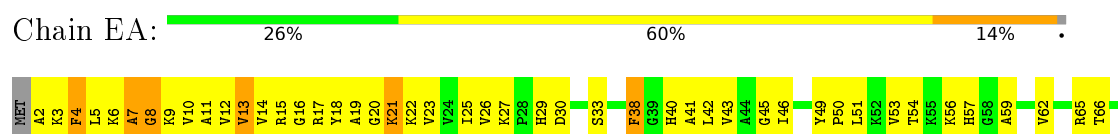
- Molecule 29: uL23 (yeast L25)

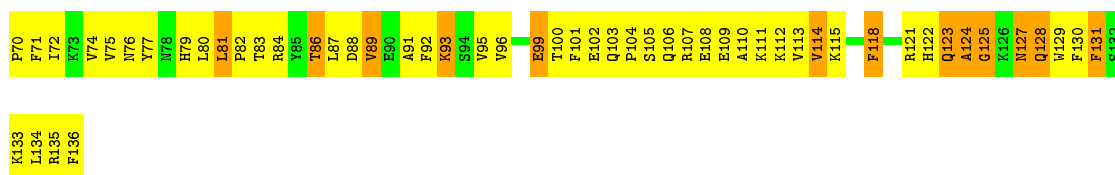


- Molecule 30: uL24 (yeast L26)



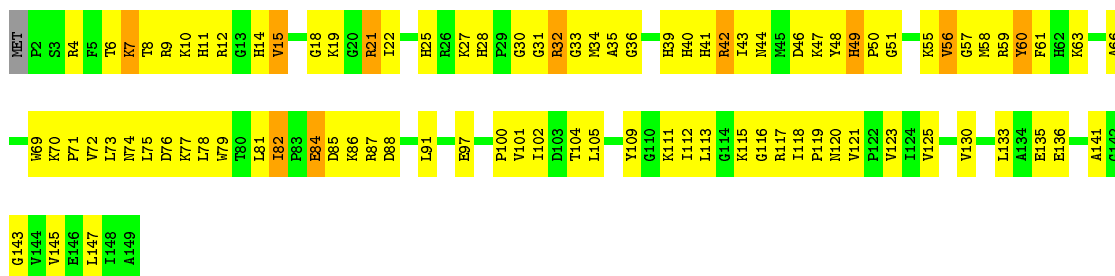
- Molecule 31: eL27 (yeast L27)





• Molecule 32: uL15 (yeast L28)

Chain FA: 38% 54% 7% .



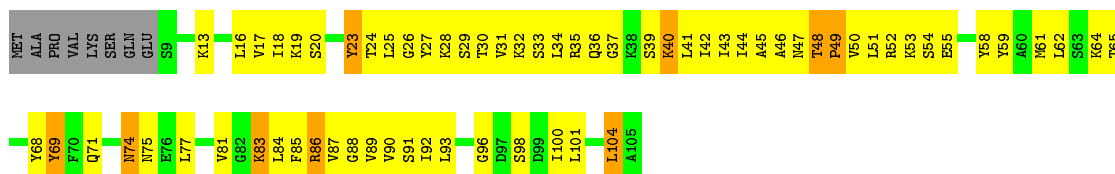
• Molecule 33: eL29 (yeast L29)

Chain GA: 46% 42% 10% .



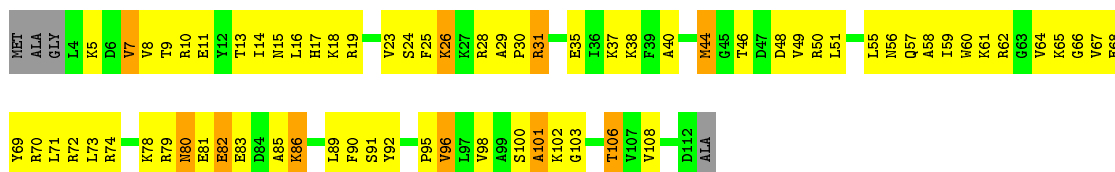
• Molecule 34: eL30 (yeast L30)

Chain HA: 29% 55% 9% 8%



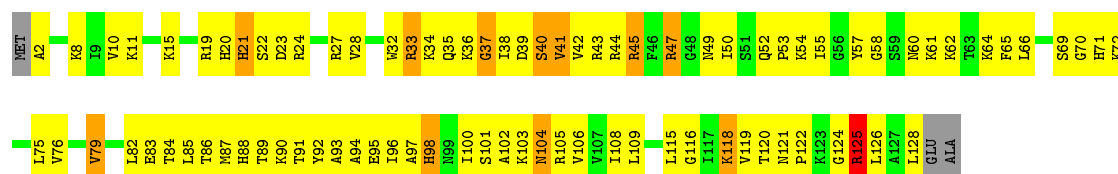
• Molecule 35: eL31 (yeast L31)

Chain IA: 34% 54% 9% .



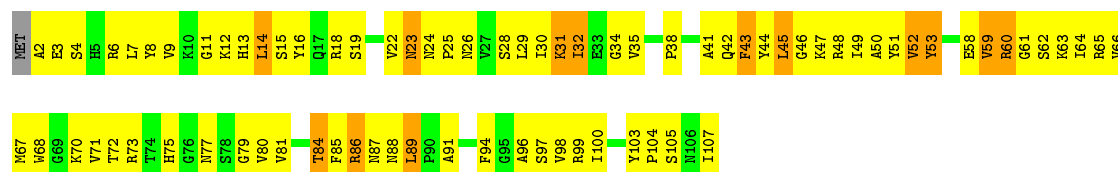
• Molecule 36: eL32 (yeast L32)

Chain JA: 32% 57% 8% ..



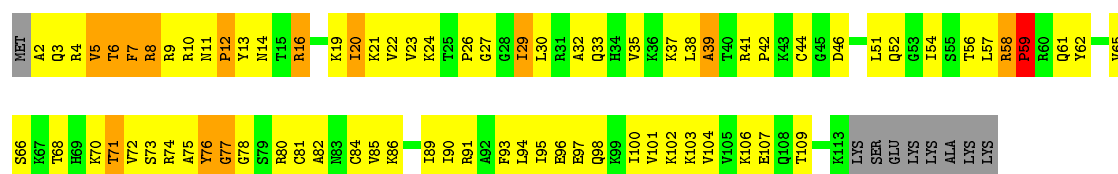
• Molecule 37: eL33 (yeast L33)

Chain KA: 26% 61% 12%



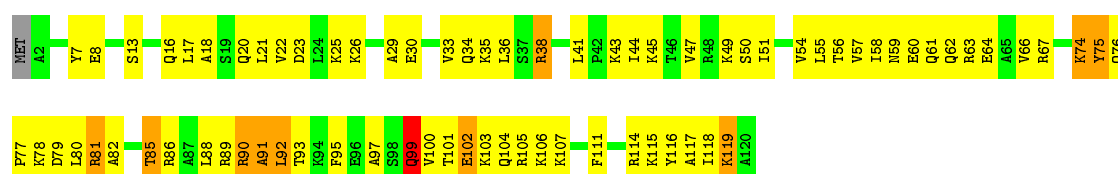
• Molecule 38: eL34 (yeast L34)

Chain LA: 28% 53% 11% 7%



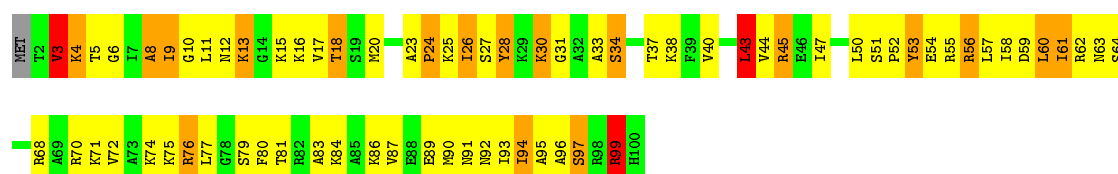
• Molecule 39: uL29 (yeast L35)

Chain MA: 37% 53% 8% ..



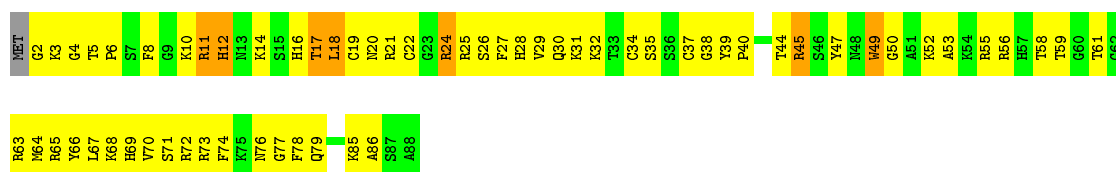
• Molecule 40: eL36 (yeast L36)

Chain NA: 27% 51% 18% ..



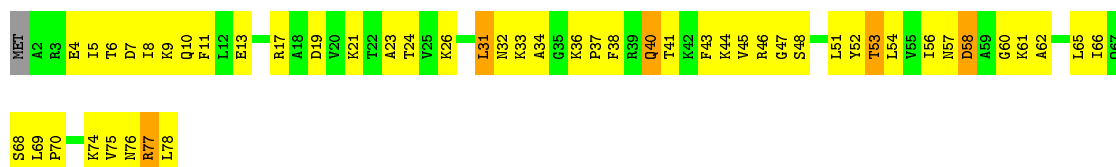
• Molecule 41: eL37 (yeast L37)

Chain OA: 28% 63% 8%



- Molecule 42: eL38 (yeast L38)

Chain PA: 35% 58% 6%



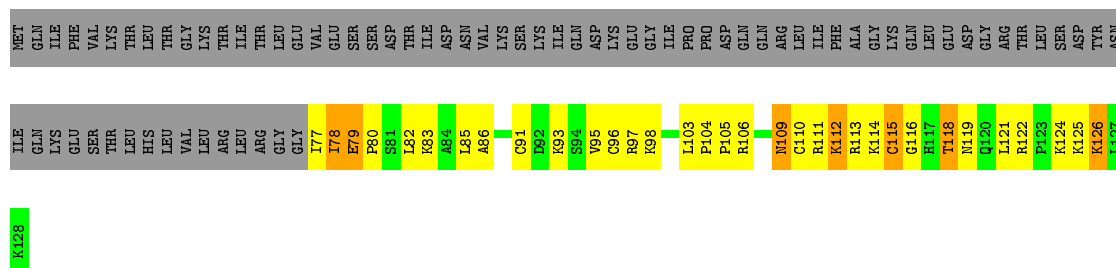
- Molecule 43: eL39 (yeast L39)

Chain QA: 24% 51% 22%



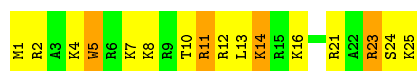
- Molecule 44: eL40 (yeast L40)

Chain RA: 15% 20% 5% 59%



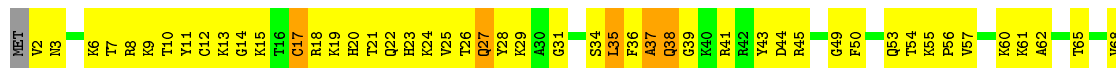
- Molecule 45: eL41 (yeast L41)

Chain SA: 36% 48% 16%



- Molecule 46: eL42 (yeast L42)

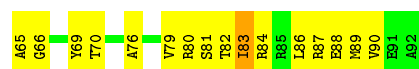
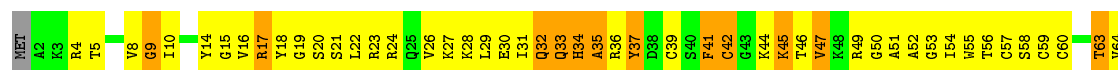
Chain TA: 31% 58% 9%





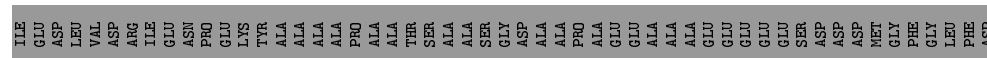
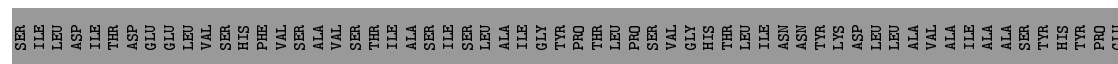
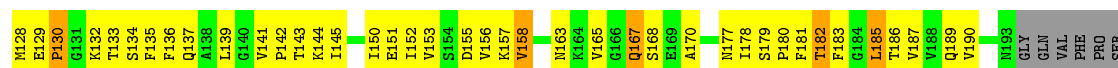
• Molecule 47: eL43 (yeast L43)

Chain UA: 28% 57% 14%



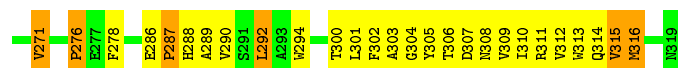
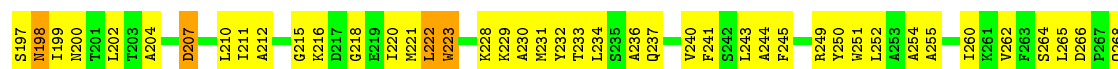
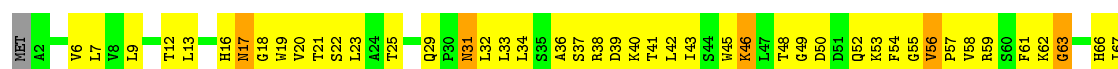
• Molecule 48: uL10 (yeast P0)

Chain VA: 17% 36% 7% 39%

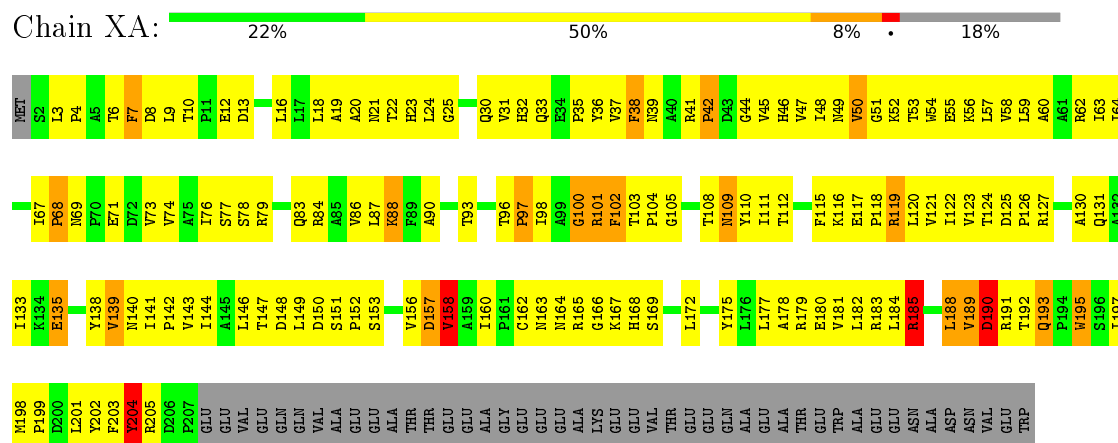


• Molecule 49: RACK1 (yeast Asc1)

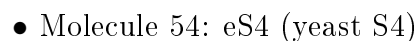
Chain WA: 35% 55% 9%



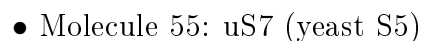
• Molecule 50: uS2 (yeast S0)



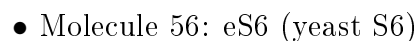
Response	Percentage
Yes	30%
No	55%
Don't know	6%
Other	7%

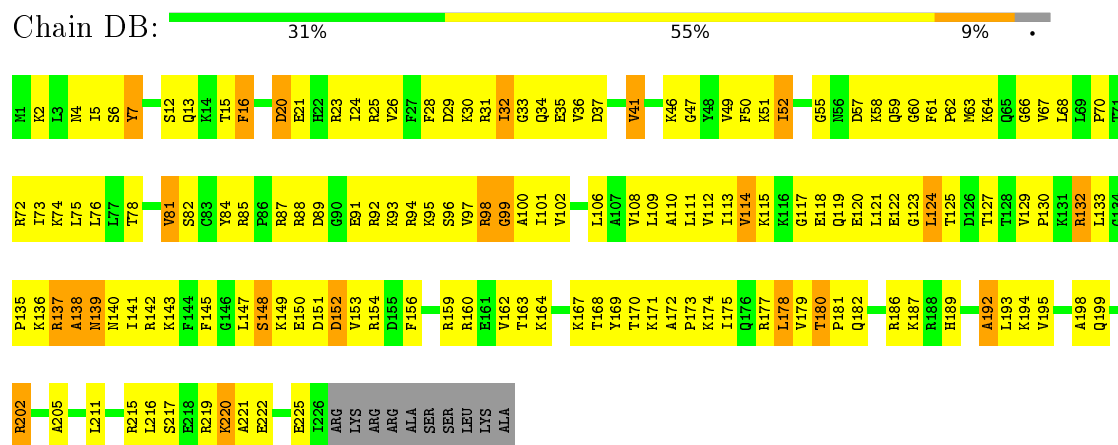


Response	Percentage
Yes	25%
No	61%
Don't know	13%

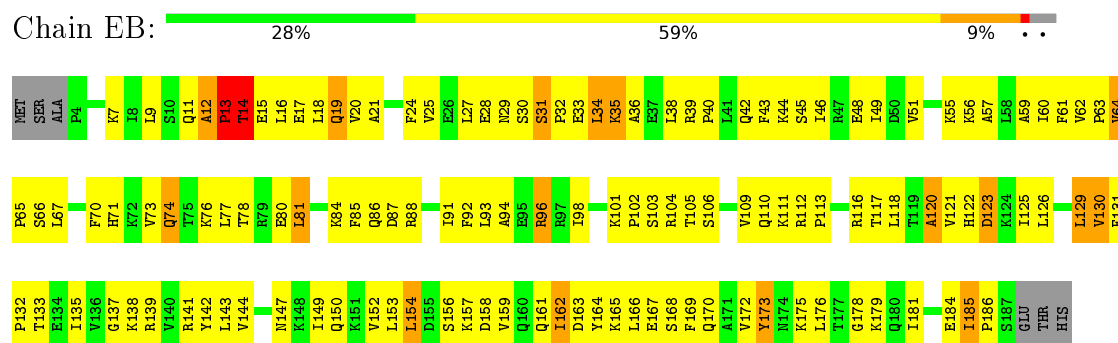


Response	Percentage
Yes, U.S. should take action to reduce greenhouse gas emissions	30%
No, U.S. should focus on other issues	54%
Don't know	8%
Refuse to answer	8%

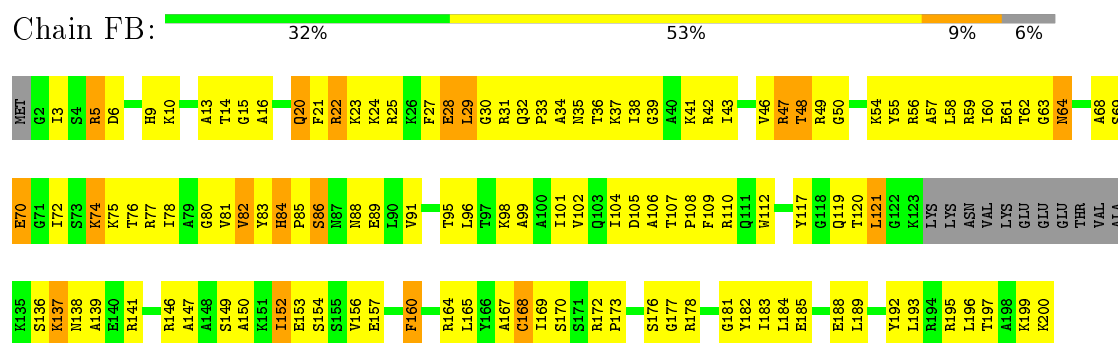




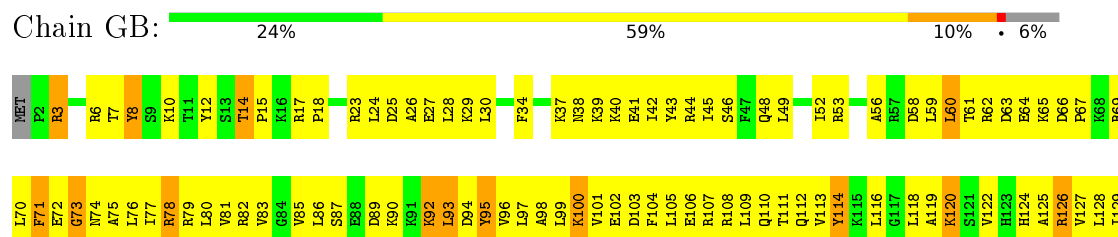
• Molecule 57: eS7 (yeast S7)

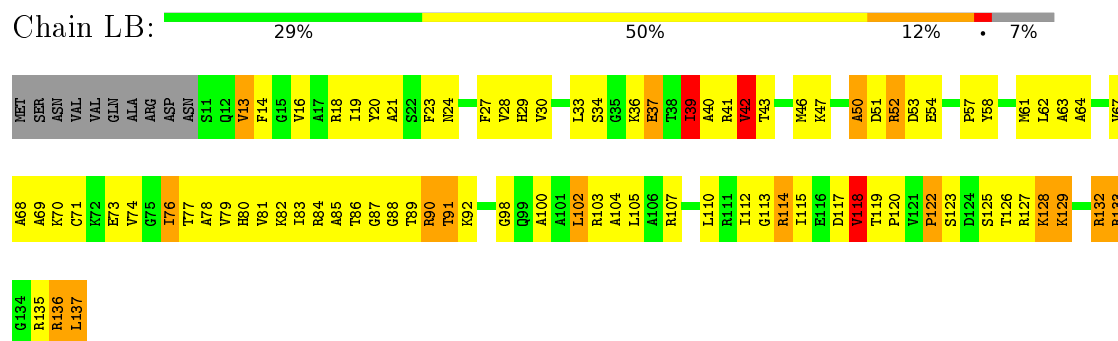


• Molecule 58: eS8 (yeast S8)

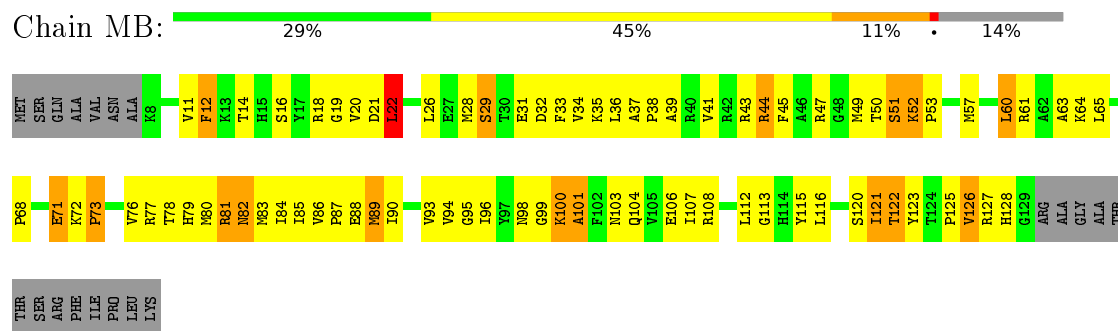


• Molecule 59: uS4 (yeast S9)

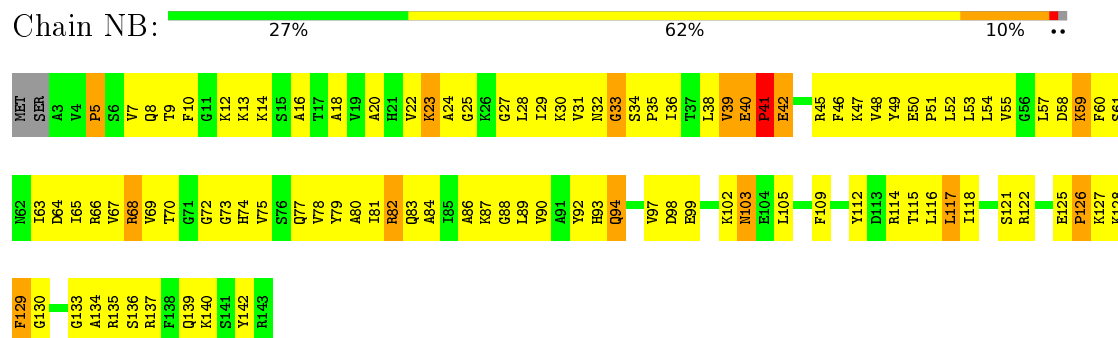




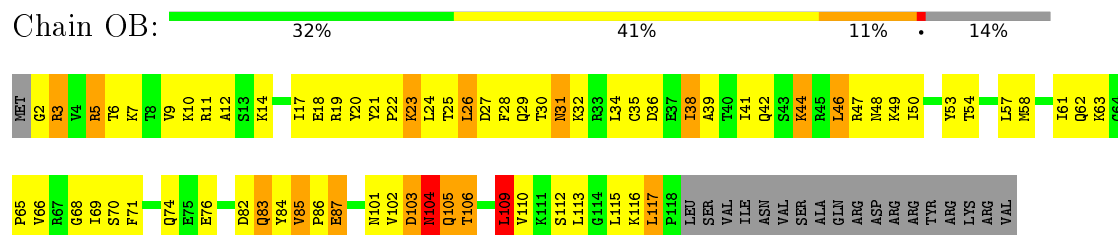
• Molecule 65: uS19 (yeast S15)



• Molecule 66: uS9 (yeast S16)



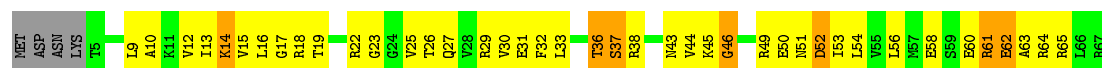
• Molecule 67: eS17 (yeast S17)



• Molecule 68: uS13 (yeast S18)



Chain ZB: 



- Molecule 79: uS14 (yeast S29)

Chain AC: 



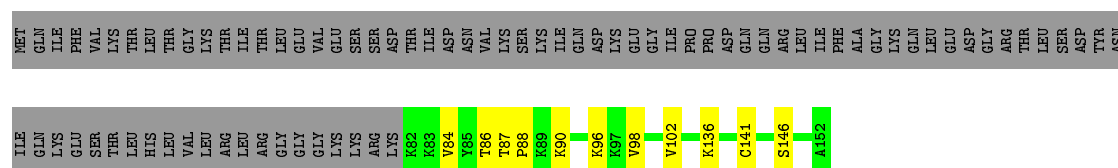
- Molecule 80: eS30 (yeast S30)

Chain BC: 




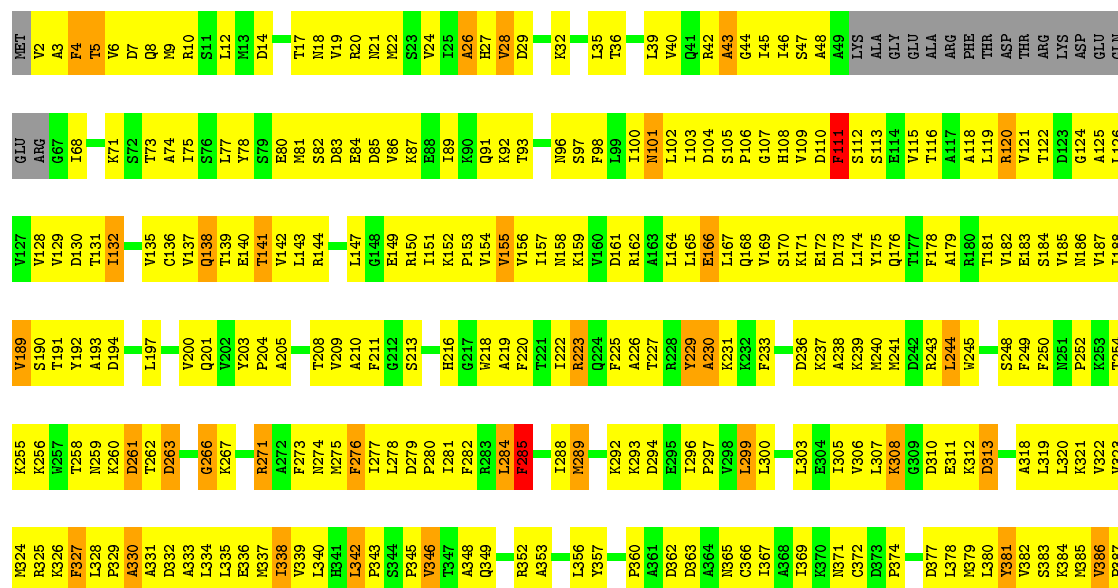
- Molecule 81: eS31 (yeast S31)

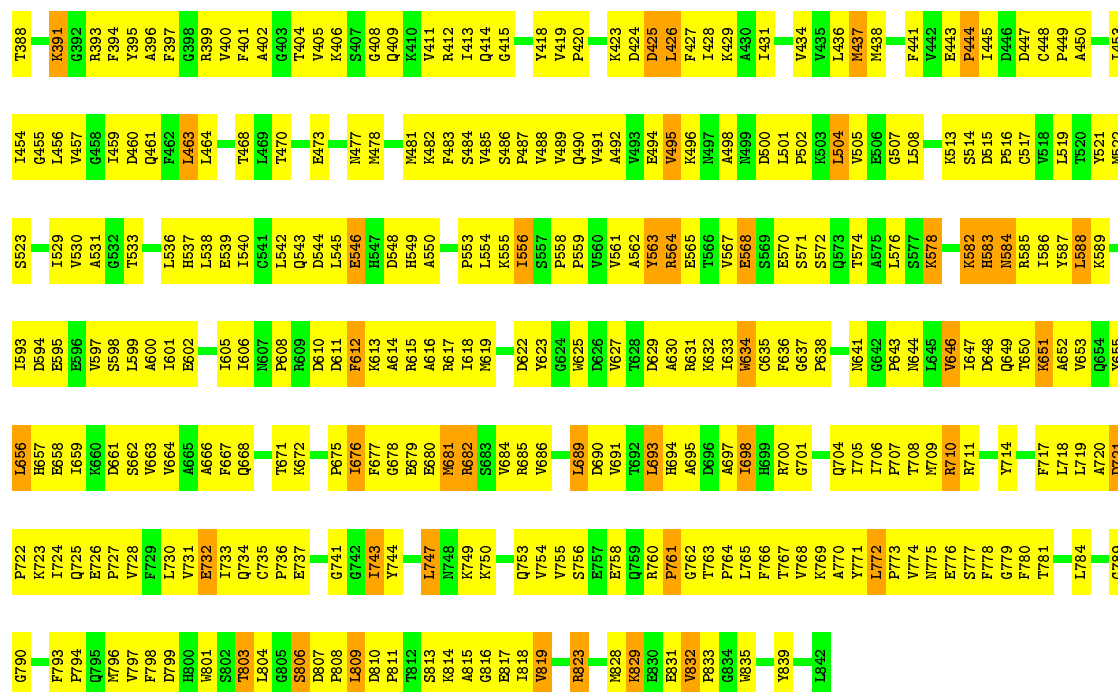
Chain CC: 



- Molecule 82: yeast eEF2

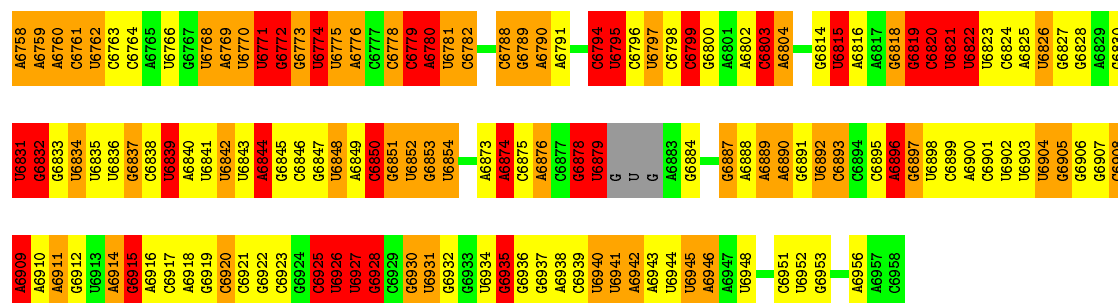
Chain DC: 





• Molecule 83: IRES

Chain EC: 28% 31% 24% 15%



4 Experimental information ⓘ

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	35045	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, SO1, MG, 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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.85	1/42096 (0.0%)	0.75	16/65570 (0.0%)
10	J	1.09	0/1425	0.76	1/1912 (0.1%)
11	K	1.13	0/1822	0.68	0/2451
12	L	0.95	0/1850	0.64	0/2495
13	M	1.05	0/1540	0.67	1/2073 (0.0%)
14	N	1.09	0/1754	0.64	0/2350
15	O	0.87	0/1375	0.63	0/1842
16	P	1.81	0/728	0.79	0/975
17	Q	1.03	0/1568	0.68	0/2106
18	R	1.16	0/1069	0.67	0/1438
19	S	1.13	0/1758	0.68	0/2354
2	B	1.16	20/78587 (0.0%)	0.77	40/122484 (0.0%)
20	T	1.11	0/1586	0.65	0/2128
21	U	1.12	0/1466	0.65	0/1968
22	V	1.09	0/1466	0.68	0/1965
23	W	0.90	0/1539	0.62	0/2050
24	X	1.18	0/1482	0.69	0/1990
25	Y	1.17	0/1301	0.68	0/1743
26	Z	0.82	0/812	0.58	0/1099
27	AA	1.04	0/1019	0.67	0/1369
28	BA	1.17	0/521	0.68	0/691
29	CA	1.06	0/984	0.66	0/1325
3	C	1.17	3/3747 (0.1%)	0.76	3/5832 (0.1%)
30	DA	1.09	0/1005	0.67	2/1341 (0.1%)
31	EA	0.85	0/1119	0.59	0/1497
32	FA	1.04	0/1205	0.65	0/1612
33	GA	1.02	0/474	0.66	0/629
34	HA	0.83	0/751	0.65	0/1008
35	IA	0.95	0/904	0.64	0/1213
36	JA	1.15	0/1041	0.62	0/1394
37	KA	1.14	0/869	0.69	0/1168
38	LA	0.98	0/891	0.67	0/1191

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	MA	1.02	0/979	0.66	0/1301
4	D	1.08	1/2884 (0.0%)	0.73	1/4491 (0.0%)
40	NA	0.94	0/779	0.70	1/1034 (0.1%)
41	OA	1.20	0/697	0.69	0/923
42	PA	0.92	0/619	0.61	0/826
43	QA	1.16	0/444	0.71	0/588
44	RA	1.11	0/424	0.65	0/562
45	SA	0.96	0/235	0.62	0/300
46	TA	1.04	0/861	0.66	0/1136
47	UA	1.02	0/702	0.65	0/934
48	VA	1.72	0/1498	0.83	1/2025 (0.0%)
49	WA	0.83	0/2498	0.58	0/3398
5	E	1.90	2/1377 (0.1%)	0.82	1/1844 (0.1%)
50	XA	0.67	0/1653	0.64	1/2261 (0.0%)
51	YA	0.71	0/1735	0.59	0/2335
52	ZA	0.71	0/1665	0.58	0/2263
53	AB	0.84	0/1759	0.60	0/2368
54	BB	0.72	0/2110	0.63	0/2839
55	CB	0.74	0/1630	0.61	0/2202
56	DB	0.74	0/1844	0.61	0/2464
57	EB	0.81	0/1506	0.61	0/2028
58	FB	0.86	0/1515	0.59	0/2021
59	GB	0.70	0/1519	0.61	0/2035
6	F	1.03	0/1952	0.71	0/2622
60	HB	0.98	0/837	0.59	0/1131
61	IB	0.92	0/1273	0.61	0/1712
62	JB	1.10	0/495	0.56	0/617
63	KB	0.80	0/1216	0.62	0/1638
64	LB	0.64	0/953	0.60	0/1279
65	MB	1.05	0/996	0.64	0/1335
66	NB	0.80	0/1126	0.60	0/1510
67	OB	0.77	0/844	0.76	1/1120 (0.1%)
68	PB	0.86	0/1212	0.62	0/1628
69	QB	0.79	0/1131	0.57	0/1517
7	G	1.00	0/3153	0.65	0/4239
70	RB	0.86	0/866	0.60	0/1169
71	SB	0.68	0/694	0.56	0/935
72	TB	0.75	0/1039	0.62	0/1395
73	UB	0.87	0/1140	0.65	1/1518 (0.1%)
74	VB	0.71	0/1088	0.59	0/1449
75	WB	0.80	0/571	0.60	0/768
76	XB	0.69	0/782	0.60	0/1047
77	YB	0.74	0/621	0.62	0/838

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
78	ZB	0.72	0/500	0.59	0/670
79	AC	0.94	0/454	0.58	0/602
8	H	1.11	0/2802	0.70	1/3792 (0.0%)
80	BC	0.83	0/483	0.57	0/643
81	CC	1.05	0/283	0.63	0/352
82	DC	1.41	0/6521	0.71	2/8830 (0.0%)
83	EC	2.21	71/4413 (1.6%)	1.02	23/6849 (0.3%)
9	I	0.93	0/2426	0.65	0/3271
All	All	1.08	98/230558 (0.0%)	0.73	96/337917 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	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 98 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	EC	6875	C	N1-C2	7.27	1.47	1.40
83	EC	6831	U	N1-C2	7.18	1.45	1.38
83	EC	6879	U	N1-C2	7.00	1.44	1.38
83	EC	6843	U	N1-C2	6.99	1.44	1.38
83	EC	6775	U	N1-C2	6.94	1.44	1.38

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	EC	6799	C	N1-C1'-C2'	8.09	124.52	114.00
48	VA	182	THR	N-CA-C	7.73	131.88	111.00
10	J	126	GLN	N-CA-C	-7.47	90.83	111.00
83	EC	6774	U	N1-C1'-C2'	7.36	123.57	114.00
2	B	3360	C	N1-C1'-C2'	7.26	123.44	114.00

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 ⓘ

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	1739	0
2	B	70248	0	35241	3748	0
3	C	3354	0	1695	184	0
4	D	2580	0	1304	123	0
5	E	1359	0	1425	113	0
6	F	1918	0	1987	279	0
7	G	3082	0	3165	364	0
8	H	2750	0	2863	343	0
9	I	2376	0	2325	266	0
10	J	1401	0	1501	161	0
11	K	1785	0	1862	230	0
12	L	1818	0	1908	203	0
13	M	1519	0	1587	161	0
14	N	1718	0	1754	166	0
15	O	1354	0	1383	182	0
16	P	723	0	774	107	0
17	Q	1543	0	1608	188	0
18	R	1054	0	1149	174	0
19	S	1721	0	1779	243	0
20	T	1556	0	1659	150	0
21	U	1443	0	1485	166	0
22	V	1442	0	1543	200	0
23	W	1522	0	1617	164	0
24	X	1446	0	1487	179	0
25	Y	1277	0	1323	152	0
26	Z	796	0	812	60	0
27	AA	1004	0	1048	113	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	BA	509	0	537	51	0
29	CA	969	0	1036	133	0
30	DA	994	0	1081	124	0
31	EA	1093	0	1155	140	0
32	FA	1174	0	1215	132	0
33	GA	463	0	491	41	0
34	HA	743	0	797	90	0
35	IA	890	0	938	84	0
36	JA	1020	0	1090	89	0
37	KA	851	0	880	121	0
38	LA	881	0	949	128	0
39	MA	970	0	1078	122	0
40	NA	772	0	849	109	0
41	OA	682	0	687	83	0
42	PA	613	0	682	52	0
43	QA	437	0	475	72	0
44	RA	418	0	459	43	0
45	SA	234	0	284	20	0
46	TA	848	0	918	69	0
47	UA	695	0	738	87	0
48	VA	1473	0	1514	176	0
49	WA	2445	0	2401	191	0
50	XA	1612	0	1623	176	0
51	YA	1709	0	1784	217	0
52	ZA	1635	0	1723	207	0
53	AB	1734	0	1817	169	0
54	BB	2069	0	2154	255	0
55	CB	1610	0	1675	180	0
56	DB	1820	0	1918	158	0
57	EB	1481	0	1572	152	0
58	FB	1490	0	1525	155	0
59	GB	1494	0	1573	181	0
60	HB	817	0	804	72	0
61	IB	1245	0	1314	123	0
62	JB	496	0	141	0	0
63	KB	1193	0	1255	126	0
64	LB	942	0	979	148	0
65	MB	975	0	1017	91	0
66	NB	1106	0	1166	141	0
67	OB	836	0	827	75	0
68	PB	1193	0	1222	100	0
69	QB	1113	0	1124	140	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	RB	856	0	917	97	0
71	SB	685	0	672	107	0
72	TB	1022	0	1060	133	0
73	UB	1122	0	1196	121	0
74	VB	1074	0	1132	119	0
75	WB	563	0	603	85	0
76	XB	769	0	818	104	0
77	YB	611	0	633	76	0
78	ZB	498	0	535	56	0
79	AC	444	0	436	61	0
80	BC	475	0	525	38	0
81	CC	284	0	76	0	0
82	DC	6419	0	6493	727	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	14774	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 14774 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	25
6	F	250/254 (98%)	165 (66%)	71 (28%)	14 (6%)	2	29
7	G	384/387 (99%)	277 (72%)	79 (21%)	28 (7%)	1	22
8	H	359/362 (99%)	253 (70%)	76 (21%)	30 (8%)	1	17
9	I	294/297 (99%)	221 (75%)	57 (19%)	16 (5%)	2	30
10	J	173/176 (98%)	117 (68%)	40 (23%)	16 (9%)	1	16
11	K	220/244 (90%)	173 (79%)	30 (14%)	17 (8%)	1	20
12	L	231/256 (90%)	165 (71%)	43 (19%)	23 (10%)	1	13
13	M	189/191 (99%)	146 (77%)	37 (20%)	6 (3%)	5	44
14	N	207/221 (94%)	157 (76%)	42 (20%)	8 (4%)	4	38
15	O	167/174 (96%)	125 (75%)	28 (17%)	14 (8%)	1	17
16	P	92/165 (56%)	63 (68%)	18 (20%)	11 (12%)	0	8
17	Q	191/199 (96%)	140 (73%)	38 (20%)	13 (7%)	1	24
18	R	134/138 (97%)	101 (75%)	24 (18%)	9 (7%)	1	25
19	S	201/204 (98%)	155 (77%)	33 (16%)	13 (6%)	1	26
20	T	195/199 (98%)	158 (81%)	30 (15%)	7 (4%)	4	41
21	U	181/184 (98%)	135 (75%)	35 (19%)	11 (6%)	2	27
22	V	183/186 (98%)	135 (74%)	34 (19%)	14 (8%)	1	20
23	W	186/189 (98%)	151 (81%)	30 (16%)	5 (3%)	6	47
24	X	170/172 (99%)	126 (74%)	25 (15%)	19 (11%)	0	10
25	Y	157/160 (98%)	102 (65%)	41 (26%)	14 (9%)	1	17
26	Z	98/121 (81%)	68 (69%)	22 (22%)	8 (8%)	1	18
27	AA	134/137 (98%)	95 (71%)	32 (24%)	7 (5%)	2	31
28	BA	59/155 (38%)	44 (75%)	8 (14%)	7 (12%)	0	8
29	CA	119/142 (84%)	90 (76%)	18 (15%)	11 (9%)	1	16
30	DA	124/127 (98%)	93 (75%)	21 (17%)	10 (8%)	1	19
31	EA	133/136 (98%)	93 (70%)	28 (21%)	12 (9%)	1	17
32	FA	146/149 (98%)	108 (74%)	31 (21%)	7 (5%)	3	32
33	GA	56/59 (95%)	45 (80%)	9 (16%)	2 (4%)	4	41
34	HA	95/105 (90%)	74 (78%)	16 (17%)	5 (5%)	2	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	IA	107/113 (95%)	84 (78%)	17 (16%)	6 (6%)	2	29
36	JA	125/130 (96%)	89 (71%)	27 (22%)	9 (7%)	1	23
37	KA	104/107 (97%)	82 (79%)	20 (19%)	2 (2%)	10	54
38	LA	110/121 (91%)	79 (72%)	23 (21%)	8 (7%)	1	22
39	MA	117/120 (98%)	89 (76%)	21 (18%)	7 (6%)	2	27
40	NA	97/100 (97%)	70 (72%)	13 (13%)	14 (14%)	0	5
41	OA	85/88 (97%)	65 (76%)	17 (20%)	3 (4%)	4	42
42	PA	75/78 (96%)	61 (81%)	14 (19%)	0	100	100
43	QA	48/51 (94%)	38 (79%)	6 (12%)	4 (8%)	1	18
44	RA	50/128 (39%)	32 (64%)	13 (26%)	5 (10%)	1	13
45	SA	23/25 (92%)	20 (87%)	3 (13%)	0	100	100
46	TA	103/106 (97%)	73 (71%)	19 (18%)	11 (11%)	0	11
47	UA	89/92 (97%)	55 (62%)	22 (25%)	12 (14%)	0	6
48	VA	187/312 (60%)	128 (68%)	42 (22%)	17 (9%)	1	16
49	WA	316/319 (99%)	229 (72%)	72 (23%)	15 (5%)	3	33
50	XA	204/252 (81%)	136 (67%)	49 (24%)	19 (9%)	1	16
51	YA	212/255 (83%)	146 (69%)	48 (23%)	18 (8%)	1	17
52	ZA	215/254 (85%)	165 (77%)	36 (17%)	14 (6%)	1	26
53	AB	221/240 (92%)	167 (76%)	39 (18%)	15 (7%)	1	24
54	BB	258/261 (99%)	178 (69%)	59 (23%)	21 (8%)	1	19
55	CB	204/225 (91%)	155 (76%)	31 (15%)	18 (9%)	1	17
56	DB	224/236 (95%)	167 (75%)	39 (17%)	18 (8%)	1	19
57	EB	182/190 (96%)	127 (70%)	40 (22%)	15 (8%)	1	18
58	FB	184/200 (92%)	149 (81%)	26 (14%)	9 (5%)	3	32
59	GB	183/197 (93%)	129 (70%)	35 (19%)	19 (10%)	1	12
60	HB	94/105 (90%)	67 (71%)	15 (16%)	12 (13%)	0	7
61	IB	153/156 (98%)	107 (70%)	34 (22%)	12 (8%)	1	20
62	JB	122/143 (85%)	74 (61%)	35 (29%)	13 (11%)	0	11
63	KB	148/151 (98%)	119 (80%)	21 (14%)	8 (5%)	2	30
64	LB	125/137 (91%)	83 (66%)	35 (28%)	7 (6%)	2	29
65	MB	120/142 (84%)	82 (68%)	25 (21%)	13 (11%)	0	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	NB	139/143 (97%)	104 (75%)	26 (19%)	9 (6%)	1	26
67	OB	115/136 (85%)	84 (73%)	21 (18%)	10 (9%)	1	17
68	PB	143/146 (98%)	109 (76%)	20 (14%)	14 (10%)	1	14
69	QB	141/144 (98%)	104 (74%)	23 (16%)	14 (10%)	1	13
70	RB	105/121 (87%)	73 (70%)	28 (27%)	4 (4%)	4	39
71	SB	85/87 (98%)	61 (72%)	14 (16%)	10 (12%)	0	9
72	TB	127/130 (98%)	93 (73%)	27 (21%)	7 (6%)	2	30
73	UB	142/145 (98%)	97 (68%)	36 (25%)	9 (6%)	2	27
74	VB	132/135 (98%)	94 (71%)	26 (20%)	12 (9%)	1	16
75	WB	68/108 (63%)	41 (60%)	21 (31%)	6 (9%)	1	17
76	XB	95/119 (80%)	52 (55%)	26 (27%)	17 (18%)	0	3
77	YB	79/82 (96%)	53 (67%)	21 (27%)	5 (6%)	2	27
78	ZB	61/67 (91%)	46 (75%)	10 (16%)	5 (8%)	1	18
79	AC	51/56 (91%)	37 (72%)	12 (24%)	2 (4%)	4	38
80	BC	58/63 (92%)	38 (66%)	15 (26%)	5 (9%)	1	17
81	CC	69/152 (45%)	41 (59%)	17 (25%)	11 (16%)	0	5
82	DC	819/842 (97%)	620 (76%)	154 (19%)	45 (6%)	2	30
All	All	12207/13416 (91%)	8881 (73%)	2429 (20%)	897 (7%)	3	22

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	19
6	F	194/196 (99%)	169 (87%)	25 (13%)	5	31
7	G	322/323 (100%)	283 (88%)	39 (12%)	6	33
8	H	288/289 (100%)	263 (91%)	25 (9%)	13	48
9	I	244/245 (100%)	220 (90%)	24 (10%)	10	43
10	J	152/153 (99%)	131 (86%)	21 (14%)	4	29
11	K	186/205 (91%)	165 (89%)	21 (11%)	7	37
12	L	191/208 (92%)	177 (93%)	14 (7%)	17	57
13	M	171/171 (100%)	152 (89%)	19 (11%)	8	38
14	N	180/187 (96%)	165 (92%)	15 (8%)	14	51
15	O	147/150 (98%)	126 (86%)	21 (14%)	4	28
16	P	81/136 (60%)	69 (85%)	12 (15%)	4	26
17	Q	154/159 (97%)	132 (86%)	22 (14%)	4	28
18	R	107/109 (98%)	94 (88%)	13 (12%)	6	33
19	S	175/176 (99%)	156 (89%)	19 (11%)	8	38
20	T	160/162 (99%)	144 (90%)	16 (10%)	9	42
21	U	145/146 (99%)	125 (86%)	20 (14%)	4	29
22	V	150/151 (99%)	140 (93%)	10 (7%)	20	60
23	W	153/154 (99%)	139 (91%)	14 (9%)	11	46
24	X	156/156 (100%)	136 (87%)	20 (13%)	5	31
25	Y	136/137 (99%)	109 (80%)	27 (20%)	1	13
26	Z	87/107 (81%)	83 (95%)	4 (5%)	33	70
27	AA	104/105 (99%)	88 (85%)	16 (15%)	3	24
28	BA	54/129 (42%)	48 (89%)	6 (11%)	8	38
29	CA	105/118 (89%)	88 (84%)	17 (16%)	3	22
30	DA	109/110 (99%)	98 (90%)	11 (10%)	9	41
31	EA	115/116 (99%)	103 (90%)	12 (10%)	9	40
32	FA	118/119 (99%)	110 (93%)	8 (7%)	20	59
33	GA	46/47 (98%)	39 (85%)	7 (15%)	3	25
34	HA	81/88 (92%)	72 (89%)	9 (11%)	8	38
35	IA	96/97 (99%)	90 (94%)	6 (6%)	22	61
36	JA	109/111 (98%)	95 (87%)	14 (13%)	5	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	KA	90/91 (99%)	77 (86%)	13 (14%)	4	27
38	LA	95/103 (92%)	85 (90%)	10 (10%)	8	40
39	MA	104/105 (99%)	95 (91%)	9 (9%)	13	48
40	NA	81/82 (99%)	66 (82%)	15 (18%)	2	15
41	OA	70/71 (99%)	61 (87%)	9 (13%)	5	31
42	PA	68/69 (99%)	60 (88%)	8 (12%)	6	35
43	QA	45/46 (98%)	36 (80%)	9 (20%)	1	13
44	RA	47/116 (40%)	41 (87%)	6 (13%)	5	31
45	SA	23/23 (100%)	19 (83%)	4 (17%)	2	18
46	TA	90/91 (99%)	80 (89%)	10 (11%)	8	38
47	UA	71/72 (99%)	64 (90%)	7 (10%)	10	43
48	VA	160/254 (63%)	145 (91%)	15 (9%)	11	45
49	WA	261/262 (100%)	233 (89%)	28 (11%)	8	39
50	XA	173/210 (82%)	153 (88%)	20 (12%)	7	36
51	YA	191/224 (85%)	174 (91%)	17 (9%)	12	48
52	ZA	176/205 (86%)	169 (96%)	7 (4%)	38	73
53	AB	182/195 (93%)	164 (90%)	18 (10%)	10	43
54	BB	221/222 (100%)	197 (89%)	24 (11%)	8	38
55	CB	173/191 (91%)	162 (94%)	11 (6%)	22	61
56	DB	193/201 (96%)	177 (92%)	16 (8%)	14	51
57	EB	165/170 (97%)	154 (93%)	11 (7%)	20	60
58	FB	150/161 (93%)	135 (90%)	15 (10%)	9	42
59	GB	158/166 (95%)	140 (89%)	18 (11%)	7	36
60	HB	89/98 (91%)	79 (89%)	10 (11%)	7	37
61	IB	136/137 (99%)	121 (89%)	15 (11%)	8	38
63	KB	127/128 (99%)	118 (93%)	9 (7%)	18	58
64	LB	96/105 (91%)	79 (82%)	17 (18%)	2	18
65	MB	103/118 (87%)	95 (92%)	8 (8%)	16	54
66	NB	117/119 (98%)	107 (92%)	10 (8%)	13	51
67	OB	82/124 (66%)	65 (79%)	17 (21%)	1	11
68	PB	128/129 (99%)	112 (88%)	16 (12%)	6	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	QB	115/116 (99%)	105 (91%)	10 (9%)	13	48
70	RB	100/114 (88%)	91 (91%)	9 (9%)	12	47
71	SB	74/74 (100%)	69 (93%)	5 (7%)	20	59
72	TB	110/111 (99%)	96 (87%)	14 (13%)	5	31
73	UB	119/120 (99%)	109 (92%)	10 (8%)	14	51
74	VB	112/113 (99%)	105 (94%)	7 (6%)	22	61
75	WB	61/89 (68%)	57 (93%)	4 (7%)	21	60
76	XB	83/101 (82%)	76 (92%)	7 (8%)	14	51
77	YB	70/71 (99%)	65 (93%)	5 (7%)	18	58
78	ZB	56/60 (93%)	53 (95%)	3 (5%)	27	67
79	AC	47/49 (96%)	44 (94%)	3 (6%)	22	61
80	BC	51/54 (94%)	49 (96%)	2 (4%)	39	74
82	DC	699/714 (98%)	622 (89%)	77 (11%)	8	38
All	All	10235/11032 (93%)	9143 (89%)	1092 (11%)	13	39

5 of 1092 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	FA	46	ASP
44	RA	115	CYS
78	ZB	52	ASP
34	HA	69	TYR
38	LA	58	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 315 such sidechains are listed below:

Mol	Chain	Res	Type
36	JA	49	ASN
49	WA	147	HIS
82	DC	21	ASN
37	KA	39	GLN
41	OA	76	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1755/1798 (97%)	359 (20%)	19 (1%)
2	B	3265/3396 (96%)	569 (17%)	29 (0%)
3	C	157/158 (99%)	25 (15%)	2 (1%)
4	D	120/121 (99%)	17 (14%)	0
83	EC	176/201 (87%)	70 (39%)	4 (2%)
All	All	5473/5674 (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	658	G
2	B	1481	A
3	C	85	G
2	B	780	A
2	B	1307	G

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	13,20,21	1.57	2 (15%)	12,28,30	2.39	4 (33%)

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	-	0/19/21/23	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	DC	699	DDE	OAG-CBI	2.14	1.27	1.23
82	DC	699	DDE	CBW-CBI	4.01	1.59	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	DC	699	DDE	CAU-CBW-CBI	-4.43	101.78	110.72
82	DC	699	DDE	CAC-NCB-CBW	2.42	116.07	110.57
82	DC	699	DDE	OAG-CBI-NAD	2.53	127.25	123.06
82	DC	699	DDE	CAU-CAT-CE1	5.10	140.08	112.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
84	GDP	DC	901	85	24,30,30	2.16	8 (33%)	26,47,47	2.47	8 (30%)
86	SO1	DC	903	-	36,39,39	2.75	20 (55%)	36,64,64	1.70	8 (22%)

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	-	0/12/32/32	0/3/3/3
86	SO1	DC	903	-	-	0/15/104/104	0/2/5/5

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	DC	903	SO1	O56-C52	-4.38	1.30	1.41
84	DC	901	GDP	C8-N7	-2.09	1.30	1.34
86	DC	903	SO1	C24-C18	2.02	1.59	1.54
86	DC	903	SO1	C2-C6	2.14	1.59	1.55
86	DC	903	SO1	C4-C13	2.20	1.59	1.54

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	DC	901	GDP	N3-C2-N1	-6.73	118.40	127.56
84	DC	901	GDP	C5-C6-N1	-4.93	117.08	123.52
86	DC	903	SO1	C12-C6-C10	-3.20	102.20	107.47
86	DC	903	SO1	C7-C2-C8	-3.08	104.60	110.16
84	DC	901	GDP	C6-C5-C4	-2.85	117.60	120.86

There are no chirality outliers.

There are no torsion outliers.

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

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.