



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:34 PM BST

PDB ID : 3JAJ
EMDB ID: : EMD-3037
Title : Structure of the engaged state of the mammalian SRP-ribosome complex
Authors : Voorhees, R.M.; Hegde, R.S.
Deposited on : 2015-06-16
Resolution : 3.75 Å(reported)
Based on PDB ID : 3J7O, 4P3E, 1WGW, 1E8S, 1QB2, 1E80, 3J7P

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 : unknown
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) : trunk27241

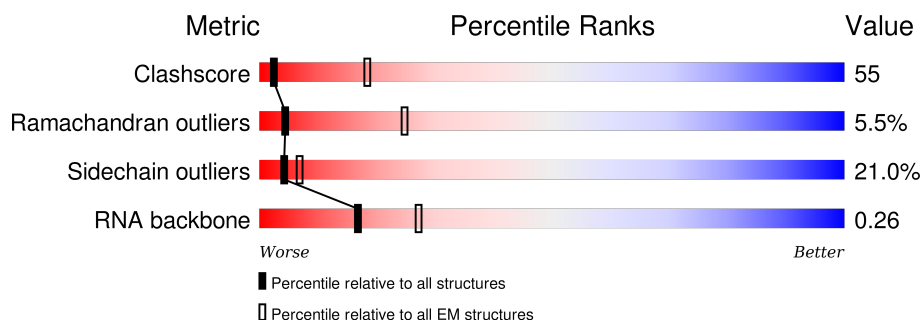
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.75 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.














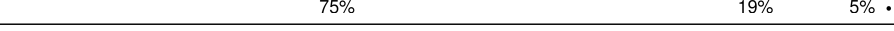







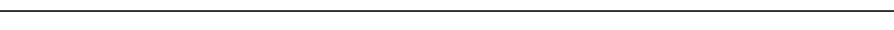

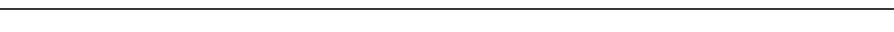
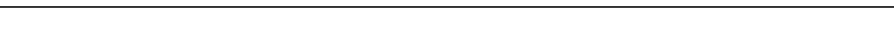


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	244	57% 25% 13% 5%
2	D	292	52% 30% 13% 5%
3	G	238	58% 28% 11% .
4	H	190	63% 25% 6% 6%
5	J	170	58% 31% 8% .
6	L	210	60% 26% 10% .
7	M	138	57% 33% 8% .
8	N	203	49% 33% 11% 6%




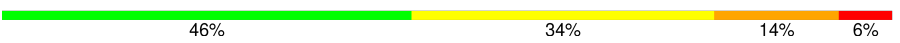







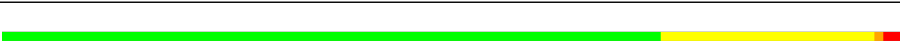
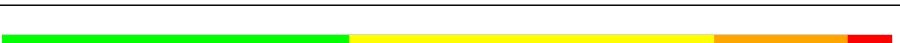



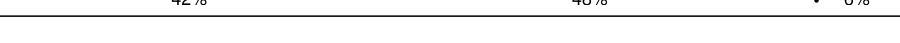
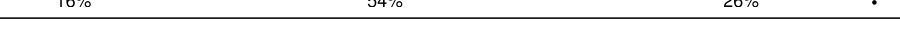
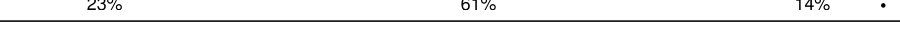




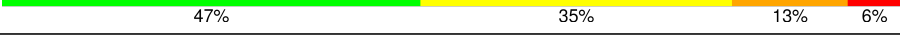

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Mol	Chain	Length	Quality of chain
9	O	201	
10	Q	187	
11	R	180	
12	S	175	
13	T	159	
14	U	99	
15	V	131	
16	X	119	
17	Y	134	
18	Z	135	
19	a	147	
20	b	75	
21	c	94	
22	d	107	
23	e	128	
24	f	109	
25	g	114	
26	h	122	
27	i	102	
28	k	69	
29	l	50	
30	m	52	
31	o	104	
32	5	3658	
33	7	120	


























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Mol	Chain	Length	Quality of chain
34	8	156	
35	B	394	
36	C	367	
37	E	236	
38	F	225	
39	I	213	
40	P	153	
41	W	63	
42	j	86	
43	n	23	
44	p	91	
45	r	125	
46	K	163	
47	q	202	
48	z	426	
49	2	31	
50	3	76	
51	4	206	
52	9	105	
53	6	179	
54	S2	1742	
55	SA	208	
56	SB	213	
57	SC	218	
58	SE	262	



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Mol	Chain	Length	Quality of chain
59	SG	237	
60	SH	189	
61	SI	206	
62	SJ	185	
63	SL	152	
64	SN	149	
65	SO	136	
66	SV	82	
67	SW	129	
68	SX	141	
69	SY	126	
70	Sa	98	
71	Sb	83	
72	Se	57	
73	SD	227	
74	SF	191	
75	SK	98	
76	SM	124	
77	SP	96	
78	SQ	141	
79	SR	129	
80	SS	137	
81	ST	141	
82	SU	104	
83	SZ	75	

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Mol	Chain	Length	Quality of chain
84	Sc	64	 84%13%•
85	Sd	52	 77%17%••
86	Sf	71	 56%30%10%•
87	Sg	313	 83%15%•
88	S1	74	 58%26%15%•
89	S4	76	 74%22%•

2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 228197 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 protein called Ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 2 is a protein called Ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	292	Total	C	N	O	S	0	0
			2380	1508	434	426	12		

- Molecule 3 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	238	Total	C	N	O	S	0	0
			1912	1218	368	322	4		

- Molecule 4 is a protein called Ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 5 is a protein called Ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 6 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 7 is a protein called Ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 8 is a protein called Ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 9 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	201	Total	C	N	O	S	0	0
			1651	1063	323	260	5		

- Molecule 10 is a protein called Ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 11 is a protein called Ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 12 is a protein called Ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 13 is a protein called Ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 14 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 15 is a protein called Ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 16 is a protein called Ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 17 is a protein called Ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 18 is a protein called Ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 19 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 20 is a protein called Ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 21 is a protein called Ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 22 is a protein called Ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 23 is a protein called Ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 24 is a protein called Ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	f	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 25 is a protein called Ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 26 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 27 is a protein called Ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	i	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 28 is a protein called Ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 29 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 30 is a protein called Ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 31 is a protein called Ribosomal protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 32 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	3658	Total	C	N	O	P	0	0
			78406	34911	14352	25486	3657		

- Molecule 33 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 34 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 35 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

- Molecule 36 is a protein called Ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

- Molecule 37 is a protein called Ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

- Molecule 38 is a protein called Ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 39 is a protein called Ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	I	213	Total	C	N	O	S	0	0
			1713	1083	331	284	15		

- Molecule 40 is a protein called Ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 41 is a protein called Ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 42 is a protein called Ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

- Molecule 43 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 44 is a protein called Ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

- Molecule 46 is a protein called Ribosomal protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	K	163	Total	C	N	O	S	0	0
			1238	773	230	230	5		

- Molecule 47 is a protein called Ribosomal protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	202	Total	C	N	O	S	0	0
			1556	989	272	286	9		

- Molecule 48 is a protein called SRP54.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	z	426	Total	C	N	O	S	0	0
			3241	2047	555	615	24		

- Molecule 49 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2	31	Total	C	N	O	S	0	0
			233	167	32	32	2		

- Molecule 50 is a RNA chain called Val tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	76	Total	C	N	O	P	0	0
			1616	723	290	528	75		

- Molecule 51 is a RNA chain called SRP 7S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	206	Total	C	N	O	P	6	0
			4551	2026	836	1477	212		

- Molecule 52 is a protein called SRP19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	9	105	Total	C	N	O	S	0	0
			844	534	152	152	6		

- Molecule 53 is a protein called SRP68.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	179	Total	C	N	O	S	0	0
			1497	939	280	271	7		

- Molecule 54 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	S2	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

- Molecule 55 is a protein called Ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SA	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 56 is a protein called Ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SB	213	Total	C	N	O	S	0	0
			1725	1093	311	308	13		

- Molecule 57 is a protein called Ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SC	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 58 is a protein called Ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 59 is a protein called Ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 60 is a protein called Ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SH	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 61 is a protein called Ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 62 is a protein called Ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 63 is a protein called Ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SL	152	Total	C	N	O	S	0	0
			1238	788	232	212	6		

- Molecule 64 is a protein called Ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 65 is a protein called Ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 66 is a protein called Ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SV	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 67 is a protein called Ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 68 is a protein called Ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SX	141	Total	C	N	O	S	0	0
			1099	694	220	182	3		

- Molecule 69 is a protein called Ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SY	126	Total	C	N	O	S	0	0
			1023	646	200	172	5		

- Molecule 70 is a protein called Ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sa	98	Total	C	N	O	S	0	0
			781	486	161	129	5		

- Molecule 71 is a protein called Ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 72 is a protein called Ribosomal protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Se	57	Total	C	N	O	S	0	0
			452	279	99	73	1		

- Molecule 73 is a protein called Ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 74 is a protein called Ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 75 is a protein called Ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 76 is a protein called Ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SM	124	Total	C	N	O	S	0	0
			960	600	171	181	8		

- Molecule 77 is a protein called Ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SP	96	Total	C	N	O	S	0	0
			805	506	158	135	6		

- Molecule 78 is a protein called Ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 79 is a protein called Ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SR	129	Total	C	N	O	S	0	0
			1047	658	193	191	5		

- Molecule 80 is a protein called Ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	SS	137	Total	C	N	O	S	0	0
			1139	714	231	193	1		

- Molecule 81 is a protein called Ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	ST	141	Total	C	N	O	S	0	0
			1101	690	212	196	3		

- Molecule 82 is a protein called Ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	SU	104	Total	C	N	O	S	0	0
			818	513	153	148	4		

- Molecule 83 is a protein called Ribosomal protein es25.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 84 is a protein called Ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 85 is a protein called Ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Sd	52	Total	C	N	O	S	0	0
			434	273	87	69	5		

- Molecule 86 is a protein called Ribosomal protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Sf	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 87 is a protein called Ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 88 is a protein called SRP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	S1	74	Total	C	N	O	S	0	0
			608	388	105	110	5		

- Molecule 89 is a protein called SRP14.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	S4	76	Total	C	N	O	S	0	0
			604	382	105	113	4		

- Molecule 90 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
90	g	1	Total	Mg	0
			1	1	
90	D	1	Total	Mg	0
			1	1	
90	S2	36	Total	Mg	0
			36	36	

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Mol	Chain	Residues	Atoms		AltConf
90	V	1	Total 1	Mg 1	0
90	7	5	Total 5	Mg 5	0
90	5	116	Total 116	Mg 116	0
90	8	6	Total 6	Mg 6	0

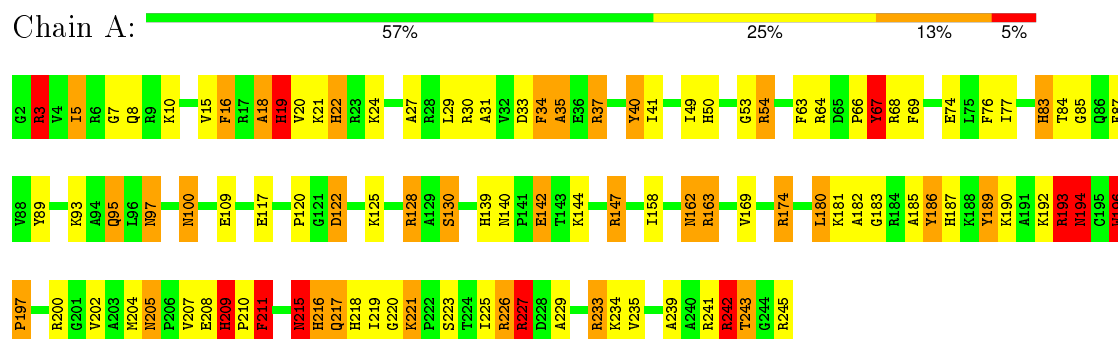
- Molecule 91 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
91	o	1	Total 1	Zn 1	0
91	j	1	Total 1	Zn 1	0
91	Sa	1	Total 1	Zn 1	0
91	m	1	Total 1	Zn 1	0

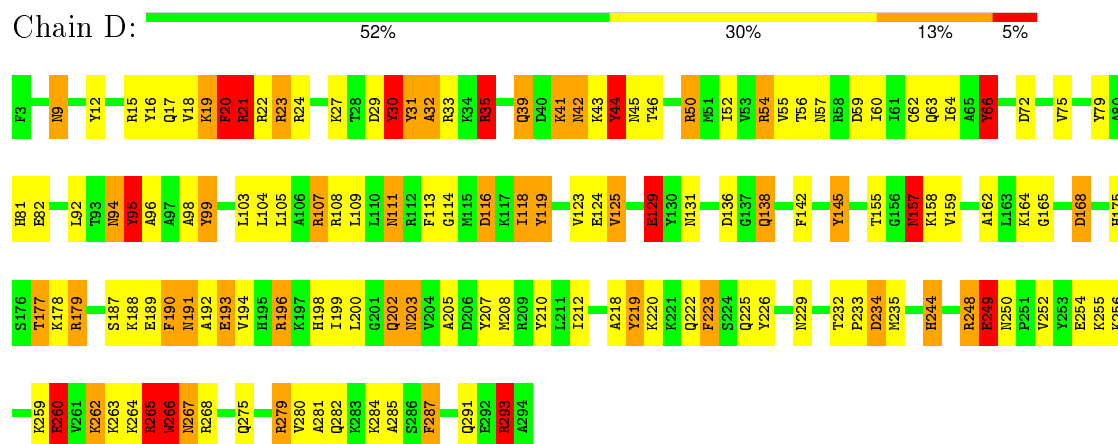
3 Residue-property plots

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.

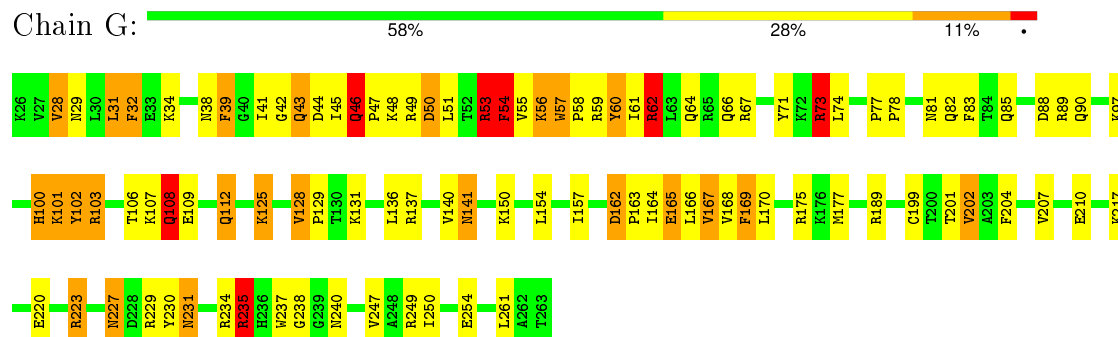
• Molecule 1: Ribosomal protein uL2



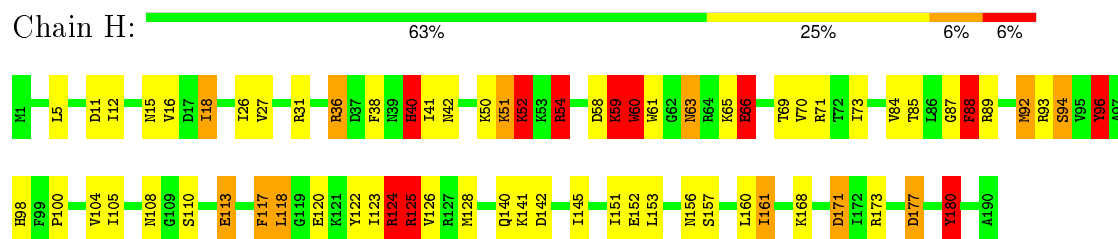
• Molecule 2: Ribosomal protein uL18



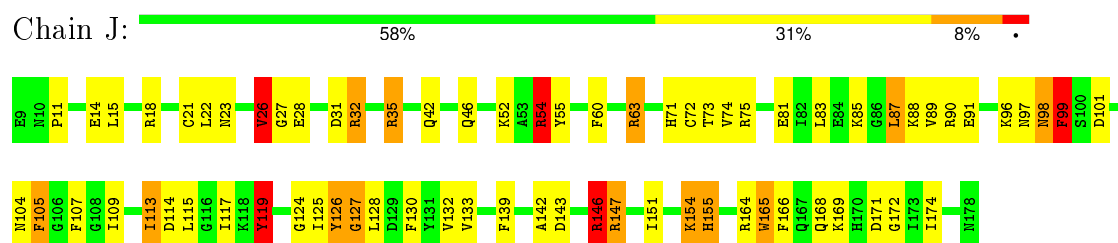
• Molecule 3: Ribosomal protein eL8



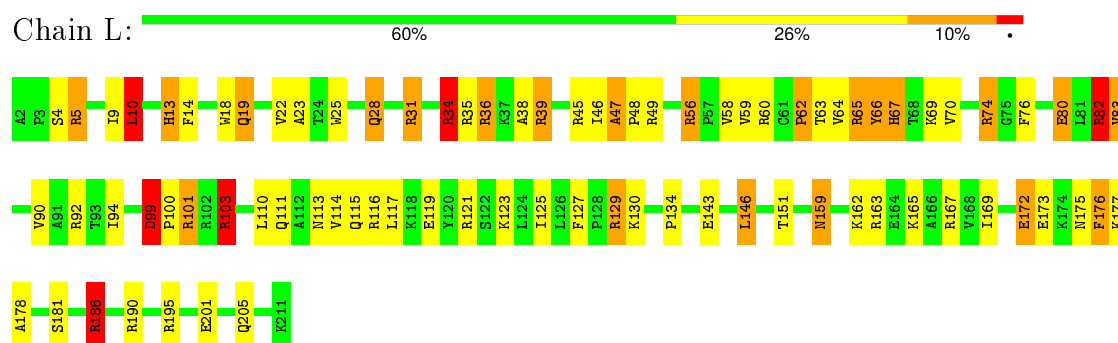
- Molecule 4: Ribosomal protein uL6



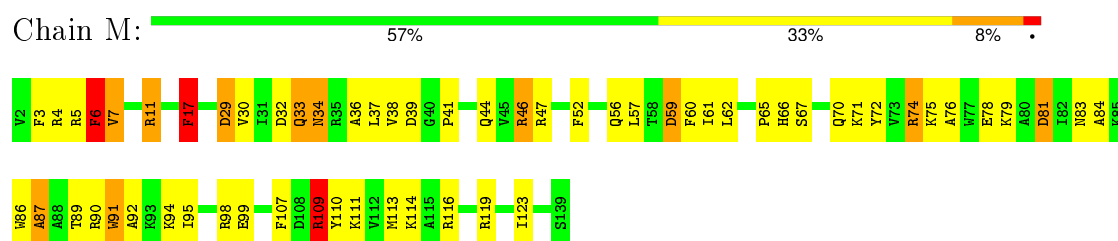
- Molecule 5: Ribosomal protein uL5



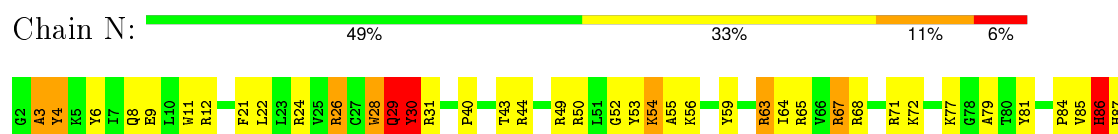
- Molecule 6: Ribosomal protein eL13

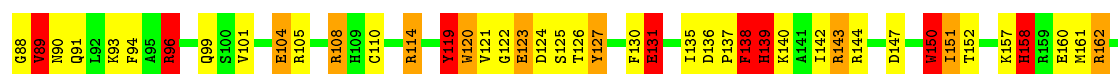


- Molecule 7: Ribosomal protein eL14

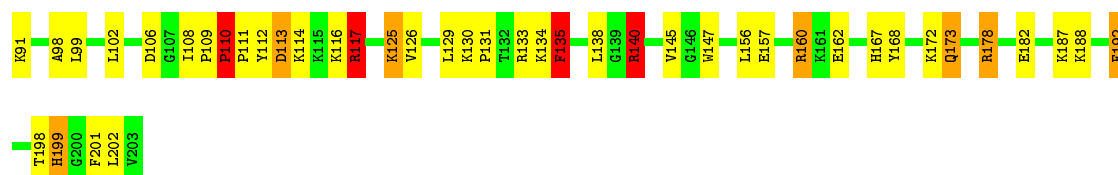
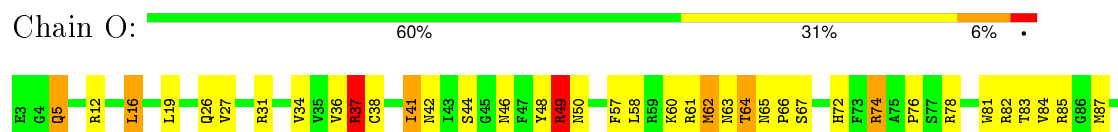


- Molecule 8: Ribosomal protein eL15

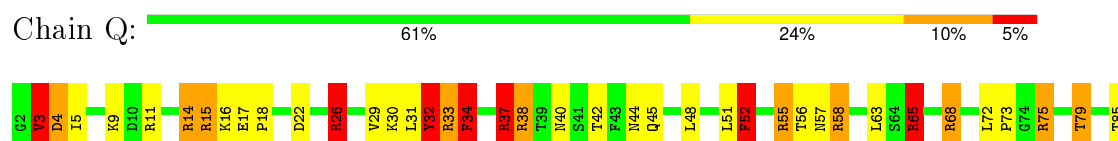




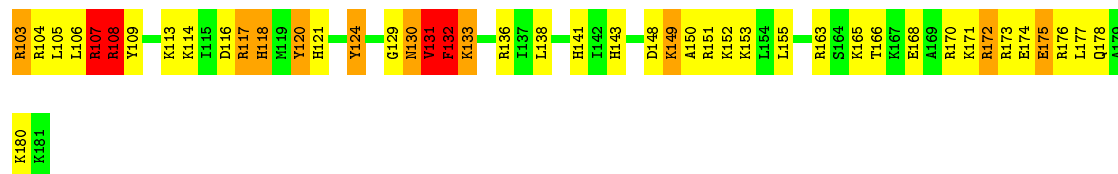
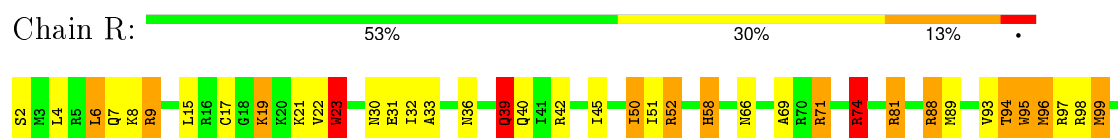
• Molecule 9: Ribosomal protein uL13



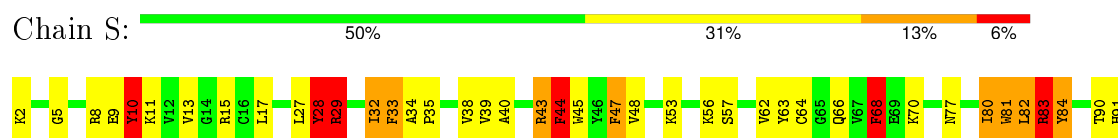
• Molecule 10: Ribosomal protein eL18



• Molecule 11: Ribosomal protein eL19



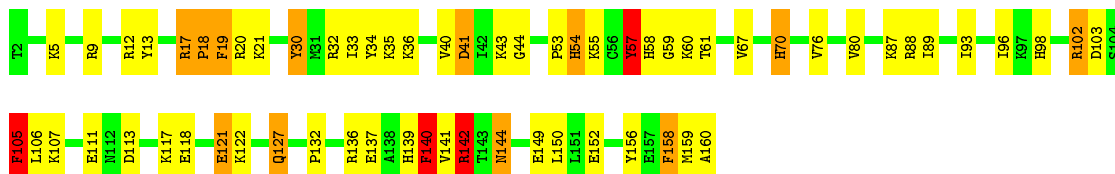
• Molecule 12: Ribosomal protein eL20



T174
F175
F176

• Molecule 13: Ribosomal protein eL21

Chain T: 



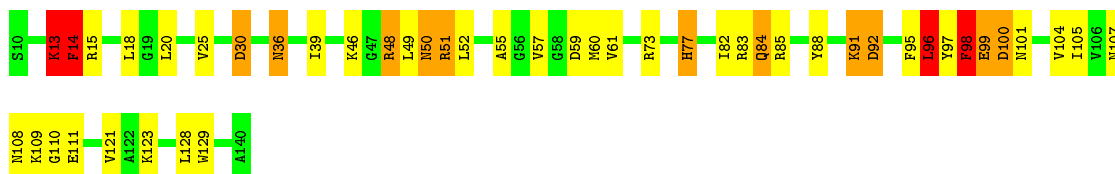
• Molecule 14: Ribosomal protein eL22

Chain U: 



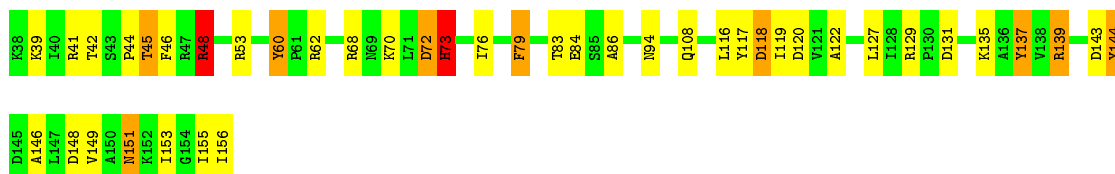
• Molecule 15: Ribosomal protein uL14

Chain V: 



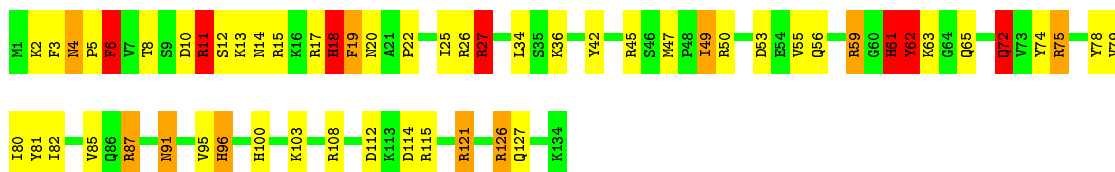
• Molecule 16: Ribosomal protein uL23

Chain X: 

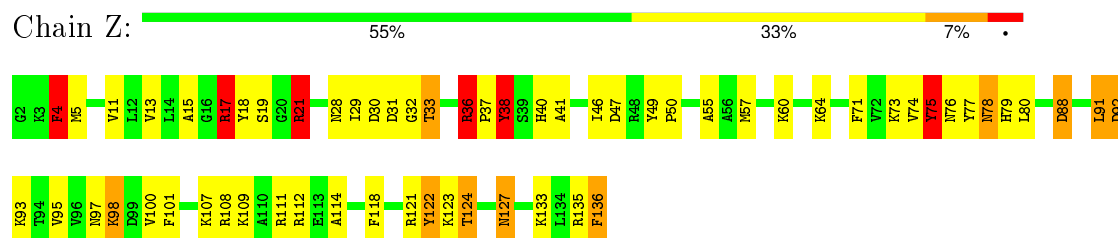


• Molecule 17: Ribosomal protein uL24

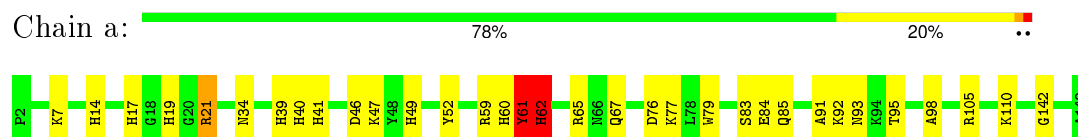
Chain Y: 



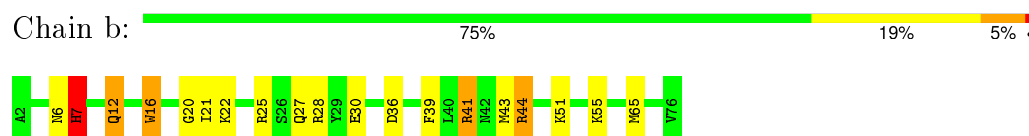
• Molecule 18: Ribosomal protein eL27



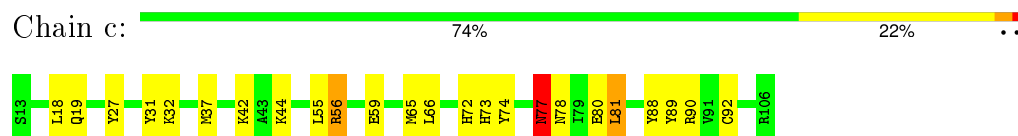
- Molecule 19: Ribosomal protein uL15



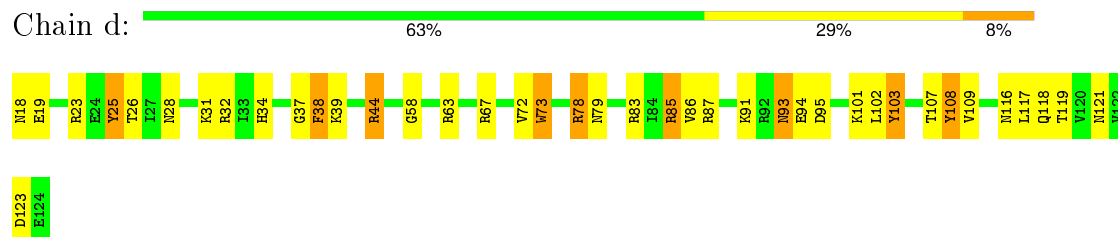
- Molecule 20: Ribosomal protein eL29



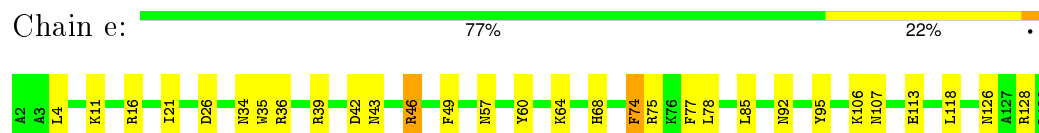
- Molecule 21: Ribosomal protein eL30



- Molecule 22: Ribosomal protein eL31

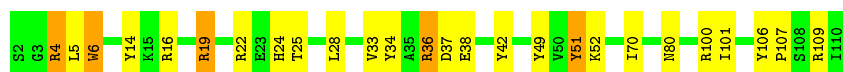


- Molecule 23: Ribosomal protein eL32

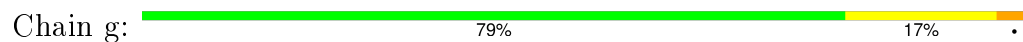


- Molecule 24: Ribosomal protein eL33

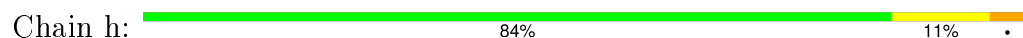




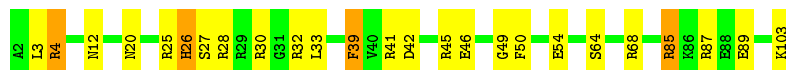
- Molecule 25: Ribosomal protein eL34



- Molecule 26: Ribosomal protein uL29



- Molecule 27: Ribosomal protein eL36



- Molecule 28: Ribosomal protein eL38



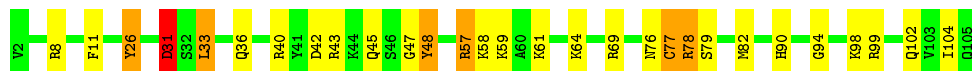
- Molecule 29: Ribosomal protein eL39



- Molecule 30: Ribosomal protein eL40

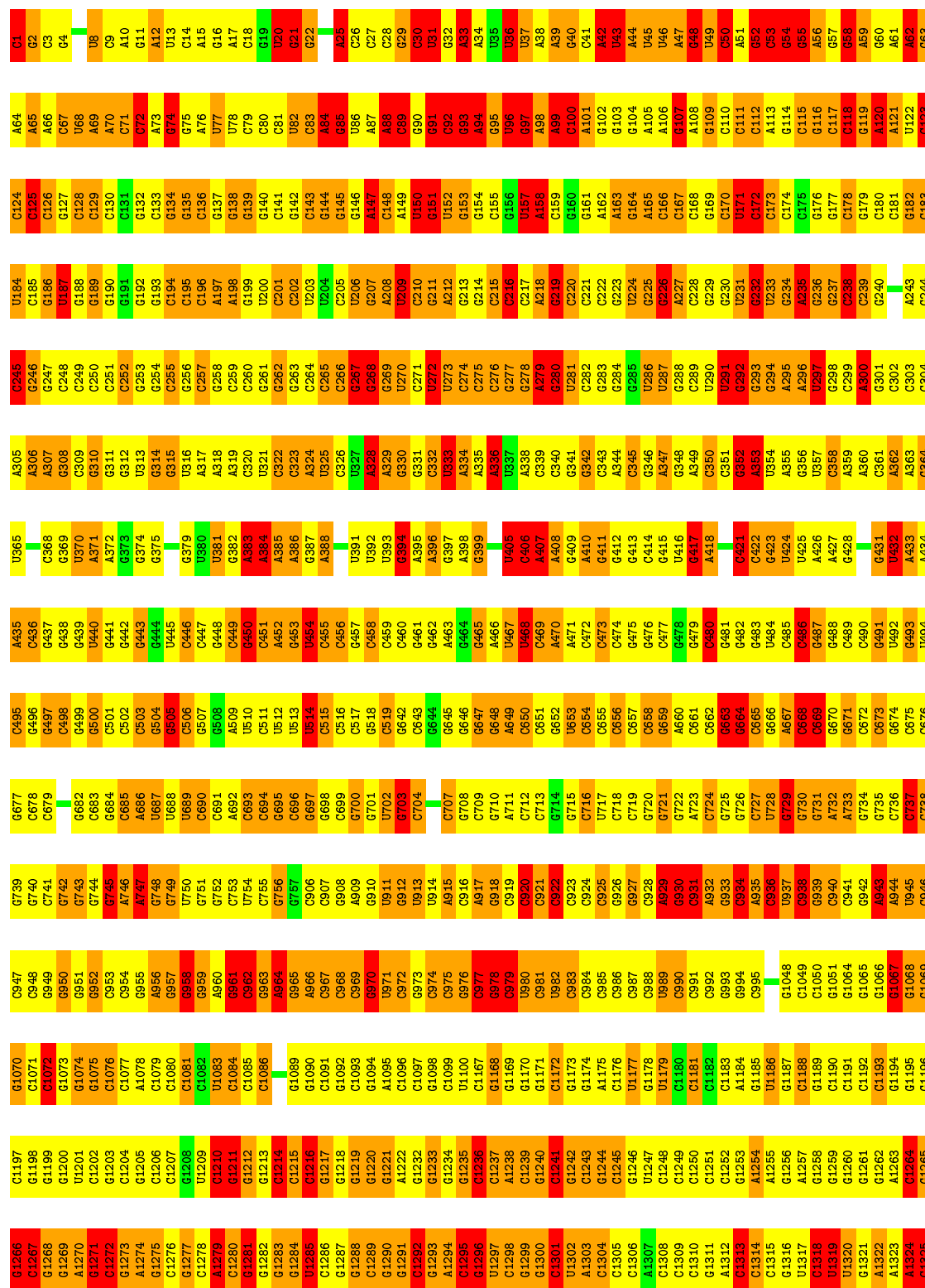


- Molecule 31: Ribosomal protein eL42



• Molecule 32: 28S ribosomal RNA

Chain 5:  8% 43% 36% 13%




C2373	C2311	G2251	U2080	A2017	U1957	A1897	G1836	A1775	C1696	A1634	U1572	G1510	C1447	A1387	A1326
G2376	U2312	G2252	C2081	C2018	A1956	C1896	A1837	A1776	G1697	C1635	G1573	U1511	G1448	A1388	C1327
C2377	G2313	A2253	G2082	C2019	U1959	C1899	A1838	C1777	C1698	U1636	G1574	G1512	C1449	A1389	G1328
G2378	G2314	G2254	C2083	U2020	A1960	C1900	U1839	C1778	A1699	A1637	A1575	U1513	C1450	G1390	G1329
A2382	G2315	C2255	C2084	G2021	A1961	C1901	G1840	U1779	C1718	U1638	G1576	U1514	G1451	A1391	A1330
G2383	G2316	G2256	G2085	C2022	A1962	G1902	G1842	A1780	A1719	U1639	G1577	A1515	A1452	A1392	
U2384	C2317	C2257	G2086	C2023	C1963	G1903	A1843	U1781	C1720	C1640	U1578	G1516	G1453	G1393	A1383
G2385	G2318	G2258	C2087	G2024	A1964	G1904	G1844	U1782	G1721	G1641	G1579	G1517	G1454	G1394	A1334
U2386	C2319	A2088	A2088	A2025	G1965	U1905	U1845	C1783	A1722	A1642	C1580	A1518	G1455	G1395	A1335
A2389	G2320	G2260	G2089	A2026	C1966	U1906	G1846	U1784	A1723	A1643	G1581	C1519	C1456	G1396	G1336
G2390	G2321	G2261	U2090	U2027	A1967	A1907	C1847	C1785	G1724	C1644	U1582	C1520	C1457	A1397	A1337
G2391	G2322	G2262	C2091		G1968	A1908	C1848	A1786	U1725	C1645	A1583	C1521	C1458	A1398	G1338
G2392	G2323	A2263	G2092	U2032	G1969	G1909	U1849	A1787	U1726		G1584	G1522	A1459	U1339	U1339
G2393	C2324	C2264	A2093	A2033	A1970	G1910	A1850	U1788	U1727	U1649	C1585	A1523	C1460	G1400	C1340
G2394	G2325	G2265	G2094	G2034	C1971	C1911	G1851	C1789	A1728	A1650	G1586	A1524		C1401	U1341
G2395	C2326	C2266	A2095	C2035	G1972	G1912	U1852	U1790	U1729	G1651	G1587	A1525	C1463	C1402	A1342
G2396	G2327	U2267	G2096	C2036	G1973	C1913	G1853	U1791	U1730	U1652	U1588	G1528	C1464	G1403	A1343
G2397	G2328	A2268	U2097	C2037	U1974	G1914	G1854	U1792	C1731	A1653	G1589	U1529	G1465	G1404	C1344
A2398	U2329	G2269	G2098	U2038	G1975	C1915	G1855	A1793	C1732	C1654	C1590	G1530	G1466	G1405	A1345
G2399	G2330	C2270	G2099	G2039	G1976	G1916	C1856	A1794	G1733	C1655	U1592		C1467	G1406	C1346
G2400	G2331	C2271	A2100	A2040	C1977	A1917	U1857	U1795	G1734	U1656	G1593		C1468	C1407	G1347
G2401	G2332	C2272	C2101	A2041	C1978	U1918	A1858	U1796	U1735	G1657	A1594	A1533	C1469	G1408	U1348
G2402	G2333	G2273	G2102	A2042	A1979	G1919	C1859	G1797	A1736	G1658	C1595	C1541	G1470	C1409	G1349
G2403	C2334	C2274	G2103	A2043	U1980	U1920	U1860	G1798		U1659	G1595	U1536	U1471	U1410	C1350
G2404	C2335	G2275	G2104	U2044	G1981	C1921	U1861	G1799	G1739	U1660	U1596	U1537	C1472	C1411	G1351
G2405	G2336	A2276	A2105	G2045	G1982	G1922	U1862	U1800	C1740	C1661	G1597	A1537	U1473	G1412	C1352
G2406	C2337	C2277	G2106	G2046	A1983	A1923	U1863	A1801	G1741	C1662	C1598	U1538	C1474	C1413	G1353
G2407	G2338	C2278	C2107	A2047	A1984	C1924	G1864	A1802	A1742	C1663	A1599	G1475	C1475	A1354	A1354
U2408	C2339	A2279	G2108	U2048	G1985	G1925	U1865	G1803	A1743	U1664	A1601	C1540	C1476	G1415	G1355
G2409	G2340	G2280	G2109	G2049	U1986	C1926	G1866	A1804	U1744	C1665	A1601	C1541	C1477	G1416	U1356
G2410	A2341	U2281	C2110	G2050	C1987	U1927	A1867	A1805	G1745	C1666	U1602	U1542	C1478	C1417	C1357
G2411	G2342	A2282	G2111	C2051	G1988	C1928	A1868	A1806	U1746	C1667	C1603	U1543	G1478	C1418	G1358
G2412	C2343	G2283	G2112	G2052	G1989	A1929	A1869	C1807	U1747	A1668	G1604	G1544	C1480	G1419	G1359
G2413	U2344	C2284	G2113	C2053	A1990	U1930	C1870	C1808	U1748	A1669	C1481	G1545	C1481	A1420	G1360
G2414	G2345	A2285	G2114	G2054	A1991	C1931	A1871	C1809	A1749	G1670	G1482	U1546	G1482	G1421	G1361
G2415	C2346	G2286	G2115	G2055	U1992	A1932	G1872	G1810	G1750	U1671	C1483	A1547	G1483	G1422	G1362
G2416	G2347	C2287	C2116	G2056	C1993	G1933	A1873	G1811	A1751	U1672	G1610	G1548	G1484	U1423	C1363
G2417	G2348	C2288	G2117	A2057	C1994	A1934	A1874	C1812	G1752	U1673	C1611	G1549	C1485	G1424	U1364
G2418	U2349	C2289	G2118	G2058	G1995	C1935	C1875	U1813	G1753	C1674	G1612	G1550	C1486	G1425	C1365
G2419	C2351	G2291	C2119	C2059	C1996	C1936	U1876	C1814	U1754	C1675	A1613	G1551	G1487	G1426	G1366
G2420	U2352	C2292	G2120	G2060	U1997	C1937	G1877	G1815	C1755	C1676	C1614	G1552	G1488	A1427	C1367
G2421	G2353	G2293	C2121	U2061	A1998	C1938	G1878	C1816	U1756	U1677	C1615	A1553	G1489	U1428	A1368
G2422	C2354	G2294	C2122	C2062	A1999	A1939	C1879	U1817	U1757	C1678	U1616	A1554	G1490	C1429	C1369
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G2424	G2357	C2296	G2124	G2064	G2001	A1941	C1881	G1819	G1759	G1680	G1618	C1556	G1492	C1431	A1371
G2425	A2360	G2297	C2125	G2065	A2002	C1942	U1882	C1820	G1760	G1681	C1557	C1557	G1493	G1432	A1372
G2426	U2362	U2298	G2126	C2066	G2003	A1943	G1883	G1821	G1761	A1682	U1620	A1558	A1497	A1433	A1373
G2427	G2363	G2299	C2127	C2067	U2004	A1944	C1884	U1822	C1762	G1683	A1621	G1559	G1498	G1434	G1374
G2428	U2364	C2300	G2128	C2068	G2005	G1945	G1885	G1823	C1763	A1684	U1622	A1560	C1499	G1435	C1375
G2429	G2365	A2300	C2129	A2069	U2006	G1946	G1886	A1825	G1764	G1685	A1623	G1561	C1499	C1436	C1376
G2430	A2366	C2301	G2130	U2070	G2007	U1947	G1887	G1826	A1765	C1686	G1624	G1562	A1500	U1437	G1377
G2431	G2367	G2302	C2131	A2071	U2008	G1948	A1888	C1827	A1766	C1687	G1625	A1563	C1501	C1438	C1378
G2432	U2368	C2303	C2243	C2072	A2009	U1949	U1889	G1828	A1767	G1688	G1626	A1564	G1502	C1439	C1379
G2433	G2369	U2304	G2073	C2073	A2010	U1950	G1890	G1829	C1768	G1689	G1627	A1565	A1503	U1440	G1380
G2434	C2370	C2244	C2244	C2074	C2011	G1951	A1891	G1830	G1769	C1690	C1628	C1566	G1504	U1381	U1381
G2435	U2371	G2245	G2074	G2074	A1892	G1952	A1892	G1831	A1770	G1691	G1629	C1505	C1505	C1442	G1382
G2436	G2372	C2246	C2246	G2075	A2012	G1953	C1893	C1832	U1771	C1692	A1630	U1567	G1506	G1443	G1383
G2437	U2373	A2307	C2247	G2076	A2013	U1954	C1894	G1833	U1772	C1693	A1631	U1569	G1507	A1444	G1384
G2438	G2374	C2308	C2248	C2077	C2014	U1955	G1895	G1834	U1773	C1694	A1632	U1570	A1508	U1445	G1385
G2439	U2375	G2310	C2249	G2078	U2015	G1955	C1896	A1835	C1774	U1695	G1633	G1571	C1509	U1446	C1386

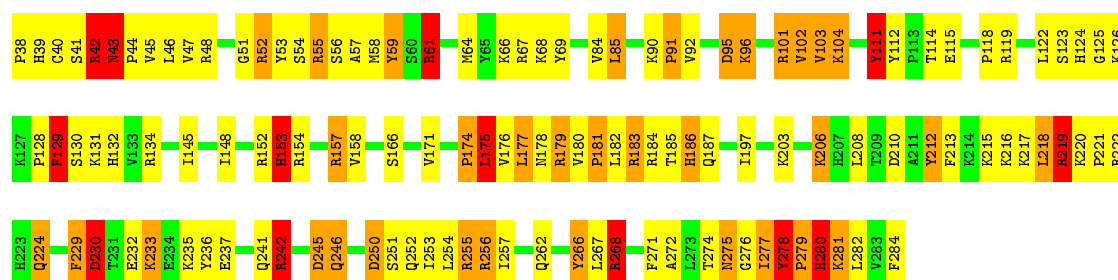
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C4146	C4088	C3911	U3851	U3789	A3727	C3667	U3606	U3868	A2807	A2744	G2682	G2618	C2558	C2498	A2438
C4149	G4089	U3932	A3852	U3790	U3728	C3668	A3608	U3870	G2808	A2745	G2683	G2620	C2559	C2499	U2440
G4150	G4090	C3913	U3853	U3791	U3729	C3669	C3609	U3871	G2811	A2746	G2684	A2621	C2560	U2500	U2441
G4152	G4091	U3914	C3854	C3792	U3730	C3670	A3610	C2872	A2812	U2747	C2685	G2622	C2561	G2501	G2442
C4153	G4093	C3916	C3855	U3793	C3731	C3671	A3611	U3873	A2813	C2748	G2686	A2623	C2562	G2502	G2443
G4154	G4094	A3917	U3857	A3732	A3732	C3672	C3612	U2874	A2814	C2749	U3887	G2624	C2563	G2503	U2444
C4155	G4095	C3917	C3858	A3733	A3733	C3673	U3613	C2875	A2815	G2750	U2687	U2625	A2564	C2504	U2445
C4156	C4096	U3796	C3859	G3735	G3735	C3675	A3614	U3878	G2816	G2752	U2688	U2626	C2565	C2505	U2446
A4157	G4097	C3797	A3860	A3736	A3736	C3676	C3615	U3879	C2817	G2753	U2689	U2627	C2566	U2506	U2447
C4158	A4098	U3798	A3861	A3737	A3737	U3677	U3616	A2879	A2818	G2754	U2691	C2628	C2568	U2508	G2448
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C4160	C4100	A3800	C3863	C3739	C3739	U3679	U3800	U3881	C2820	G2756	U2693	U2630	U2570	G2510	G2450
G4161	C4101	U3801	C3864	C3740	C3740	U3680	U3801	U3882	U2821	A2757	U2694	U2631	C2571	A2511	A2451
C4162	C4102	U3802	A3865	G3741	G3741	C3681	A3621	U3884	U2822	G2758	A2695	U2632	C2572	A2512	G2452
U4163	C4103	C3926	C3866	G3742	G3742	A3682	C3622	U2889	G2823	G2759	A2696	U2633	A2573	A2513	A2453
C4164	G4104	U3927	A3867	G3743	G3743	C3683	C3623	C2890	C2824	G2760	A2697	C2634	C2574	U2454	U2454
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U4167	G4107	U3930	C3870	A3746	A3746	U3686	G3626	U2893	G2827	U2763	G2700	G2638	C2577	A2517	G2457
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C4169	G4109	U3932	C3872	A3748	A3748	U3688	G3628	A2895	U2829	A2765	G2702	G2640	C2579	U2519	G2459
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C4174	C4114	C3936	C3877	G3753	G3753	U3693	C3633	U2900	C2834	U2770	G2707	G2645	C2584	U2524	C2464
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G4182	G4122	A3945	G3885	C3761	C3761	C3701	U3641	C2909	G2842	G2778	G2715	C2654	C2592	C2532	A2472
C4183	C4123	G3946	G3886	U3762	U3762	A3702	A3642	C2909	U2843	G2781	C2716	C2655	C2593	C2533	A2473
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G4198	C4137	U3840	G3900	G3776	G3776	A3716	A3656	U3595	A2857	U2795	G2733	C2669	C2607	G2546	G2487
C4199	U4138	C3841	A3901	G3777	G3777	C3717	U3657	A3596	A2858	G2796	U2734	C2670	G2608	C2548	C2488
G4200	G4139	C3842	C3902	U3778	U3778	A3718	C3658	C3597	G2859	C2797	G2735	C2671	G2609	G2549	C2489
C4201	C4140	C3843	A3903	A3779	A3779	A3719	G3659	C3598	C2860	A2798	G2736	C2672	C2610	C2550	U2490
U4202	G4141	U3844	C3904	G3780	G3780	G3720	C3660	A3599	C2861	G2799	G2737	G2673	A2611	A2551	C2491
C4203	C4142	G3811	C3781	C3781	C3781	U3721	G3661	G3600	G2862	G2799	G2738	A2674	C2612	G2552	C2492
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C4206	U4145	C3848	A3724	A3784	A3784	C3724	G3664	C3603	U2865	C2804	G2677	C2615	C2615	U2555	U2495
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A4220	U4285	C4345	U4406	U4467	G4529	A4590	C4653	G4718	G4863	U4924	C4987	G5051
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	A4315	A4376	U4436	G4497	A4559	A4622	C4688	U4748	A4894	C4957	G5018	
	G4316	G4377	U4437	U4500	C4560	G4623	U4689	C4749	G4895	C4958	C5019	
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	C4270	G4329	U4452	G4515	U4575	U4638	C4704	U4764	A4910	G4973	G5033	
	G4330	G4331	C4391	C4392	C4452	G4639	C4705	G4765	G4911	C4974	A5034	
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• Molecule 33: 5S ribosomal RNA

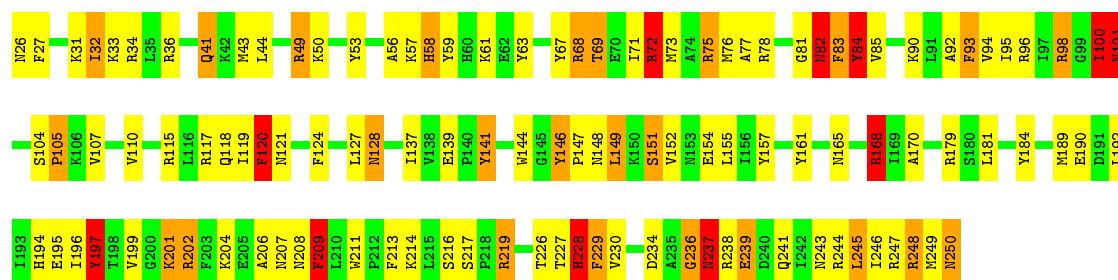
Chain 7:  15% 54% 22% 9%

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U2	C63
A5	G64
C6	G65
G6	A5042
C67	A5043
A5044	C68
G5045	G69
U5046	C70
C5047	G71
A5048	U72
G5049	U73
C5050	A74
G5051	G75
C5052	
U5053	U79
C5054	U80
G5055	G81
A5056	G82
C5057	A83
A5058	U84
C5059	G85
A5060	
G5061	A88
U5062	G89
G5063	A90
C5064	C91
U5065	C92
A5066	G93
C5067	C94
U5068	C95
U5069	
	G98
	G99
	A100
	C101
	U102
	A103
	C104
	C105
	G106
	U107
	G108
	U109
	G110
	C111
	U112
	G113
	A49
	U114
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	U117
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	U60
	G61



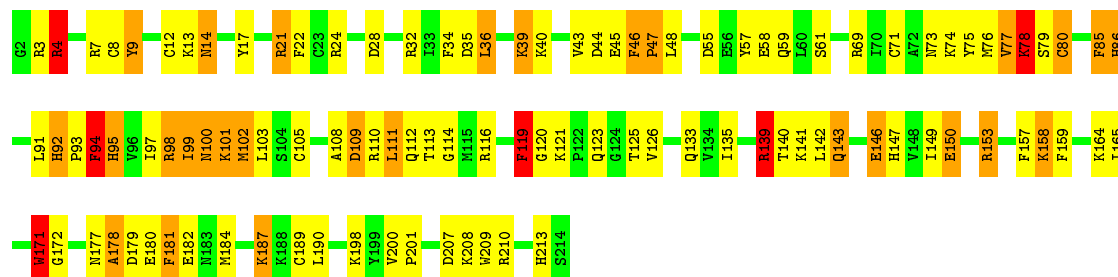
• Molecule 38: Ribosomal protein uL30

Chain F: 48% 36% 11% 5%



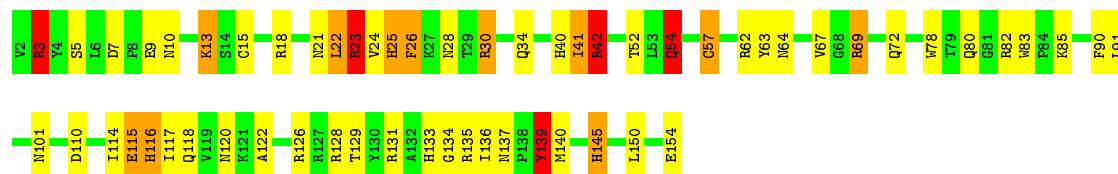
• Molecule 39: Ribosomal protein uL16

Chain I: 50% 34% 13% 1%

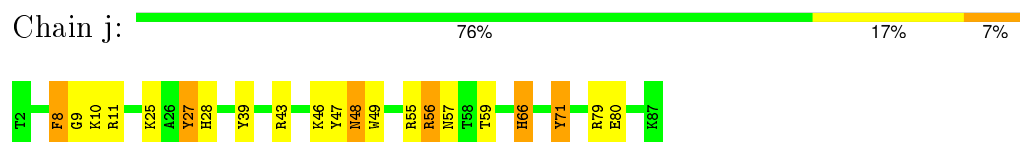


• Molecule 40: Ribosomal protein uL22

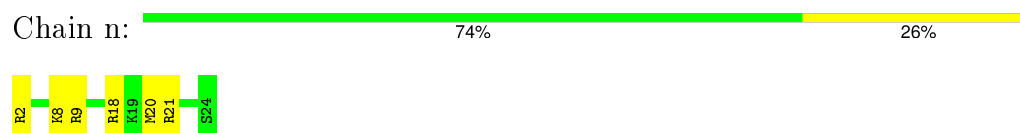
Chain P: 61% 28% 7% 1%



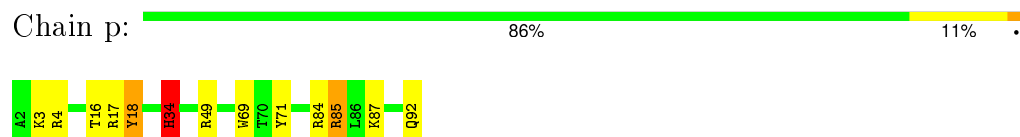
- Molecule 42: Ribosomal protein eL37



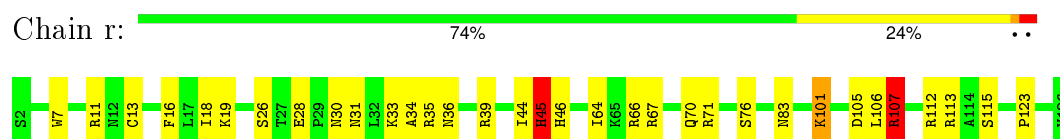
- Molecule 43: Ribosomal protein eL41



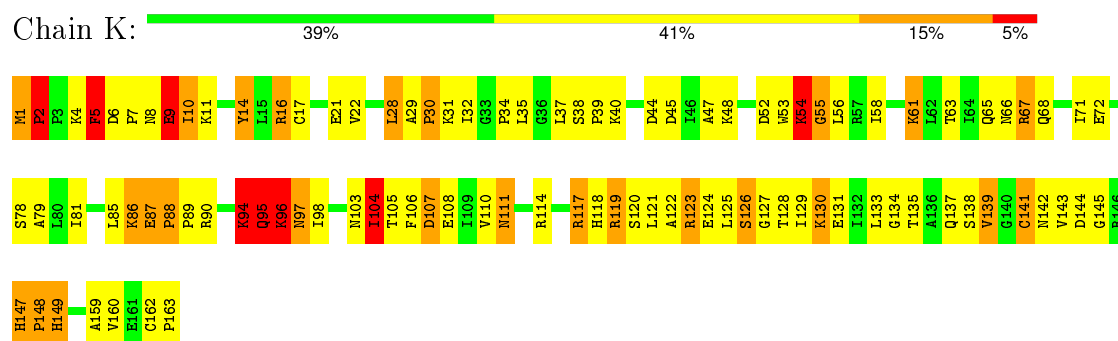
- Molecule 44: Ribosomal protein eL43



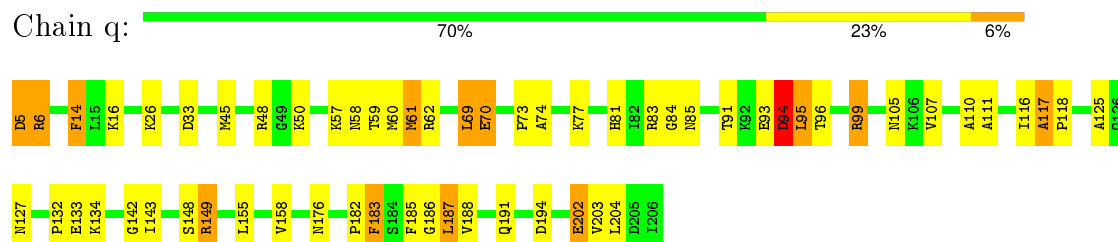
- Molecule 45: Ribosomal protein eL28




- Molecule 46: Ribosomal protein uL11



- Molecule 47: Ribosomal protein uL10

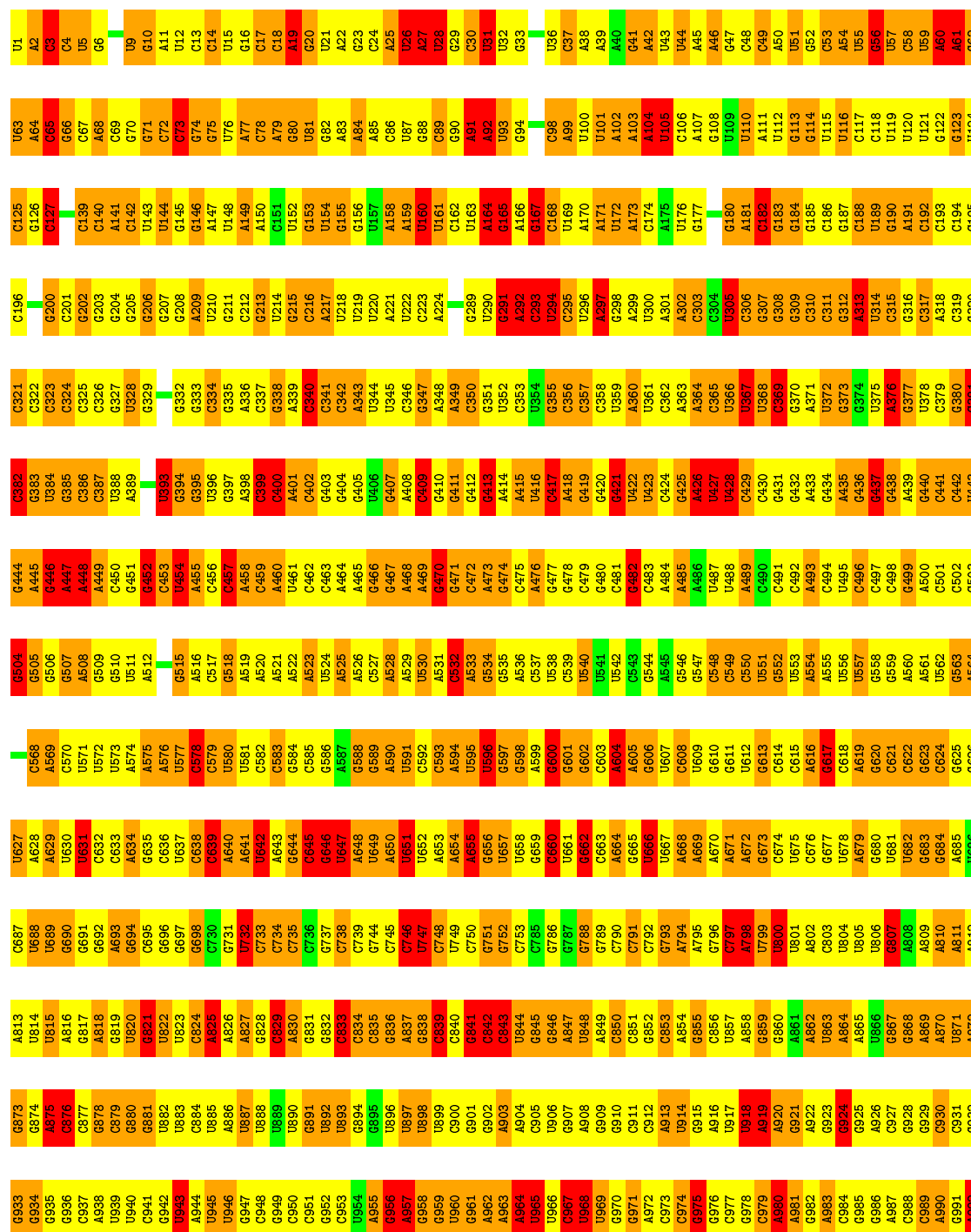


Chain 6:  80% 18%



• Molecule 54: 18S ribosomal RNA

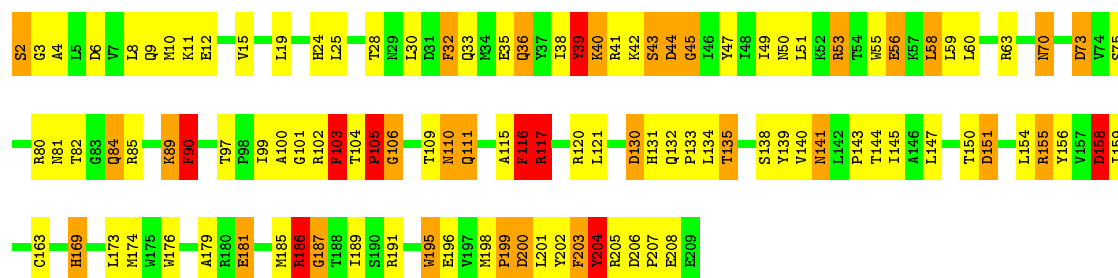
Chain S2:  8% 42% 38% 11%



G1856	G1794	G1726	A1663	U1602	C1542	G1481	C1418	A1357	U1297	G1237	G1176	C1116	A1055	G993
G1857	G1795	G1727	A1664	G1603	U1543	C1482	C1419	U1358	G1298	U1238	U1177	C1117	U1056	G994
G1858	G1796	U1728	G1665	G1604	C1544	C1483	G1420	U1359	A1299	C1239	U1178	A1119	C1057	G995
G1859	U1797	U1729	G1666	G1605	A1545	A1484	A1421	U1360	U1300	A1240	G1179	A1118	A1058	A996
A1860	C1798	U1730	U1667	G1606	U1495	G1485	G1422	G1361	A1301	U1241	C1180	G1121	G1059	A997
G1861	U1731	A1730	U1668	A1607	C1547	U1486	G1423	U1362	G1302	U1242	A1181	G1120	A1060	A998
G1862	A1800	U1732	U1669	U1608	C1548	A1487	G1424	C1363	C1303	U1243	A1182	A1122	U1061	G999
A1863	A1801	U1733	U1670	C1609	U1549	C1488	G1425	U1364	U1304	U1244	A1183	C1123	A1062	C1000
A1864		U1734	G1671	G1610	G1550	A1489	G1426	U1365	C1305	G1245	A1184	C1124	G1063	A1001
U1804	U1804	A1735	U1672	U1611	U1551	G1490	A1427	G1366	U1306	A1246	C1185	C1125	C1064	U1002
G1805	G1805	U1736	U1673	G1612	C1552	G1491	G1428	U1367	U1307	C1247	U1186	G1126	G1065	U1003
A1806	A1806	G1737	G1674	C1553	C1553	U1492	G1429	U1368	U1308	U1248	G1187	C1127	U1066	U1004
G1807	C1807	U1738	A1675	C1554	C1554	C1493	C1430	A1369	C1309	U1249	A1188	C1128	C1067	G1005
A1868	U1808	C1739	U1676	U1555	U1555	U1494	G1431	A1370	U1310	A1250	A1189	G1129	C1068	C1006
	A1809	C1740	A1677	A1556	A1556	A1495	U1432	A1371	U1311	A1251	A1190	G1130	U1069	C1007
	U1810	U1741	A1678	U1496	C1557	U1496	U1433	U1372	G1312	C1252	A1191	G1131	U1070	A1008
	C1811	C1742	A1679	C1558	C1558	A1497	G1434	C1373	A1313	A1253	U1192	C1132	G1071	A1009
	U1812	G1743	G1680	A1620	C1559	A1498	C1435	C1374	U1314	C1254	U1193	A1133	C1072	A1010
	A1813	G1744	U1681	U1621	U1560	U1499	G1436	G1375	U1315	G1255	A1194	G1134	U1073	A1011
	G1814	U1745	C1682	U1622	A1561	G1500	A1437	A1376	C1316	G1256	A1195	C1135	C1074	U1015
	A1815	U1746	C1683	A1623	C1562	C1501	A1438	U1377	C1317	G1257		U1136	C1075	U1016
	G1816	C1747	G1684	U1624	G1563	C1502	A1439	A1378	G1318	A1258	G1198	U1137	G1076	U1017
	U1817	G1748	U1685	U1625	C1564	C1503	C1440	A1379	U1319	A1259	A1199	C1138	A1077	U1018
	A1818	G1749	G1686	C1626	C1565		U1441	G1380	G1320	A1260	A1200	C1139	C1078	U1019
	U1819	C1750	C1687	C1627	G1566		U1442	G1381	G1321	C1261	U1201	G1140	C1079	C1019
	G1820	C1751	C1688	C1628	G1567	G1507	C1443	A1382	G1322	C1262	U1202	G1141	A1080	A1020
	A1821	C1752	C1689	A1629	C1568	A1508	U1444	A1383	G1323	U1263	G1203	G1142	U1081	U1021
	U1822	C1753	U1690	C1630	A1509	C1509	U1445	C1384	G1324	C1264	A1204	A1143	U1082	U1022
	A1823	G1754	U1691	U1631	G1570	G1510	A1446	C1385	G1325	A1265	C1205	A1144	A1083	A1023
	C1824	C1755		G1632	G1571	U1511	G1447	A1386	U1326	C1266	G1206	A1145	A1084	A1024
	A1825	C1756		A1633	C1572	C1512	A1448	G1387	G1327	C1267	G1207	G1146	G1085	U1025
	G1826	G1757		A1634	G1573	C1513	G1449		G1328	C1268	A1208	C1147	C1026	A1026
	U1827	U1758		C1635	C1574	G1514	U1450	U1390	U1329	C1269	A1209	A1148	G1087	A1027
	C1828	G1759		G1636	G1575	G1515	G1451	C1391	G1330	C1270	G1210	A1149	U1088	A1028
	U1829	G1760		A1637	G1576	G1516	C1452	U1392	C1331	C1271	G1211	A1150	G1029	G1029
	A1830	U1761		G1638	G1577	G1517	C1453	G1393	A1332	C1272	G1212	G1151	A1030	A1030
	A1831			U1639	U1578	C1518	A1454	G1394	U1333	C1273	G1213	U1152	G1092	A1031
				A1640	A1579	U1519	A1455	C1395	G1334	G1274	A1214	C1153	A1093	C1032
				A1641	A1580	G1520	G1456	A1396	G1335	G1275	C1215	U1154	C1094	G1033
				C1581	C1581	C1521	U1457	U1397	C1336	A1276	C1216	U1155	U1095	A1034
				U1643	C1582	A1522	G1458	G1398	C1337	C1277	A1217	U1156	G1096	A1035
				C1644	C1583	C1523	G1459	C1399	G1338	A1278	C1218	G1157	G1097	A1036
				U1645	G1584	G1524	C1460	U1400	U1339	C1279	A1219	G1158	G1098	G1037
				C1646	U1585	C1525	G1461	A1401	C1340	G1280	A1220	U1159	U1038	U1038
				A1647	U1586	G1526	U1462	A1402	C1341	G1281	G1221	U1160	C1039	C1039
				C1592	G1587	C1527	U1463	C1403	G1342	A1282	G1222	U1161	U1101	G1040
				U1588	A1588	G1528	C1464	U1404	U1343	C1283	C1223	C1162	G1102	G1041
				U1589	A1589	C1529	G1465	A1405	U1344	A1284	G1224	C1163	C1103	A1042
				C1590	C1590	U1530	G1466	G1406	G1345	G1285	U1225	G1164	G1104	G1043
				C1591	C1591	A1531	C1467	U1407	U1346	G1286	G1226	G1165	G1105	G1044
				C1592	C1592	C1532	U1468	U1408	U1347	A1287	G1227	G1166	C1106	U1045
				U1593	A1593	A1533		A1409	G1348	U1288	A1228	G1167	G1107	U1046
				A1594	C1534	C1534	G1473	C1410	U1349	U1289	G1229	G1168	G1108	C1047
				U1595	U1535	C1535	A1474	G1411	U1350	C1290	C1230	G1169	C1109	G1048
				U1596	G1536	G1536	G1475	C1412	G1351	A1291	C1231	A1170	G1110	A1049
				C1597	A1537	A1537	A1476	G1413	G1352	C1292	U1232	G1171	U1111	A1050
				G1598	C1538	C1538	U1477	A1414	A1353	A1293	G1233	U1172	U1112	G1051
				U1599	U1539	C1539	U1478	C1415	G1354	G1294	C1234	U1173	A1113	A1052
				G1600	G1600	G1600	U1479	C1416	C1355	A1295	U1174	U1174	U1114	C1053
				A1601	A1601	G1541	A1480	C1417	G1356	U1296	G1236	G1175	U1115	G1054

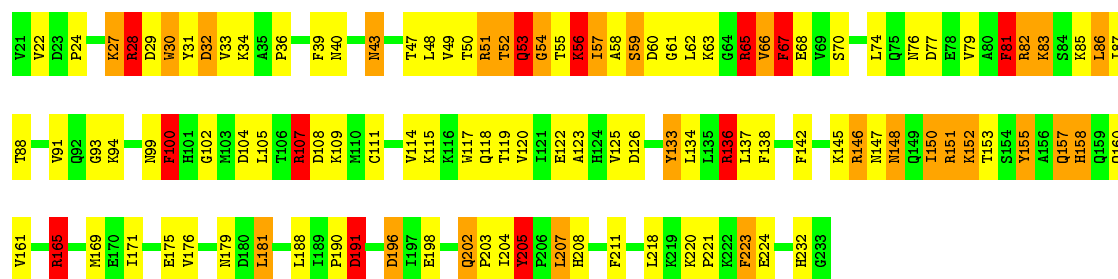
• Molecule 55: Ribosomal protein uS2

Chain SA: 47% 35% 14%



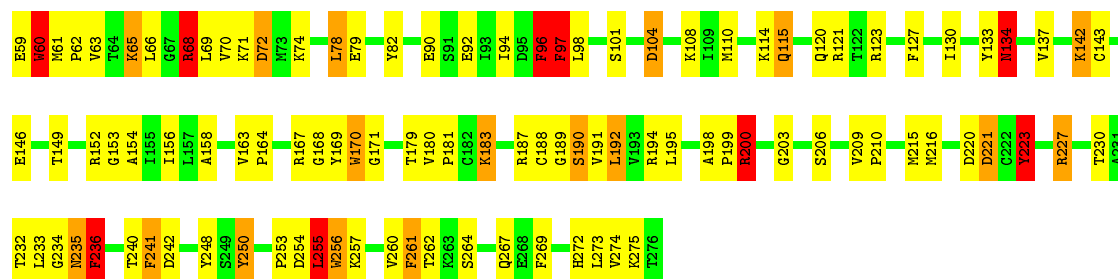
- Molecule 56: Ribosomal protein eS1

Chain SB: 47% 35% 13% 6%



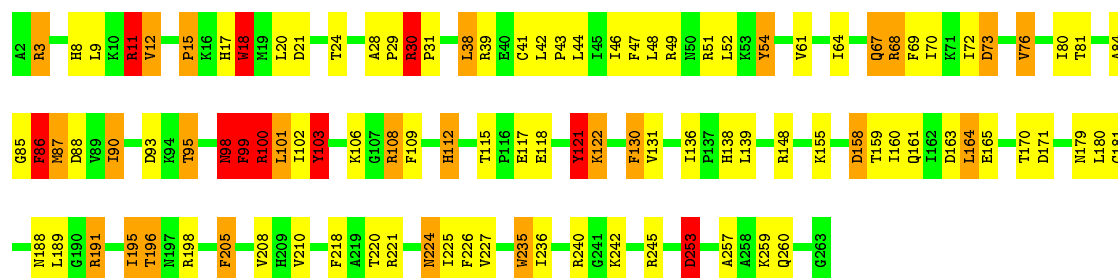
- Molecule 57: Ribosomal protein uS5

Chain SC: 53% 35% 8% 1%



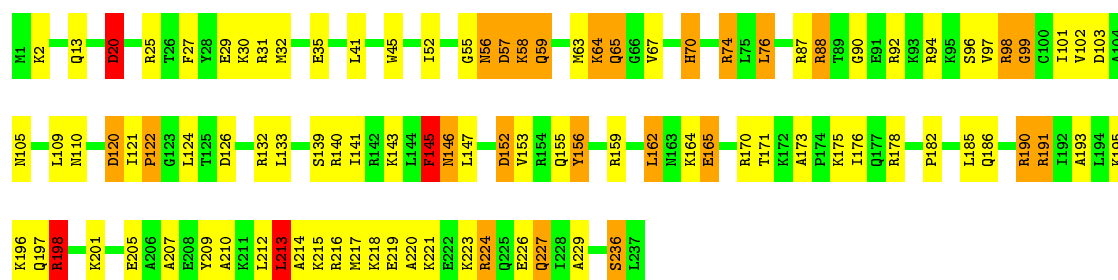
- Molecule 58: Ribosomal protein eS4

Chain SE: 60% 27% 10% 1%

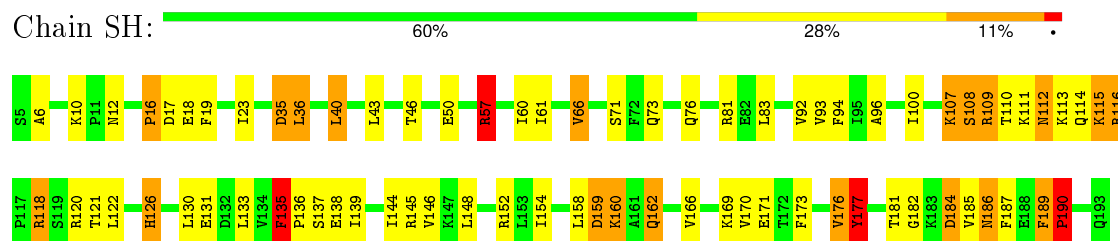


- Molecule 59: Ribosomal protein eS6

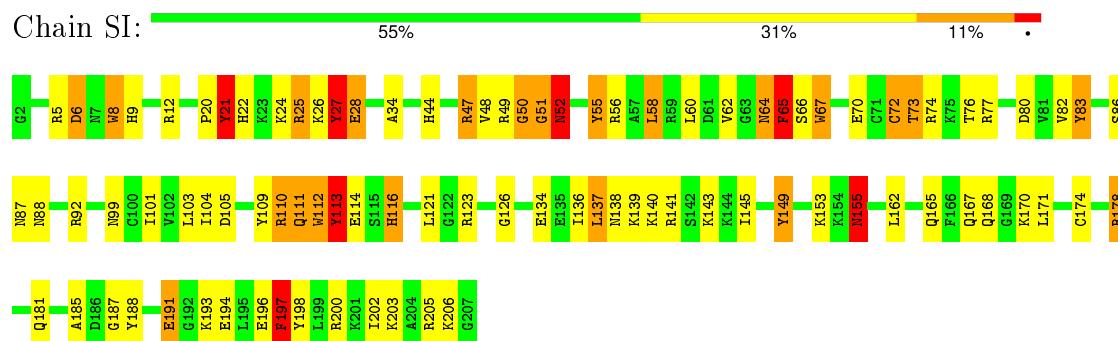
Chain SG: 58% 30% 10% 1%



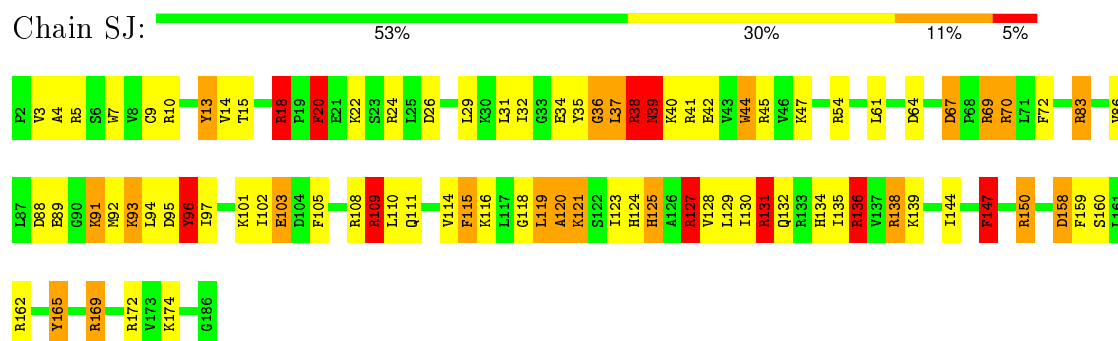
• Molecule 60: Ribosomal protein eS7



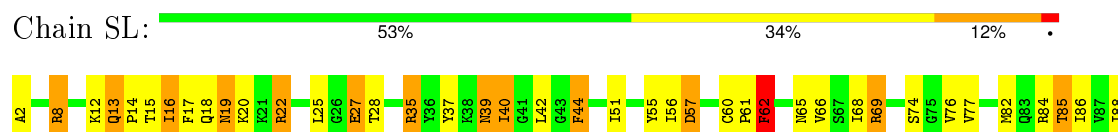
• Molecule 61: Ribosomal protein eS8



• Molecule 62: Ribosomal protein uS4



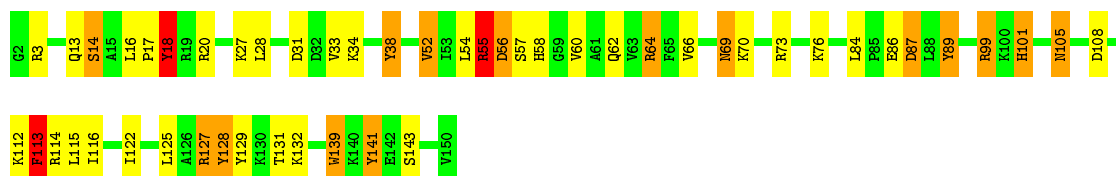
• Molecule 63: Ribosomal protein uS17





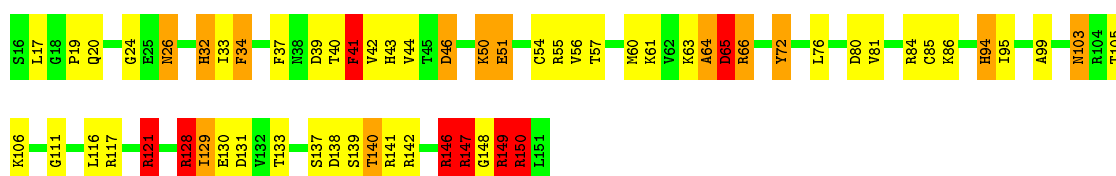
- Molecule 64: Ribosomal protein uS15

Chain SN: 66% 21% 10% .



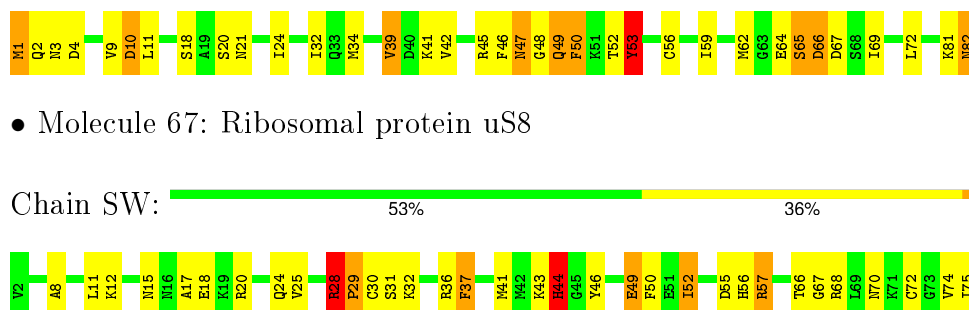
- Molecule 65: Ribosomal protein uS11

Chain SO: 55% 29% 10% 6% .



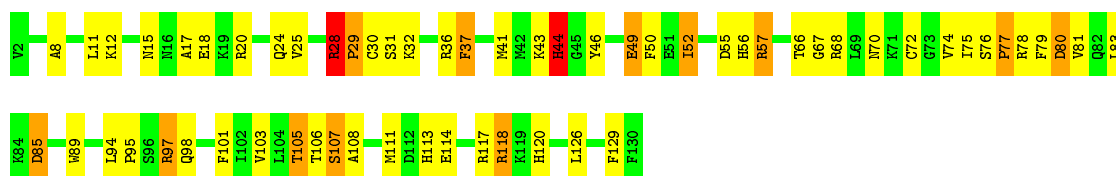
- Molecule 66: Ribosomal protein eS21

Chain SV: 57% 30% 11% .



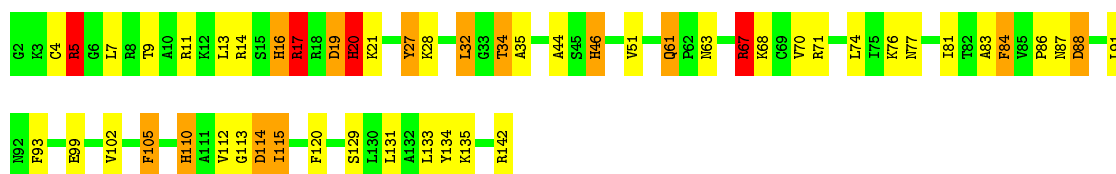
- Molecule 67: Ribosomal protein uS8

Chain SW: 53% 36% 9% .

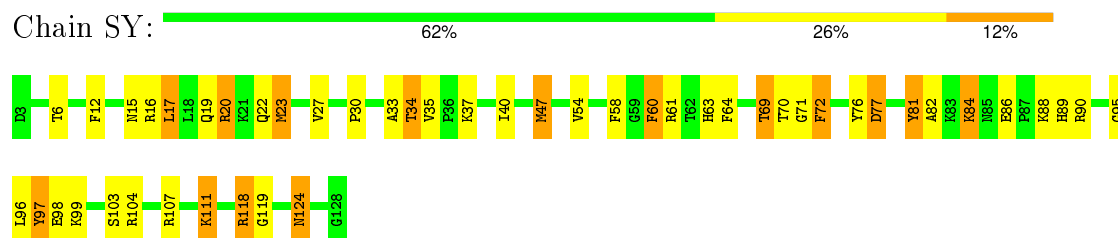


- Molecule 68: Ribosomal protein uS12

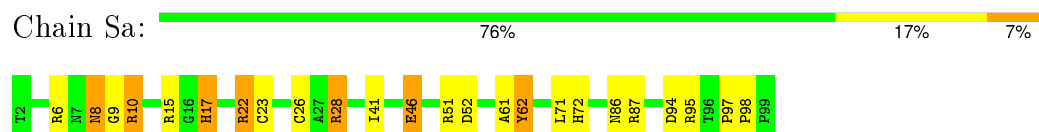
Chain SX: 63% 25% 9% .



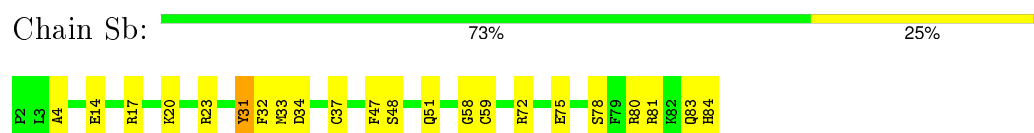
- Molecule 69: Ribosomal protein eS24



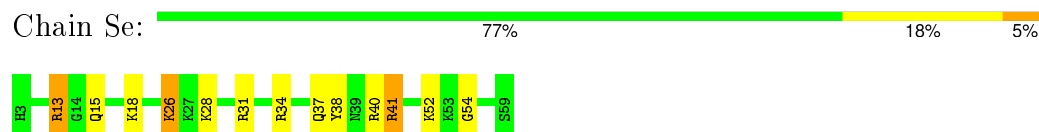
- Molecule 70: Ribosomal protein eS26



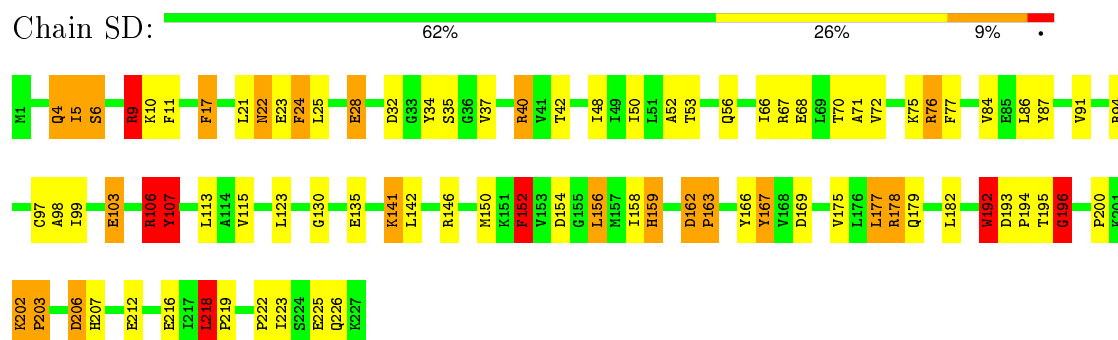
- Molecule 71: Ribosomal protein eS27



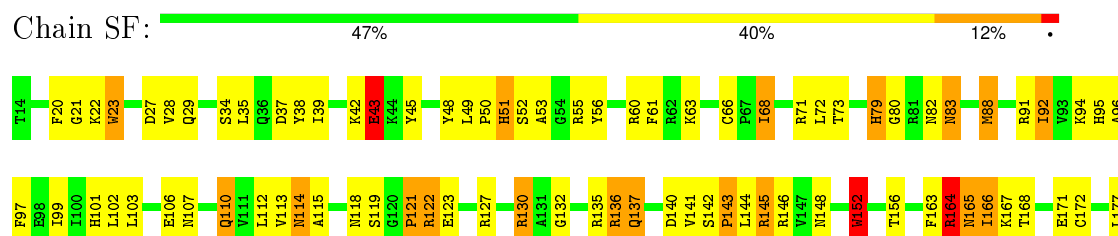
- Molecule 72: Ribosomal protein eS30



- Molecule 73: Ribosomal protein uS3



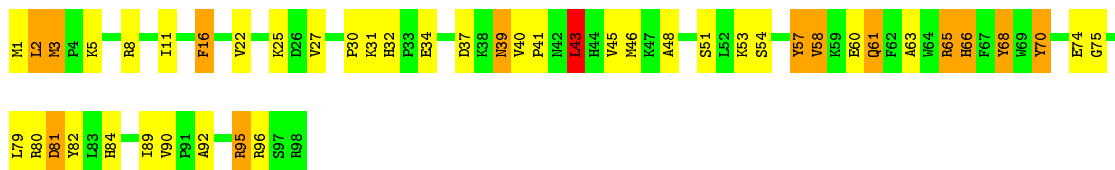
- Molecule 74: Ribosomal protein uS7





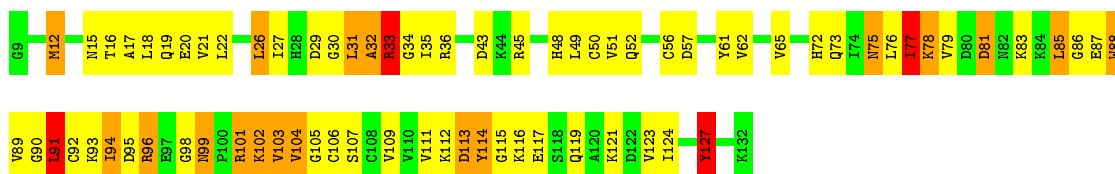
• Molecule 75: Ribosomal protein eS10

Chain SK: 53% 33% 13% .



• Molecule 76: Ribosomal protein eS12

Chain SM: 40% 42% 15% .



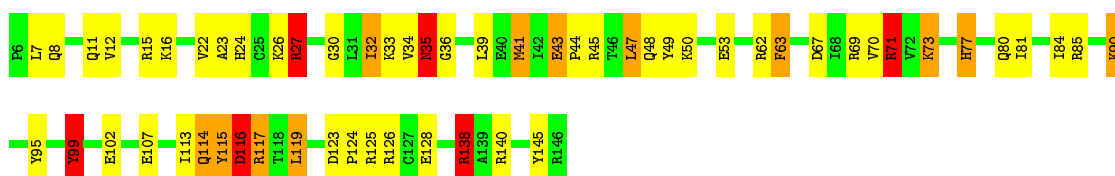
• Molecule 77: Ribosomal protein uS19

Chain SP: 59% 29% 7% .



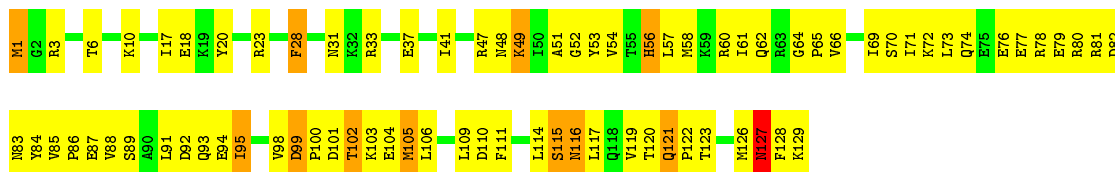
• Molecule 78: Ribosomal protein uS9

Chain SQ: 59% 28% 9% .

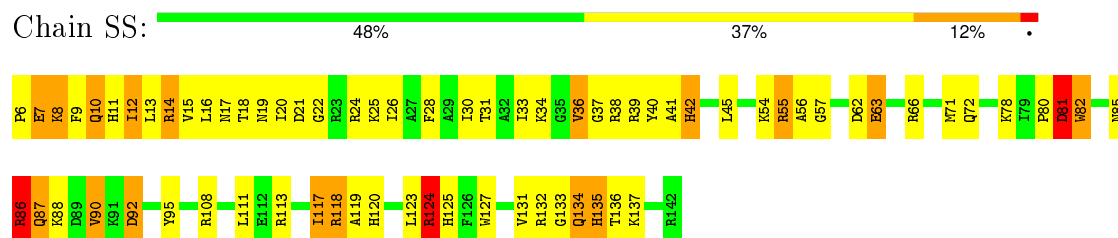


• Molecule 79: Ribosomal protein eS17

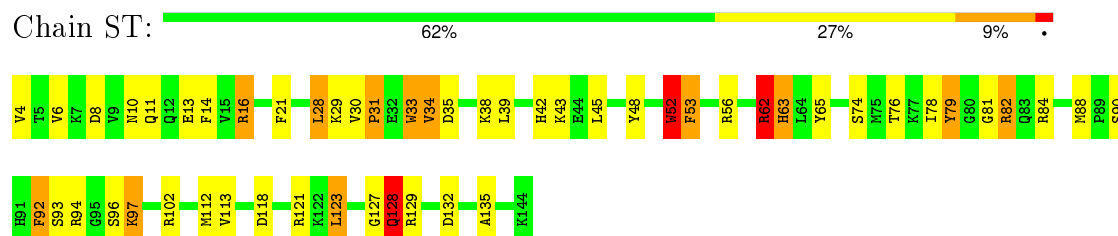
Chain SR: 39% 52% 9% .



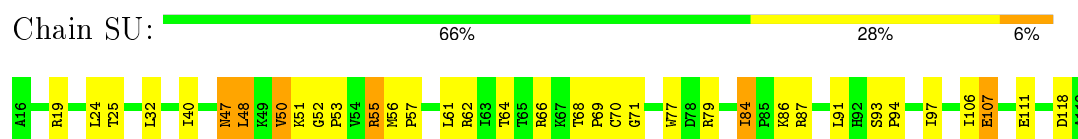
• Molecule 80: Ribosomal protein uS13



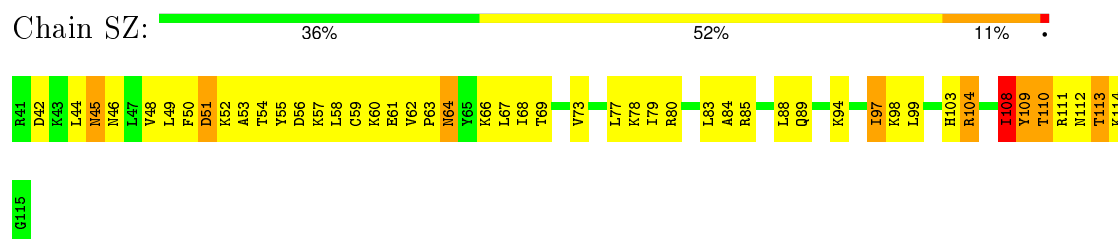
- Molecule 81: Ribosomal protein eS19



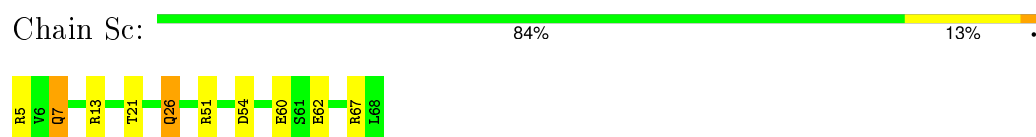
- Molecule 82: Ribosomal protein uS10



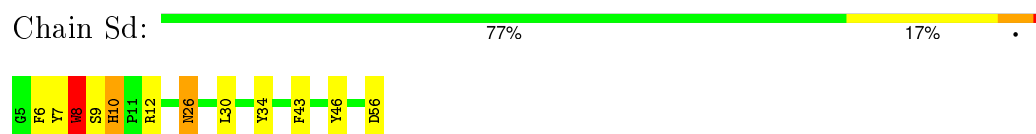
- Molecule 83: Ribosomal protein es25



- Molecule 84: Ribosomal protein eS28



- Molecule 85: Ribosomal protein uS14




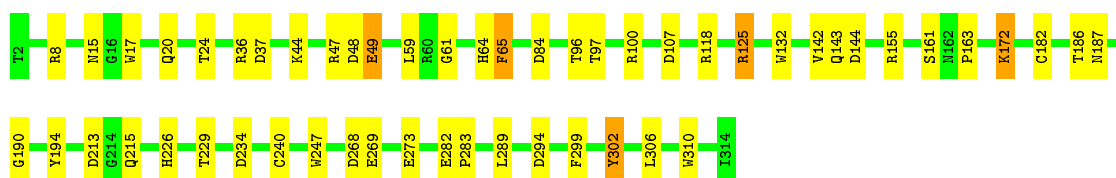
- Molecule 86: Ribosomal protein eS31

Chain Sf:  56% 30% 10% .



- Molecule 87: Ribosomal protein RACK1

Chain Sg:  83% 15% .



- Molecule 88: SRP9

Chain S1:  58% 26% 15% .



- Molecule 89: SRP14

Chain S4:  74% 22% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	52061	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.70	1/1906 (0.1%)	1.25	19/2556 (0.7%)
10	Q	0.68	2/1530 (0.1%)	1.31	32/2041 (1.6%)
11	R	0.81	3/1524 (0.2%)	1.24	19/2013 (0.9%)
12	S	1.07	10/1493 (0.7%)	1.36	28/2002 (1.4%)
13	T	0.62	1/1326 (0.1%)	0.99	4/1770 (0.2%)
14	U	0.61	1/822 (0.1%)	0.99	2/1103 (0.2%)
15	V	0.57	0/993	0.98	2/1332 (0.2%)
16	X	0.56	0/993	0.95	3/1334 (0.2%)
17	Y	0.64	0/1132	1.17	12/1504 (0.8%)
18	Z	0.65	0/1130	1.14	8/1507 (0.5%)
19	a	0.66	0/1192	1.12	6/1591 (0.4%)
2	D	0.67	2/2426 (0.1%)	1.17	25/3252 (0.8%)
20	b	0.75	2/620 (0.3%)	1.17	7/819 (0.9%)
21	c	0.60	0/742	1.11	4/996 (0.4%)
22	d	0.69	2/903 (0.2%)	1.28	11/1216 (0.9%)
23	e	0.73	1/1071 (0.1%)	1.13	7/1429 (0.5%)
24	f	0.83	1/895 (0.1%)	1.28	10/1198 (0.8%)
25	g	0.59	0/916	1.14	8/1220 (0.7%)
26	h	0.55	0/1023	1.17	13/1350 (1.0%)
27	i	0.62	0/843	1.17	8/1115 (0.7%)
28	k	0.51	0/575	0.88	0/761
29	l	0.60	0/454	1.07	1/599 (0.2%)
3	G	0.78	8/1944 (0.4%)	1.10	14/2618 (0.5%)
30	m	0.47	0/435	0.95	1/575 (0.2%)
31	o	0.60	0/864	1.24	7/1140 (0.6%)
32	5	0.59	37/87703 (0.0%)	1.15	801/136805 (0.6%)
33	7	0.52	0/2858	1.01	19/4455 (0.4%)
34	8	0.60	1/3701 (0.0%)	1.17	40/5766 (0.7%)
35	B	0.76	6/3214 (0.2%)	1.10	13/4308 (0.3%)
36	C	0.68	4/2973 (0.1%)	1.07	14/3990 (0.4%)
37	E	0.68	3/1941 (0.2%)	1.17	15/2601 (0.6%)
38	F	0.68	0/1905	1.17	13/2539 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	I	0.59	1/1753 (0.1%)	1.05	8/2343 (0.3%)
4	H	0.77	2/1537 (0.1%)	1.10	10/2066 (0.5%)
40	P	0.77	3/1268 (0.2%)	1.15	12/1701 (0.7%)
41	W	0.73	0/541	1.17	3/720 (0.4%)
42	j	0.82	1/721 (0.1%)	1.31	12/953 (1.3%)
43	n	0.72	0/223	1.11	0/284
44	p	0.60	1/718 (0.1%)	1.00	4/953 (0.4%)
45	r	0.57	0/1017	1.05	4/1365 (0.3%)
46	K	0.76	2/1256 (0.2%)	1.17	6/1694 (0.4%)
47	q	0.73	2/1580 (0.1%)	0.93	5/2133 (0.2%)
48	z	0.92	7/3171 (0.2%)	0.95	10/4257 (0.2%)
49	2	0.50	0/234	0.99	1/317 (0.3%)
5	J	0.69	2/1382 (0.1%)	1.09	15/1849 (0.8%)
50	3	1.56	2/1804 (0.1%)	1.07	7/2805 (0.2%)
51	4	0.77	1/5090 (0.0%)	1.05	13/7936 (0.2%)
52	9	0.35	0/858	0.58	0/1156
53	6	0.29	0/1521	0.49	0/2039
54	S2	0.59	27/41241 (0.1%)	1.15	365/64249 (0.6%)
55	SA	0.63	1/1679 (0.1%)	1.05	10/2283 (0.4%)
56	SB	0.74	6/1753 (0.3%)	1.12	15/2350 (0.6%)
57	SC	0.69	1/1726 (0.1%)	1.05	14/2332 (0.6%)
58	SE	0.64	2/2118 (0.1%)	1.09	15/2849 (0.5%)
59	SG	0.69	4/1946 (0.2%)	1.05	8/2590 (0.3%)
6	L	0.68	3/1734 (0.2%)	1.05	7/2318 (0.3%)
60	SH	0.51	0/1544	0.94	5/2068 (0.2%)
61	SI	0.76	3/1715 (0.2%)	1.11	12/2287 (0.5%)
62	SJ	0.59	1/1550 (0.1%)	1.20	12/2069 (0.6%)
63	SL	0.66	1/1259 (0.1%)	1.05	4/1684 (0.2%)
64	SN	0.60	0/1226	1.05	7/1649 (0.4%)
65	SO	0.61	0/1029	1.23	13/1380 (0.9%)
66	SV	0.54	0/631	0.93	0/844
67	SW	0.65	1/1051 (0.1%)	1.04	6/1406 (0.4%)
68	SX	0.60	0/1118	1.06	9/1493 (0.6%)
69	SY	0.54	0/1040	0.94	0/1382
7	M	0.63	1/1152 (0.1%)	1.10	5/1539 (0.3%)
70	Sa	0.71	1/794 (0.1%)	1.17	6/1065 (0.6%)
71	Sb	0.48	0/665	0.90	1/891 (0.1%)
72	Se	0.50	0/458	0.97	3/602 (0.5%)
73	SD	0.60	1/1793 (0.1%)	1.01	5/2414 (0.2%)
74	SF	0.62	2/1531 (0.1%)	1.00	6/2059 (0.3%)
75	SK	0.58	0/851	1.01	5/1147 (0.4%)
76	SM	0.69	0/970	1.05	6/1300 (0.5%)
77	SP	0.87	2/816 (0.2%)	1.19	10/1084 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
78	SQ	0.51	0/1142	1.08	12/1528 (0.8%)
79	SR	0.50	0/1060	0.73	0/1421
8	N	0.72	3/1746 (0.2%)	1.25	11/2338 (0.5%)
80	SS	0.46	0/1157	0.99	5/1548 (0.3%)
81	ST	0.61	1/1119 (0.1%)	1.05	3/1499 (0.2%)
82	SU	0.52	0/828	0.92	0/1112
83	SZ	0.47	0/604	0.84	0/810
84	Sc	0.57	2/507 (0.4%)	0.75	0/677
85	Sd	0.66	0/445	1.12	2/589 (0.3%)
86	Sf	0.96	3/593 (0.5%)	1.61	15/786 (1.9%)
87	Sg	0.56	0/2493	0.85	3/3394 (0.1%)
88	S1	1.04	4/619 (0.6%)	0.90	1/832 (0.1%)
89	S4	0.88	2/608 (0.3%)	0.77	0/809
9	O	0.63	2/1684 (0.1%)	1.08	11/2251 (0.5%)
All	All	0.64	183/244716 (0.1%)	1.12	1888/359004 (0.5%)

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	8
10	Q	0	5
11	R	0	7
12	S	0	8
13	T	0	2
15	V	0	3
16	X	0	2
17	Y	0	3
18	Z	0	1
19	a	0	6
2	D	0	9
20	b	0	2
21	c	0	1
22	d	0	5
23	e	0	1
24	f	0	2
25	g	0	2
26	h	0	1
27	i	0	3
28	k	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	G	0	4
30	m	0	1
31	o	0	3
32	5	0	175
33	7	0	2
34	8	0	11
35	B	0	12
36	C	0	4
37	E	0	16
38	F	0	8
39	I	0	3
4	H	0	2
40	P	0	4
41	W	0	1
42	j	0	4
44	p	0	2
45	r	0	3
46	K	0	10
47	q	0	8
48	z	0	7
49	2	0	1
5	J	0	2
54	S2	0	59
55	SA	0	5
56	SB	0	7
57	SC	0	7
58	SE	0	6
59	SG	0	1
6	L	0	4
60	SH	0	2
61	SI	0	9
62	SJ	0	3
63	SL	0	3
64	SN	0	5
65	SO	0	1
66	SV	0	3
67	SW	0	3
68	SX	0	2
69	SY	0	1
7	M	0	3
70	Sa	0	3
71	Sb	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
73	SD	0	3
74	SF	0	4
75	SK	0	1
76	SM	0	2
77	SP	0	3
78	SQ	0	1
8	N	0	9
80	SS	0	1
81	ST	0	2
82	SU	0	1
83	SZ	0	1
85	Sd	0	3
86	Sf	0	4
87	Sg	0	3
88	S1	0	4
9	O	0	4
All	All	0	529

The worst 5 of 183 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	3	31	C	O3'-P	-62.24	0.86	1.61
51	4	183	A	O3'-P	-44.16	1.08	1.61
32	5	1823	G	O3'-P	35.59	2.03	1.61
48	z	340	MET	C-N	22.92	1.86	1.34
48	z	345	PHE	C-N	-18.40	0.91	1.34

The worst 5 of 1888 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	3	38	C	P-O3'-C3'	-20.63	94.95	119.70
48	z	340	MET	O-C-N	19.47	153.86	122.70
50	3	31	C	O3'-P-O5'	-18.73	68.40	104.00
48	z	340	MET	C-N-CA	-18.61	75.16	121.70
86	Sf	146	LEU	CA-CB-CG	16.39	153.01	115.30

There are no chirality outliers.

5 of 529 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	18	ALA	Peptide

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Mol	Chain	Res	Type	Group
1	A	194	ASN	Peptide
1	A	196	TRP	Peptide
1	A	66	PRO	Peptide
1	A	67	TYR	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	1868	0	1959	130	0
2	D	2380	0	2412	119	0
3	G	1912	0	2059	94	0
4	H	1518	0	1601	69	0
5	J	1359	0	1390	62	0
6	L	1703	0	1818	59	0
7	M	1131	0	1209	55	0
8	N	1701	0	1749	109	0
9	O	1651	0	1786	64	0
10	Q	1506	0	1623	66	0
11	R	1508	0	1663	118	0
12	S	1454	0	1496	115	0
13	T	1298	0	1366	54	0
14	U	808	0	831	15	0
15	V	979	0	1039	43	0
16	X	976	0	1053	37	0
17	Y	1115	0	1205	49	0
18	Z	1107	0	1182	50	0
19	a	1163	0	1211	0	0
20	b	610	0	650	0	0
21	c	732	0	769	0	0
22	d	888	0	930	0	0
23	e	1053	0	1147	0	0
24	f	876	0	912	0	0
25	g	906	0	1002	0	0
26	h	1015	0	1150	0	0
27	i	832	0	917	0	0
28	k	569	0	637	0	0
29	l	444	0	483	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	m	429	0	466	0	0
31	o	851	0	923	0	0
32	5	78406	0	39609	10754	0
33	7	2558	0	1296	325	0
34	8	3314	0	1683	569	0
35	B	3147	0	3280	198	0
36	C	2919	0	3100	118	0
37	E	1904	0	2055	110	0
38	F	1870	0	1996	127	0
39	I	1713	0	1752	122	0
40	P	1242	0	1269	60	0
41	W	528	0	541	55	0
42	j	706	0	742	0	0
43	n	222	0	257	0	0
44	p	708	0	760	0	0
45	r	1001	0	1062	0	0
46	K	1238	0	1293	99	0
47	q	1556	0	1612	0	0
48	z	3241	0	3211	0	0
49	2	233	0	291	25	0
50	3	1616	0	824	176	0
51	4	4551	0	2297	271	0
52	9	844	0	861	25	0
53	6	1497	0	1504	25	0
54	S2	36900	0	18592	5093	0
55	SA	1642	0	1646	167	0
56	SB	1725	0	1794	154	0
57	SC	1690	0	1777	73	0
58	SE	2076	0	2177	69	0
59	SG	1923	0	2089	74	0
60	SH	1521	0	1615	92	0
61	SI	1686	0	1772	85	0
62	SJ	1525	0	1640	62	0
63	SL	1238	0	1313	63	0
64	SN	1202	0	1289	50	0
65	SO	1016	0	1037	43	0
66	SV	625	0	628	16	0
67	SW	1034	0	1080	47	0
68	SX	1099	0	1166	43	0
69	SY	1023	0	1090	37	0
70	Sa	781	0	832	0	0
71	Sb	651	0	672	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	Se	452	0	494	0	0
73	SD	1765	0	1865	67	0
74	SF	1509	0	1563	86	0
75	SK	827	0	854	28	0
76	SM	960	0	989	62	0
77	SP	805	0	861	17	0
78	SQ	1124	0	1193	38	0
79	SR	1047	0	1101	215	0
80	SS	1139	0	1190	137	0
81	ST	1101	0	1135	58	0
82	SU	818	0	883	21	0
83	SZ	598	0	655	124	0
84	Sc	506	0	531	0	0
85	Sd	434	0	427	0	0
86	Sf	581	0	599	0	0
87	Sg	2436	0	2393	0	0
88	S1	608	0	617	28	0
89	S4	604	0	638	12	0
90	5	116	0	0	0	0
90	7	5	0	0	0	0
90	8	6	0	0	0	0
90	D	1	0	0	0	0
90	S2	36	0	0	1	0
90	V	1	0	0	0	0
90	g	1	0	0	0	0
91	Sa	1	0	0	0	0
91	j	1	0	0	0	0
91	m	1	0	0	0	0
91	o	1	0	0	0	0
All	All	228197	0	170130	19961	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 55.

The worst 5 of 19961 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)
50:3:31:C:H4'	54:S2:1640:A:C2	1.26	1.69
39:I:101:LYS:HE2	39:I:121:LYS:CG	1.28	1.61
32:5:294:G:C5'	32:5:296:A:H4'	1.19	1.57
54:S2:870:A:C5	54:S2:915:G:N7	1.72	1.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:R:166:THR:HG21	54:S2:872:A:C3'	1.15	1.56

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	
1	A	242/244 (99%)	194 (80%)	38 (16%)	10 (4%)	3	37
2	D	290/292 (99%)	228 (79%)	41 (14%)	21 (7%)	1	22
3	G	236/238 (99%)	188 (80%)	41 (17%)	7 (3%)	5	46
4	H	188/190 (99%)	162 (86%)	20 (11%)	6 (3%)	5	44
5	J	168/170 (99%)	126 (75%)	33 (20%)	9 (5%)	2	30
6	L	208/210 (99%)	166 (80%)	29 (14%)	13 (6%)	2	26
7	M	136/138 (99%)	111 (82%)	21 (15%)	4 (3%)	6	46
8	N	201/203 (99%)	159 (79%)	31 (15%)	11 (6%)	2	30
9	O	199/201 (99%)	177 (89%)	19 (10%)	3 (2%)	13	59
10	Q	185/187 (99%)	154 (83%)	24 (13%)	7 (4%)	4	39
11	R	178/180 (99%)	148 (83%)	23 (13%)	7 (4%)	4	38
12	S	173/175 (99%)	139 (80%)	27 (16%)	7 (4%)	4	38
13	T	157/159 (99%)	132 (84%)	20 (13%)	5 (3%)	5	44
14	U	97/99 (98%)	80 (82%)	14 (14%)	3 (3%)	5	45
15	V	129/131 (98%)	110 (85%)	14 (11%)	5 (4%)	4	38
16	X	117/119 (98%)	102 (87%)	12 (10%)	3 (3%)	7	48
17	Y	132/134 (98%)	105 (80%)	21 (16%)	6 (4%)	3	34
18	Z	133/135 (98%)	111 (84%)	15 (11%)	7 (5%)	2	30
19	a	145/147 (99%)	114 (79%)	24 (17%)	7 (5%)	3	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	b	73/75 (97%)	60 (82%)	10 (14%)	3 (4%)	3	37
21	c	92/94 (98%)	78 (85%)	10 (11%)	4 (4%)	3	36
22	d	105/107 (98%)	85 (81%)	16 (15%)	4 (4%)	4	39
23	e	126/128 (98%)	110 (87%)	14 (11%)	2 (2%)	12	58
24	f	107/109 (98%)	89 (83%)	11 (10%)	7 (6%)	1	26
25	g	112/114 (98%)	100 (89%)	10 (9%)	2 (2%)	11	56
26	h	120/122 (98%)	97 (81%)	21 (18%)	2 (2%)	11	57
27	i	100/102 (98%)	85 (85%)	13 (13%)	2 (2%)	9	54
28	k	67/69 (97%)	53 (79%)	11 (16%)	3 (4%)	3	34
29	l	48/50 (96%)	42 (88%)	5 (10%)	1 (2%)	9	53
30	m	50/52 (96%)	44 (88%)	6 (12%)	0	100	100
31	o	102/104 (98%)	79 (78%)	17 (17%)	6 (6%)	2	28
35	B	392/394 (100%)	309 (79%)	54 (14%)	29 (7%)	1	21
36	C	365/367 (100%)	292 (80%)	55 (15%)	18 (5%)	3	32
37	E	232/236 (98%)	144 (62%)	55 (24%)	33 (14%)	0	6
38	F	223/225 (99%)	180 (81%)	35 (16%)	8 (4%)	4	41
39	I	211/213 (99%)	170 (81%)	28 (13%)	13 (6%)	2	27
40	P	151/153 (99%)	134 (89%)	15 (10%)	2 (1%)	15	61
41	W	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
42	j	84/86 (98%)	64 (76%)	18 (21%)	2 (2%)	7	50
43	n	21/23 (91%)	20 (95%)	1 (5%)	0	100	100
44	p	89/91 (98%)	75 (84%)	14 (16%)	0	100	100
45	r	123/125 (98%)	96 (78%)	20 (16%)	7 (6%)	2	28
46	K	159/163 (98%)	91 (57%)	34 (21%)	34 (21%)	0	2
47	q	200/202 (99%)	141 (70%)	31 (16%)	28 (14%)	0	6
48	z	399/426 (94%)	350 (88%)	31 (8%)	18 (4%)	3	34
49	2	27/31 (87%)	15 (56%)	9 (33%)	3 (11%)	0	10
52	9	103/105 (98%)	96 (93%)	7 (7%)	0	100	100
53	6	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
55	SA	206/208 (99%)	163 (79%)	30 (15%)	13 (6%)	2	26
56	SB	211/213 (99%)	154 (73%)	36 (17%)	21 (10%)	1	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	SC	216/218 (99%)	182 (84%)	27 (12%)	7 (3%)	5	44
58	SE	260/262 (99%)	198 (76%)	44 (17%)	18 (7%)	1	24
59	SG	235/237 (99%)	195 (83%)	32 (14%)	8 (3%)	5	43
60	SH	187/189 (99%)	141 (75%)	29 (16%)	17 (9%)	1	16
61	SI	204/206 (99%)	165 (81%)	30 (15%)	9 (4%)	3	35
62	SJ	183/185 (99%)	133 (73%)	35 (19%)	15 (8%)	1	18
63	SL	150/152 (99%)	122 (81%)	22 (15%)	6 (4%)	4	38
64	SN	147/149 (99%)	115 (78%)	28 (19%)	4 (3%)	6	48
65	SO	134/136 (98%)	99 (74%)	21 (16%)	14 (10%)	1	12
66	SV	80/82 (98%)	58 (72%)	15 (19%)	7 (9%)	1	16
67	SW	127/129 (98%)	108 (85%)	16 (13%)	3 (2%)	7	50
68	SX	139/141 (99%)	109 (78%)	26 (19%)	4 (3%)	6	46
69	SY	124/126 (98%)	101 (82%)	16 (13%)	7 (6%)	2	29
70	Sa	96/98 (98%)	69 (72%)	18 (19%)	9 (9%)	1	15
71	Sb	81/83 (98%)	61 (75%)	16 (20%)	4 (5%)	3	32
72	Se	55/57 (96%)	41 (74%)	12 (22%)	2 (4%)	4	41
73	SD	225/227 (99%)	174 (77%)	41 (18%)	10 (4%)	3	35
74	SF	189/191 (99%)	145 (77%)	34 (18%)	10 (5%)	2	30
75	SK	96/98 (98%)	58 (60%)	26 (27%)	12 (12%)	0	8
76	SM	122/124 (98%)	78 (64%)	24 (20%)	20 (16%)	0	5
77	SP	94/96 (98%)	67 (71%)	17 (18%)	10 (11%)	0	11
78	SQ	139/141 (99%)	111 (80%)	20 (14%)	8 (6%)	2	28
79	SR	127/129 (98%)	111 (87%)	11 (9%)	5 (4%)	4	38
80	SS	135/137 (98%)	114 (84%)	12 (9%)	9 (7%)	1	25
81	ST	139/141 (99%)	115 (83%)	18 (13%)	6 (4%)	3	36
82	SU	102/104 (98%)	83 (81%)	13 (13%)	6 (6%)	2	28
83	SZ	73/75 (97%)	59 (81%)	9 (12%)	5 (7%)	1	24
84	Sc	60/64 (94%)	47 (78%)	12 (20%)	1 (2%)	11	57
85	Sd	50/52 (96%)	36 (72%)	11 (22%)	3 (6%)	2	27
86	Sf	69/71 (97%)	42 (61%)	15 (22%)	12 (17%)	0	4
87	Sg	311/313 (99%)	240 (77%)	56 (18%)	15 (5%)	3	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
88	S1	72/74 (97%)	61 (85%)	6 (8%)	5 (7%)	1 24
89	S4	72/76 (95%)	68 (94%)	4 (6%)	0	100 100
All	All	12341/12544 (98%)	9853 (80%)	1811 (15%)	677 (6%)	4 30

5 of 677 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	HIS
1	A	196	TRP
1	A	197	PRO
2	D	9	ASN
2	D	19	LYS

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
1	A	187/187 (100%)	137 (73%)	50 (27%)	0 5
2	D	246/247 (100%)	183 (74%)	63 (26%)	0 6
3	G	204/206 (99%)	150 (74%)	54 (26%)	0 5
4	H	169/169 (100%)	131 (78%)	38 (22%)	1 9
5	J	143/143 (100%)	108 (76%)	35 (24%)	1 7
6	L	176/176 (100%)	133 (76%)	43 (24%)	1 7
7	M	116/116 (100%)	87 (75%)	29 (25%)	1 6
8	N	171/171 (100%)	126 (74%)	45 (26%)	0 5
9	O	172/172 (100%)	138 (80%)	34 (20%)	1 12
10	Q	163/163 (100%)	126 (77%)	37 (23%)	1 8
11	R	159/159 (100%)	120 (76%)	39 (24%)	1 7
12	S	156/156 (100%)	124 (80%)	32 (20%)	1 11
13	T	139/139 (100%)	105 (76%)	34 (24%)	1 7
14	U	89/89 (100%)	65 (73%)	24 (27%)	0 5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	V	101/101 (100%)	78 (77%)	23 (23%)	1	8
16	X	107/107 (100%)	88 (82%)	19 (18%)	2	17
17	Y	124/124 (100%)	94 (76%)	30 (24%)	1	7
18	Z	117/117 (100%)	93 (80%)	24 (20%)	1	11
19	a	119/119 (100%)	99 (83%)	20 (17%)	2	19
20	b	63/63 (100%)	48 (76%)	15 (24%)	1	7
21	c	79/79 (100%)	59 (75%)	20 (25%)	1	6
22	d	98/98 (100%)	65 (66%)	33 (34%)	0	2
23	e	114/114 (100%)	91 (80%)	23 (20%)	1	12
24	f	88/88 (100%)	73 (83%)	15 (17%)	2	19
25	g	98/98 (100%)	78 (80%)	20 (20%)	1	11
26	h	109/109 (100%)	91 (84%)	18 (16%)	3	20
27	i	86/86 (100%)	68 (79%)	18 (21%)	1	11
28	k	64/64 (100%)	51 (80%)	13 (20%)	1	11
29	l	47/47 (100%)	37 (79%)	10 (21%)	1	10
30	m	48/48 (100%)	33 (69%)	15 (31%)	0	3
31	o	92/92 (100%)	70 (76%)	22 (24%)	1	7
35	B	335/335 (100%)	260 (78%)	75 (22%)	1	9
36	C	305/305 (100%)	233 (76%)	72 (24%)	1	7
37	E	209/209 (100%)	163 (78%)	46 (22%)	1	9
38	F	194/194 (100%)	141 (73%)	53 (27%)	0	5
39	I	180/180 (100%)	126 (70%)	54 (30%)	0	4
40	P	134/134 (100%)	108 (81%)	26 (19%)	2	13
41	W	55/55 (100%)	38 (69%)	17 (31%)	0	3
42	j	73/73 (100%)	60 (82%)	13 (18%)	2	17
43	n	22/22 (100%)	16 (73%)	6 (27%)	0	5
44	p	74/74 (100%)	62 (84%)	12 (16%)	3	21
45	r	109/109 (100%)	83 (76%)	26 (24%)	1	7
46	K	136/136 (100%)	118 (87%)	18 (13%)	5	31
47	q	170/170 (100%)	134 (79%)	36 (21%)	1	10
48	z	340/340 (100%)	321 (94%)	19 (6%)	26	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	2	29/29 (100%)	26 (90%)	3 (10%)	9	42
52	9	92/94 (98%)	88 (96%)	4 (4%)	35	74
53	6	157/157 (100%)	151 (96%)	6 (4%)	40	76
55	SA	174/174 (100%)	132 (76%)	42 (24%)	1	7
56	SB	194/194 (100%)	155 (80%)	39 (20%)	1	12
57	SC	184/184 (100%)	141 (77%)	43 (23%)	1	7
58	SE	224/224 (100%)	172 (77%)	52 (23%)	1	8
59	SG	207/207 (100%)	166 (80%)	41 (20%)	1	12
60	SH	169/169 (100%)	145 (86%)	24 (14%)	4	29
61	SI	178/178 (100%)	144 (81%)	34 (19%)	2	13
62	SJ	161/161 (100%)	116 (72%)	45 (28%)	0	4
63	SL	136/136 (100%)	104 (76%)	32 (24%)	1	7
64	SN	130/130 (100%)	103 (79%)	27 (21%)	1	11
65	SO	106/106 (100%)	74 (70%)	32 (30%)	0	4
66	SV	66/66 (100%)	50 (76%)	16 (24%)	1	7
67	SW	112/112 (100%)	90 (80%)	22 (20%)	1	13
68	SX	113/113 (100%)	95 (84%)	18 (16%)	3	23
69	SY	108/108 (100%)	85 (79%)	23 (21%)	1	10
70	Sa	85/85 (100%)	71 (84%)	14 (16%)	3	20
71	Sb	75/75 (100%)	58 (77%)	17 (23%)	1	8
72	Se	46/46 (100%)	35 (76%)	11 (24%)	1	7
73	SD	190/190 (100%)	149 (78%)	41 (22%)	1	9
74	SF	161/161 (100%)	123 (76%)	38 (24%)	1	7
75	SK	89/89 (100%)	68 (76%)	21 (24%)	1	7
76	SM	104/104 (100%)	74 (71%)	30 (29%)	0	4
77	SP	88/88 (100%)	70 (80%)	18 (20%)	1	11
78	SQ	117/117 (100%)	91 (78%)	26 (22%)	1	9
79	SR	117/117 (100%)	102 (87%)	15 (13%)	5	32
80	SS	119/119 (100%)	96 (81%)	23 (19%)	2	13
81	ST	112/112 (100%)	88 (79%)	24 (21%)	1	10
82	SU	94/94 (100%)	82 (87%)	12 (13%)	5	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
83	SZ	66/66 (100%)	57 (86%)	9 (14%)	5	30
84	Sc	57/57 (100%)	47 (82%)	10 (18%)	2	18
85	Sd	45/45 (100%)	36 (80%)	9 (20%)	1	12
86	Sf	64/64 (100%)	45 (70%)	19 (30%)	0	4
87	Sg	272/272 (100%)	235 (86%)	37 (14%)	5	30
88	S1	67/67 (100%)	59 (88%)	8 (12%)	6	35
89	S4	69/69 (100%)	60 (87%)	9 (13%)	5	32
All	All	10757/10762 (100%)	8495 (79%)	2262 (21%)	4	10

5 of 2262 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	C	267	TRP
44	p	85	ARG
79	SR	28	PHE
37	E	112	TYR
39	I	21	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 269 such sidechains are listed below:

Mol	Chain	Res	Type
37	E	178	ASN
46	K	147	HIS
80	SS	120	HIS
38	F	82	ASN
40	P	64	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	5	3642/3658 (99%)	1678 (46%)	666 (18%)
33	7	119/120 (99%)	38 (31%)	15 (12%)
34	8	155/156 (99%)	63 (40%)	30 (19%)
50	3	73/76 (96%)	27 (36%)	5 (6%)
51	4	197/206 (95%)	43 (21%)	10 (5%)
54	S2	1714/1742 (98%)	829 (48%)	303 (17%)
All	All	5900/5958 (99%)	2678 (45%)	1029 (17%)

5 of 2678 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
32	5	2	G
32	5	8	U
32	5	12	A
32	5	13	U
32	5	20	U

5 of 1029 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
32	5	3671	G
32	5	4452	U
54	S2	1433	C
32	5	3774	A
32	5	4119	C

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 170 ligands modelled in this entry, 170 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.