



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Jan 17, 2017 – 09:27 PM EST

PDB ID : 5T2A
EMDB ID: : EMD-8343
Title : CryoEM structure of the Leishmania donovani 80S ribosome at 2.9 Angstrom resolution
Authors : Zhang, X.; Lai, M.; Zhou, Z.H.
Deposited on : 2016-08-23
Resolution : 2.90 Å(reported)

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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) : rb-20028442

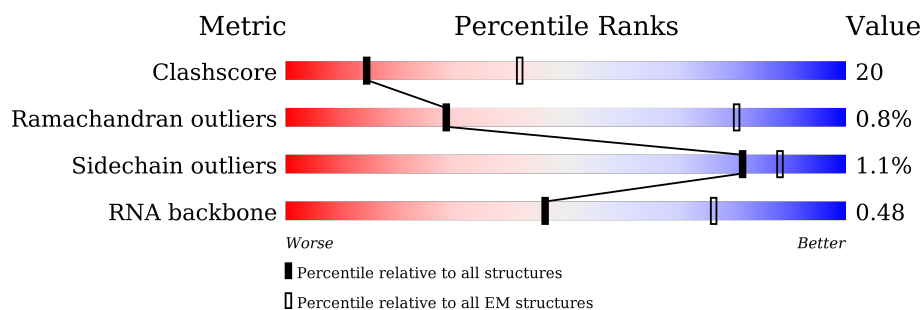
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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	1781	53% 31% 6% 10%
2	B	1465	49% 20% • 27%
3	C	262	31% 25% 5% • 38%
4	D	120	65% 33% ••
5	E	213	57% 22% 21%
6	F	73	38% 48% 10% ••
7	G	183	72% 23% ••
8	H	127	49% 22% • 27%


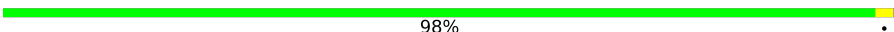










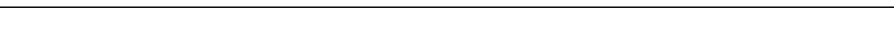

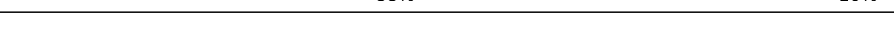

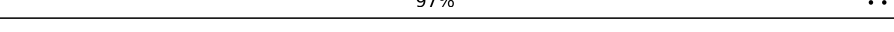







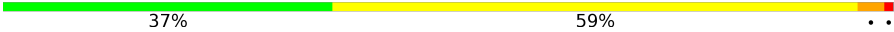
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Mol	Chain	Length	Quality of chain
9	I	198	
10	J	213	
11	K	188	
12	L	220	
13	M	222	
14	N	175	
15	O	204	
16	P	166	
17	Q	179	
18	R	245	
19	S	159	
20	T	129	
21	U	139	
22	V	145	
23	W	124	
24	X	143	
25	Y	134	
26	Z	145	
27	a	147	
28	b	70	
29	c	260	
30	d	419	
31	e	104	
32	f	183	
33	g	133	


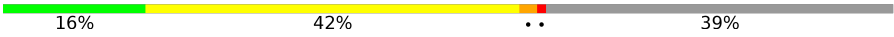



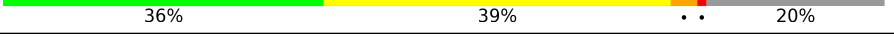


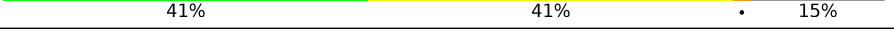


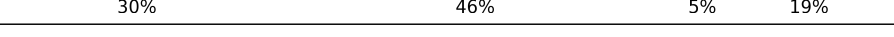

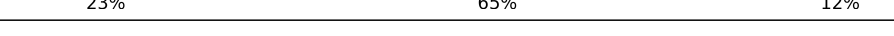


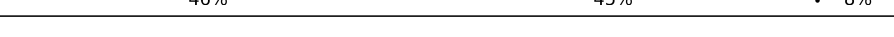

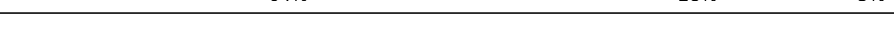



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Mol	Chain	Length	Quality of chain
34	h	168	
35	i	127	
36	j	144	
37	k	105	
38	l	83	
39	m	92	
40	n	83	
41	o	51	
42	p	373	
43	q	128	
44	r	106	
45	s	305	
46	t	195	
47	u	252	
48	v	348	
49	w	190	
50	0	264	
51	1	273	
52	2	2205	
53	3	249	
54	4	200	
55	5	220	
56	6	190	
57	7	312	
58	8	57	

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Mol	Chain	Length	Quality of chain
59	AC	246	
60	AD	153	
61	AE	173	
62	AG	151	
63	AH	144	
64	AI	152	
65	AJ	130	
66	AK	149	
67	AL	143	
68	AM	153	
69	AN	190	
70	AO	179	
71	AP	265	
72	AQ	116	
73	AR	164	
74	AS	143	
75	AT	137	
76	AV	112	
77	AW	86	
78	AX	219	
79	AY	66	
80	AZ	87	

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 200172 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 LSU-alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1603	Total	C	N	O	P	0	0
			34365	15347	6297	11118	1603		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	761	U	A	conflict	GB 322500086
A	1393	G	A	conflict	GB 322500086
A	?	-	A	deletion	GB 322500086

- Molecule 2 is a RNA chain called LSU-beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1064	Total	C	N	O	P	0	0
			22723	10152	4100	7407	1064		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	162	Total	C	N	O	P	0	0
			3449	1542	615	1130	162		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	141	C	U	conflict	GB 79677111
C	182	G	A	conflict	GB 79677111
C	185	C	G	conflict	GB 79677111
C	226	A	U	conflict	GB 79677111
C	228	C	U	conflict	GB 79677111
C	246	C	U	conflict	GB 79677111

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	119	Total	C	N	O	P	0	0
			2531	1132	452	828	119		

- Molecule 5 is a RNA chain called srRNA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	169	Total	C	N	O	P	0	0
			3589	1604	626	1190	169		

- Molecule 6 is a RNA chain called srRNA3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	71	Total	C	N	O	P	0	0
			1508	676	273	488	71		

- Molecule 7 is a RNA chain called srRNA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	183	Total	C	N	O	P	0	0
			3911	1744	704	1280	183		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	169	U	A	conflict	GB 5019758
G	171	U	A	conflict	GB 5019758

- Molecule 8 is a RNA chain called srRNA4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	93	Total	C	N	O	P	0	0
			1996	889	369	645	93		

- Molecule 9 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	197	Total	C	N	O	S	0	0
			1539	968	307	258	6		

- Molecule 10 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	211	Total	C	N	O	S	0	0
			1704	1071	338	279	16		

- Molecule 11 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	167	Total	C	N	O	S	0	0
			1339	844	249	238	8		

- Molecule 12 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	179	Total	C	N	O	S	0	0
			1435	901	296	230	8		

- Molecule 13 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	221	Total	C	N	O	S	0	0
			1780	1126	354	293	7		

- Molecule 14 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	168	Total	C	N	O	S	0	0
			1336	832	265	231	8		

- Molecule 15 is a protein called eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	203	Total	C	N	O	S	0	0
			1714	1080	362	264	8		

- Molecule 16 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	155	Total	C	N	O	S	0	1
			1245	776	246	212	11		

- Molecule 17 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	178	Total	C	N	O	S	0	0
			1456	927	280	244	5		

- Molecule 18 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	196	Total	C	N	O	S	0	0
			1646	1010	360	271	5		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	158	Total	C	N	O	S	0	0
			1261	803	245	208	5		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	123	Total	C	N	O	S	0	1
			997	642	179	173	3		

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	137	Total	C	N	O	S	0	0
			1035	653	195	181	6		

- Molecule 22 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	120	Total	C	N	O	S	0	0
			963	611	182	169	1		

- Molecule 23 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	65	Total	C	N	O	S	0	0
			563	368	110	81	4		

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	120	Total	C	N	O	S	0	0
			965	601	201	159	4		

- Molecule 25 is a protein called eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	133	Total	C	N	O	S	0	0
			1079	688	215	173	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	144	Total	C	N	O	S	0	0
			1126	708	226	186	6		

- Molecule 27 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	146	Total	C	N	O	S	0	0
			1140	698	243	194	5		

- Molecule 28 is a protein called eL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	b	69	Total	C	N	O	0	0
			554	339	127	88		

- Molecule 29 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	253	Total	C	N	O	S	0	1
			1921	1193	392	326	10		

- Molecule 30 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	399	Total	C	N	O	S	0	0
			3183	2003	629	538	13		

- Molecule 31 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	94	Total	C	N	O	S	0	0
			720	448	131	136	5		

- Molecule 32 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	110	Total	C	N	O	S	0	0
			878	561	166	149	2		

- Molecule 33 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	129	Total	C	N	O	S	0	0
			1050	664	209	174	3		

- Molecule 34 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	124	Total	C	N	O	S	0	0
			1014	624	221	163	6		

- Molecule 35 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	126	Total	C	N	O	S	0	0
			1056	658	218	176	4		

- Molecule 36 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	132	Total	C	N	O	S	0	0
			1060	663	221	171	5		

- Molecule 37 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	99	Total	C	N	O	S	0	0
			787	497	160	128	2		

- Molecule 38 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	81	Total	C	N	O	S	0	0
			674	410	154	104	6		

- Molecule 39 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	91	Total	C	N	O	S	0	0
			712	443	146	117	6		

- Molecule 40 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	75	Total	C	N	O	S	0	0
			605	383	118	101	3		

- Molecule 41 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	o	50	Total	C	N	O	S	0	0
			450	291	95	63	1		

- Molecule 42 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	p	365	Total	C	N	O	S	0	1
			2825	1761	563	486	15		

- Molecule 43 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	52	Total	C	N	O	S	0	0
			425	266	88	64	7		

- Molecule 44 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	r	96	Total	C	N	O	S	0	0
			779	493	157	124	5		

- Molecule 45 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	s	266	Total	C	N	O	S	0	0
			2094	1334	397	357	6		

- Molecule 46 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	t	137	Total	C	N	O	S	0	0
			1054	668	197	187	2		

- Molecule 47 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	u	228	Total	C	N	O	S	0	0
			1857	1180	358	308	11		

- Molecule 48 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	230	Total	C	N	O	S	0	0
			1850	1160	368	315	7		

- Molecule 49 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	w	187	Total	C	N	O	S	0	0
			1484	938	273	267	6		

- Molecule 50 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	0	221	Total	C	N	O	S	0	0
			1786	1121	338	316	11		

- Molecule 51 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	258	Total	C	N	O	S	0	0
			2037	1291	387	350	9		

- Molecule 52 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	2	1814	Total	C	N	O	P	0	0
			38724	17307	6969	12635	1813		

- Molecule 53 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	249	Total	C	N	O	S	0	0
			1994	1243	409	339	3		

- Molecule 54 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	200	Total	C	N	O	S	0	0
			1667	1059	324	276	8		

- Molecule 55 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	183	Total	C	N	O	S	0	1
			1473	921	308	242	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	220	ARG	LYS	conflict	UNP E9BH78

- Molecule 56 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	6	164	Total	C	N	O	S	0	0
			1362	862	265	227	8		

- Molecule 57 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	308	Total	C	N	O	S	0	0
			2394	1500	426	456	12		

- Molecule 58 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	38	Total	C	N	O	S	0	0
			314	194	63	52	5		

- Molecule 59 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AC	203	Total	C	N	O	S	0	0
			1622	1033	294	283	12		

- Molecule 60 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AD	93	Total	C	N	O	S	0	0
			767	491	136	133	7		

- Molecule 61 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AE	140	Total	C	N	O	S	0	0
			1148	725	229	189	5		

- Molecule 62 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AG	141	Total	C	N	O	S	0	0
			1157	730	229	190	8		

- Molecule 63 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AH	136	Total	C	N	O	S	0	0
			1023	631	200	184	8		

- Molecule 64 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AI	121	Total	C	N	O	S	0	0
			984	626	188	166	4		

- Molecule 65 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AJ	129	Total	C	N	O	S	0	0
			1020	646	188	178	8		

- Molecule 66 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AK	140	Total	C	N	O	S	0	0
			1108	710	206	189	3		

- Molecule 67 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AL	121	Total	C	N	O	S	0	0
			983	613	192	173	5		

- Molecule 68 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AM	148	Total	C	N	O	S	0	0
			1186	743	237	202	4		

- Molecule 69 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AN	190	Total	C	N	O	S	0	0
			1493	927	287	271	8		

- Molecule 70 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AO	145	Total	C	N	O	S	0	0
			1150	729	224	193	4		

- Molecule 71 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AP	224	Total	C	N	O	S	0	1
			1722	1096	304	312	10		

- Molecule 72 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AQ	102	Total	C	N	O	S	0	0
			807	504	148	153	2		

- Molecule 73 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AR	83	Total	C	N	O	S	0	0
			630	388	116	122	4		

- Molecule 74 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AS	142	Total	C	N	O	S	0	0
			1114	703	222	187	2		

- Molecule 75 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AT	126	Total	C	N	O	S	0	0
			1033	661	198	172	2		

- Molecule 76 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	AV	104	Total	C	N	O	S	0	0
			828	515	175	130	8		

- Molecule 77 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AW	82	Total	C	N	O	S	0	0
			646	396	128	114	8		

- Molecule 78 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	AX	203	Total	C	N	O	S	0	0
			1595	1003	295	284	13		

- Molecule 79 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	AY	56	Total	C	N	O	S	0	0
			452	285	94	72	1		

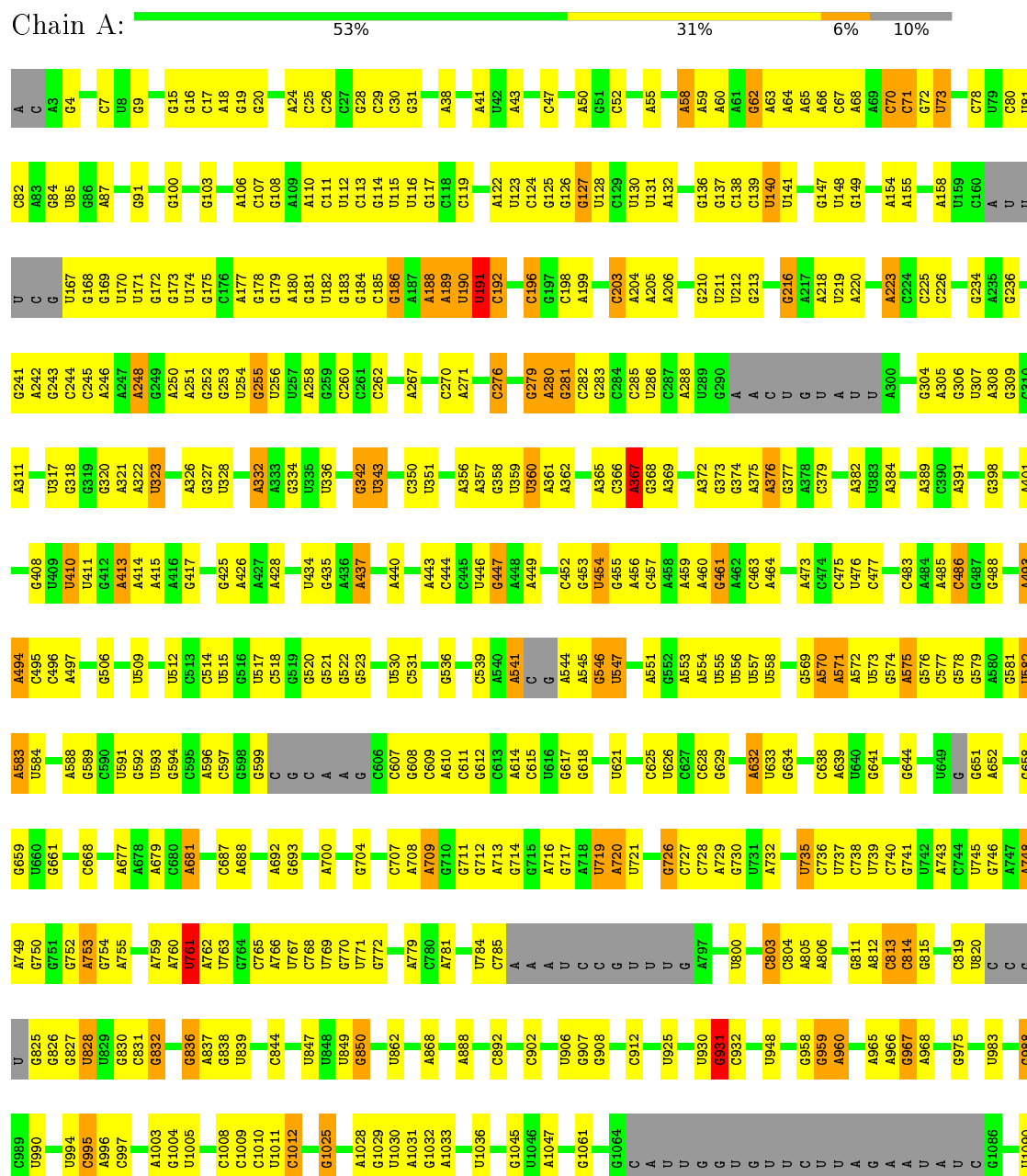
- Molecule 80 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	AZ	68	Total	C	N	O	S	0	0
			526	319	106	97	4		

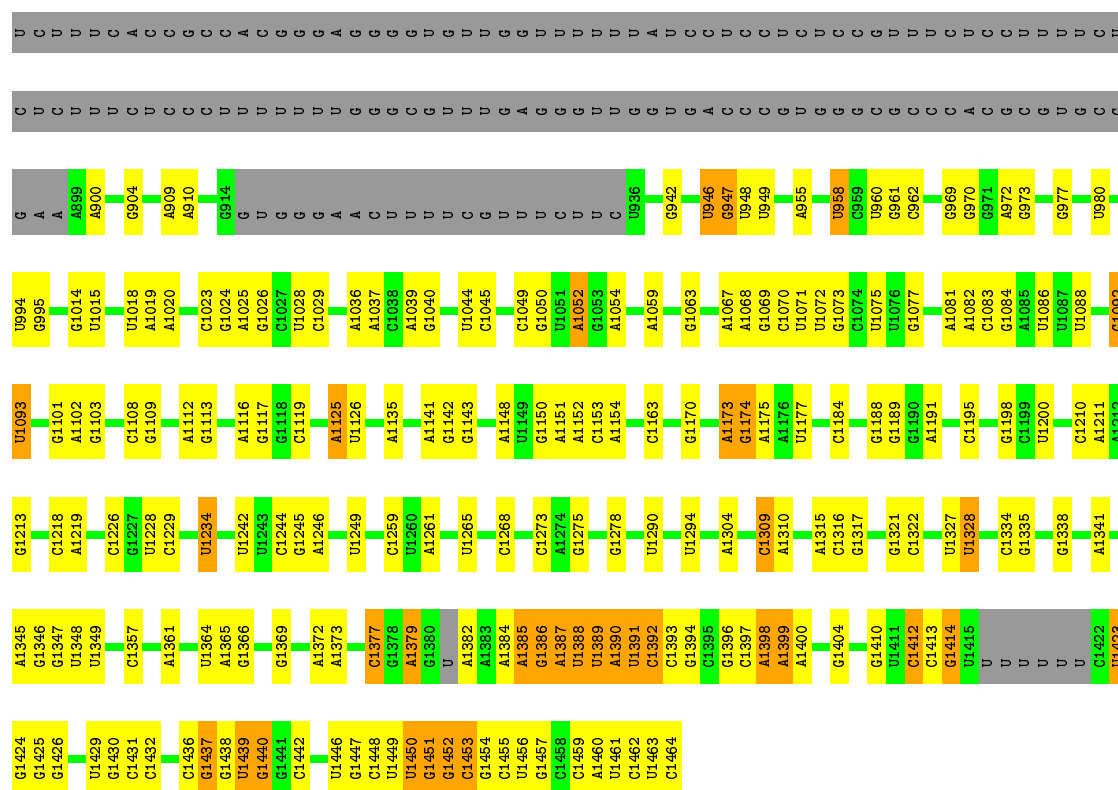
3 Residue-property plots

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.

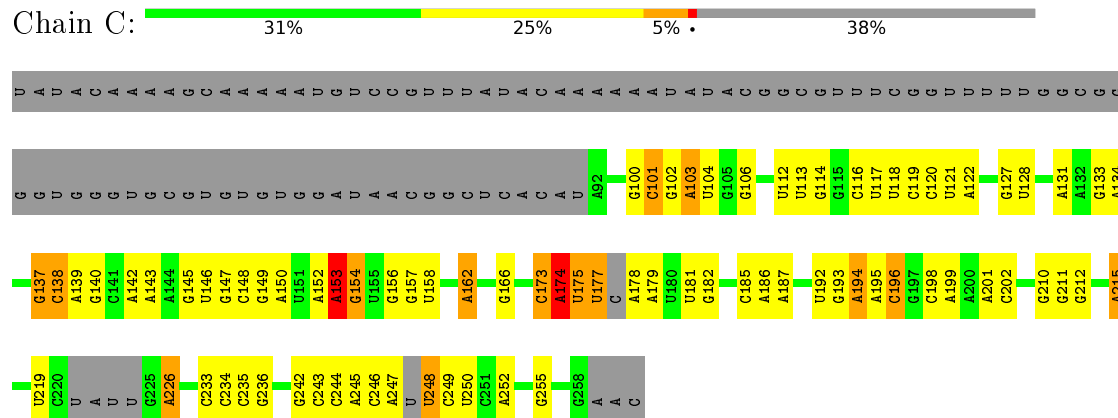
• Molecule 1: LSU-alpha



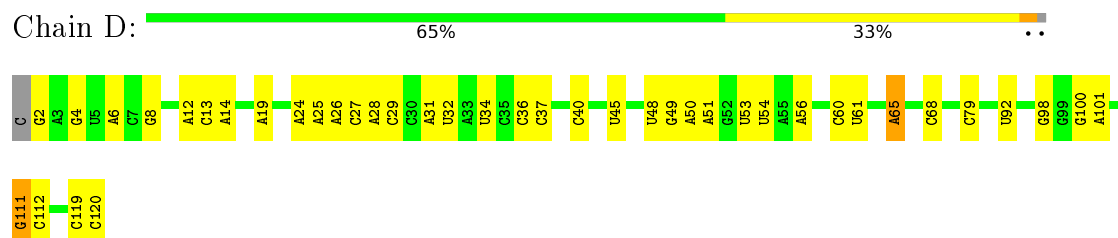




• Molecule 3: 5.8S rRNA

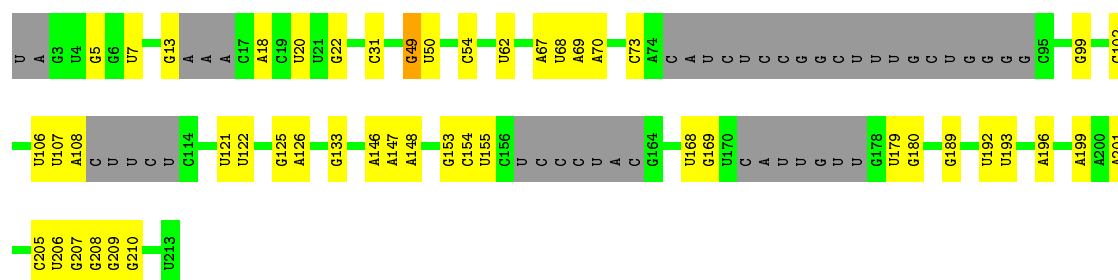


• Molecule 4: 5S rRNA



• Molecule 5: srRNA1

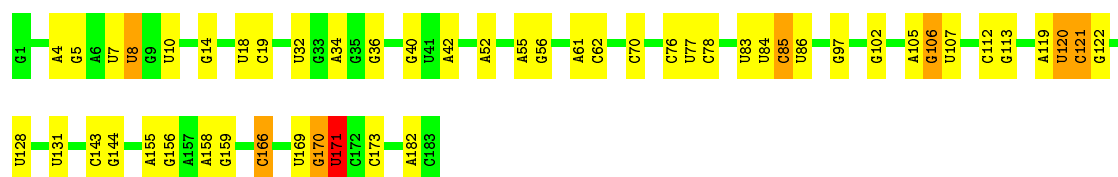




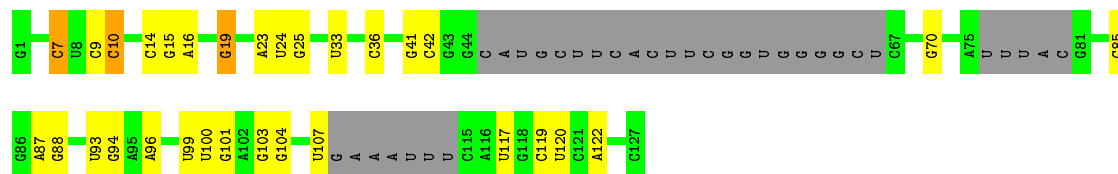
- Molecule 6: srRNA3



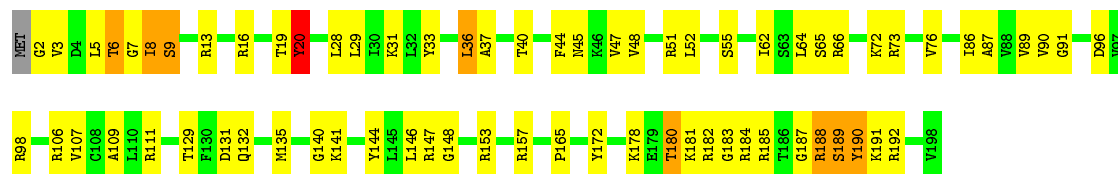
- Molecule 7: srRNA2



- Molecule 8: srRNA4



- Molecule 9: eL18



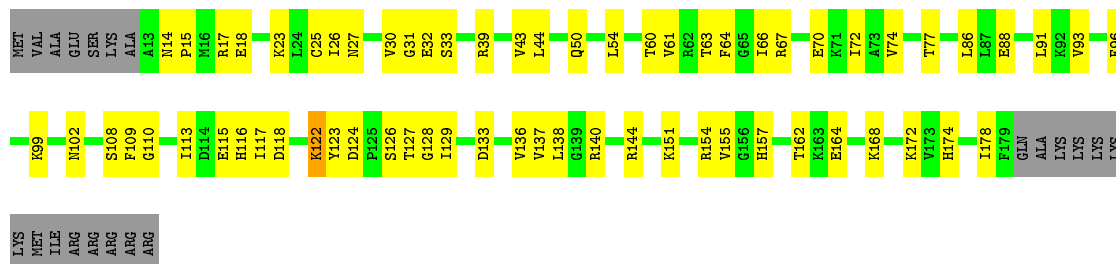
- Molecule 10: uL16





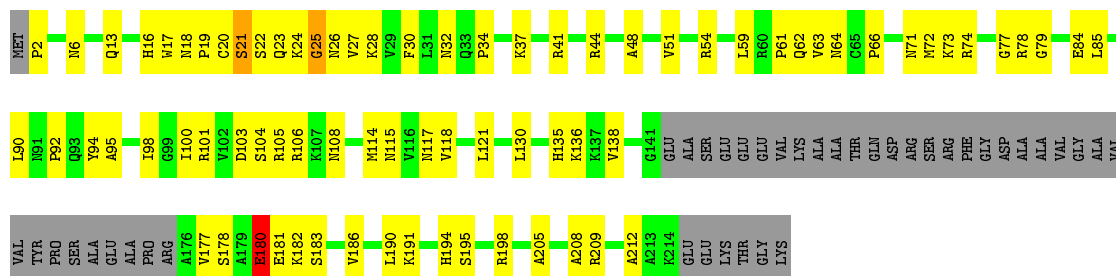
- Molecule 11: uL5

Chain K: 54% 34% • 11%



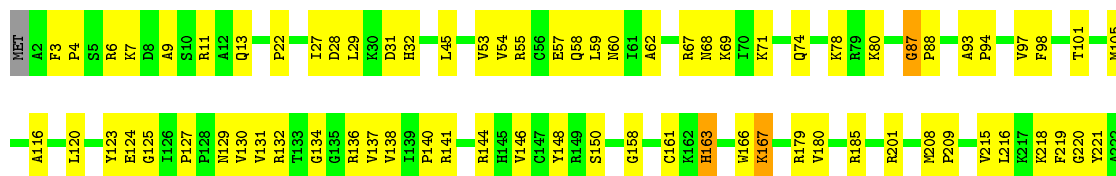
- Molecule 12: eL13

Chain L:  46% 34% 1% 19%



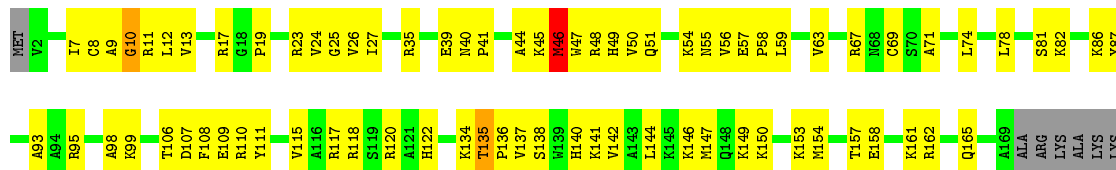
- Molecule 13: uL13

Chain M:  66% 32%



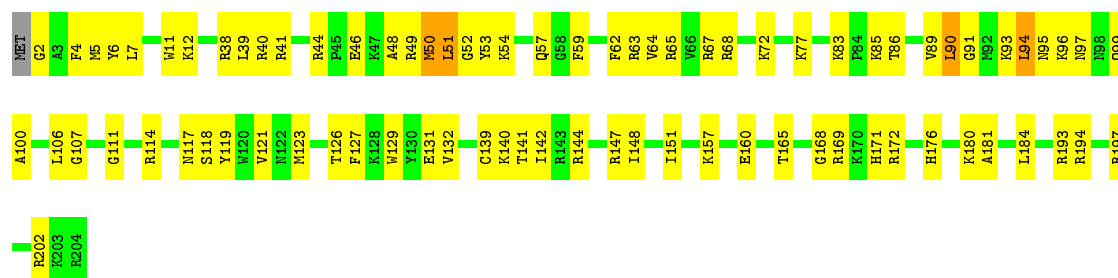
- Molecule 14: eL14

Chain N: 52% 42% ..



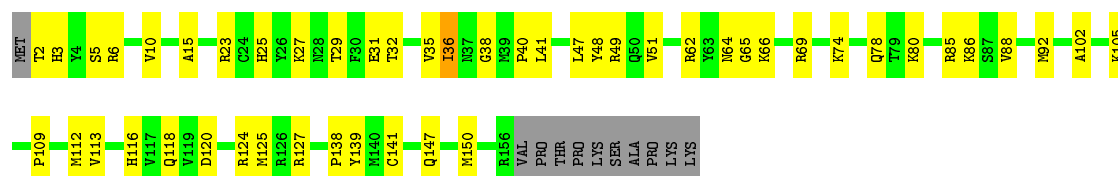
- Molecule 15: eL15

Chain 0: 60% 37% .



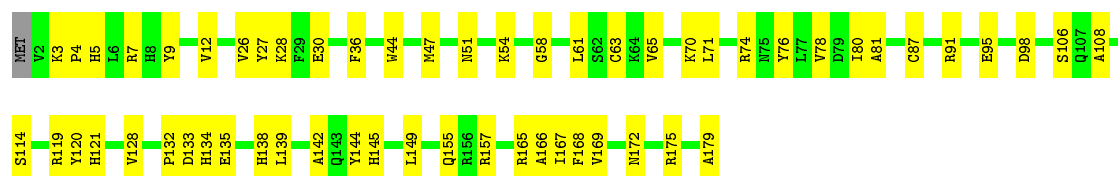
- Molecule 16: uL22

Chain P: 64% 29% 7%



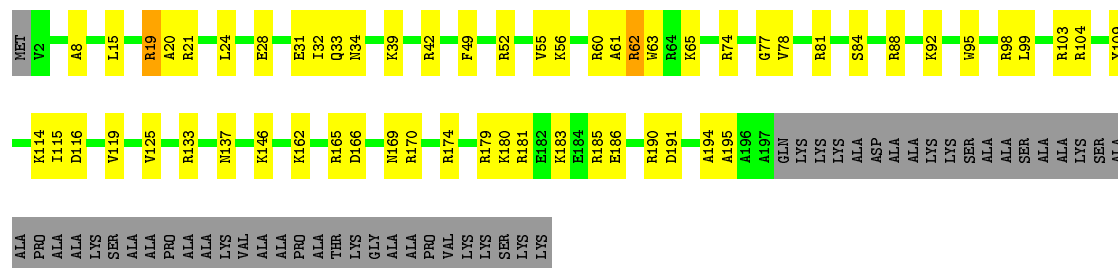
- Molecule 17: eL20

Chain Q: 68% 32%



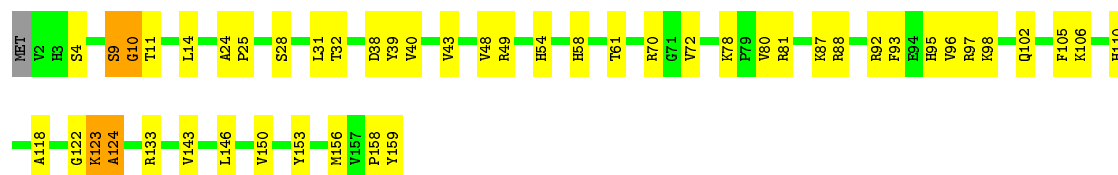
- Molecule 18: eL19

Chain R: 56% 23% 20%



- Molecule 19: eL21

Chain S: 69% 28%



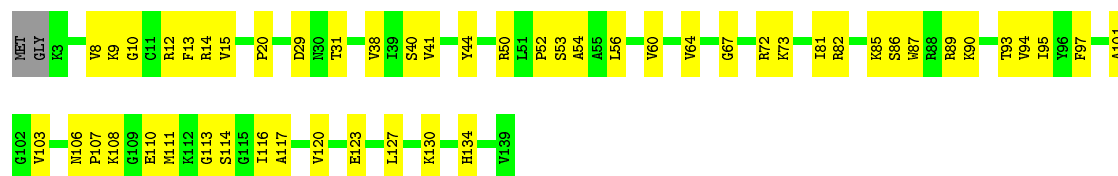
- Molecule 20: eL22

Chain T:  69% 26% 5%



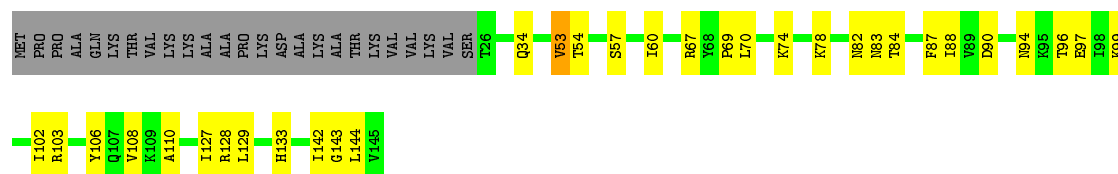
- Molecule 21: uL14

Chain U: 62% 37%



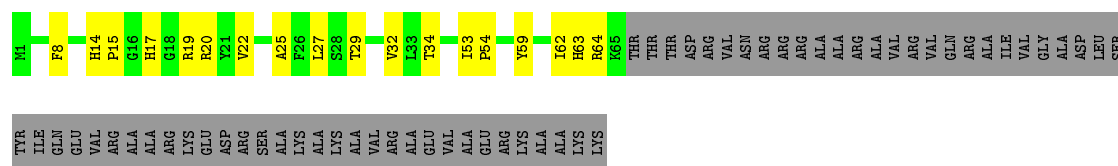
- Molecule 22: uL23

Chain V:  61% 21% • 17%



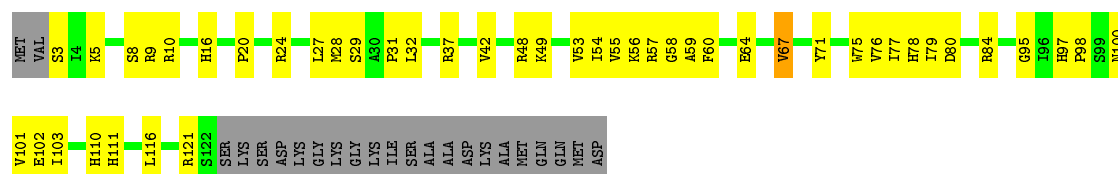
- Molecule 23: eL24

Chain W:  38% 15% 48%



- Molecule 24: uL24

Chain X:  52% 31% • 16%



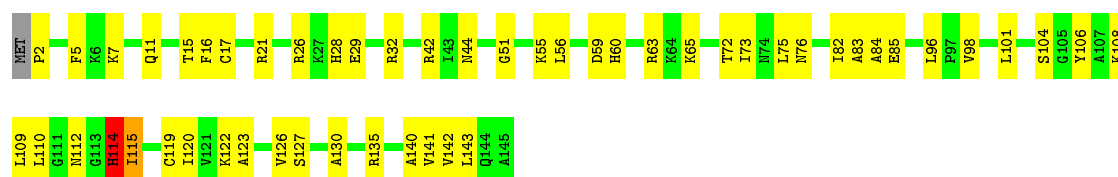
- Molecule 25: eL27

Chain Y:  70% 28% ..



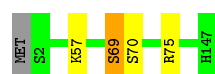
- Molecule 26: uL15

Chain Z: 63% 34% ...



- Molecule 27: eL28

Chain a: 97% ...



- Molecule 28: eL29

Chain b: 96% ..



- Molecule 29: uL2

Chain c: 94% ...



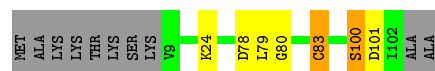
- Molecule 30: uL3

Chain d: 94% . 5%



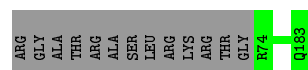
- Molecule 31: eL30

Chain e: 84% 5% • 10%



- Molecule 32: eL31

Chain f:  60% 40%



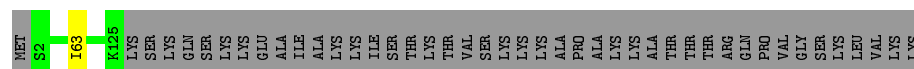
- Molecule 33: eL32

Chain g:  95% . . .



- Molecule 34: eL34

Chain h:  73% . 26%



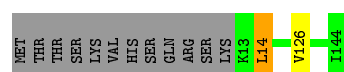
- Molecule 35: uL29

Chain i: 98%



- Molecule 36: eL33

Chain j: 90% .. 8%



- Molecule 37: eL36

Chain k: 93% . 6%

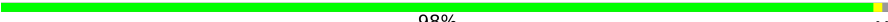


- Molecule 38: eL37

Chain 1: 93% . . .




- Molecule 39: eL43

Chain m:  98% ..



- Molecule 40: eL38

Chain n:  89% • 10%



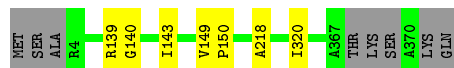
- Molecule 41: eL39

Chain o:  98% •



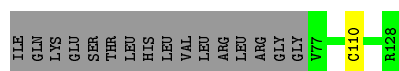
- Molecule 42: uL4

Chain p:  96% • •




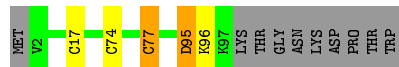
- Molecule 43: eL40

Chain q:  40% • 59%




- Molecule 44: eL42

Chain r:  86% • • 9%



- Molecule 45: uL18

Chain s:  87% 13%



- Molecule 46: eL6

SER
LYS
ALA
GLY
LYS
LYS
THR
LEU
V146
W195

MET	THR	HIS	SER	VAL	TYR	GLY	ASN	ALA	ALA	ASP	MET	PRO	VAL	VAL	ALA	ALA	PRO	GLU	SER	ALA	ILE	LYS	R25	A186	G223	M224	R225	Q226	G234	I252
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[illegible]

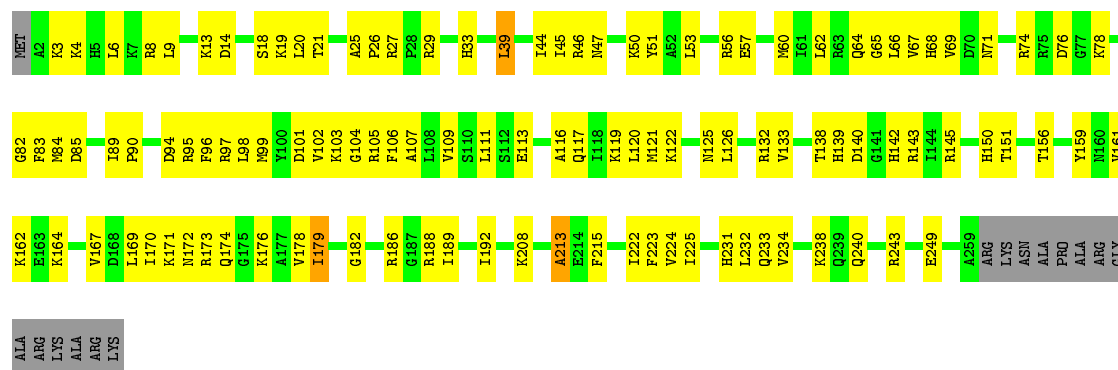
GLN

[illegible]

L157	L158	L159	L160	L161	L162	L163	L164	L165	L166	L167	L168	L169	L170	L171	L172	L173	L174	L175	L176	L177	L178	L179	L180	L181	L182	L183	L184	L185	L186	L187	L188	L189	L190	L191	L192	L193	L194	L195	L196	L197	L198	L199	L200	L201	L202	L203	L204	L205	L206	L207	L208	L209	L210	L211	L212	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L228	L229	L230	L231	L232	L233	L234	L235	L236	L237	L238	L239	L240	L241	L242	L243	L244	L245	L246	L247	L248	L249	L250	L251	L252	L253	L254	L255	L256	L257	L258	L259	L260	L261	L262	L263	L264	L265	L266	L267	L268	L269	L270	L271	L272	L273	L274	L275	L276	L277	L278	L279	L280	L281	L282	L283	L284	L285	L286	L287	L288	L289	L290	L291	L292	L293	L294	L295	L296	L297	L298	L299	L300	L301	L302	L303	L304	L305	L306	L307	L308	L309	L310	L311	L312	L313	L314	L315	L316	L317	L318	L319	L320	L321	L322	L323	L324	L325	L326	L327	L328	L329	L330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667
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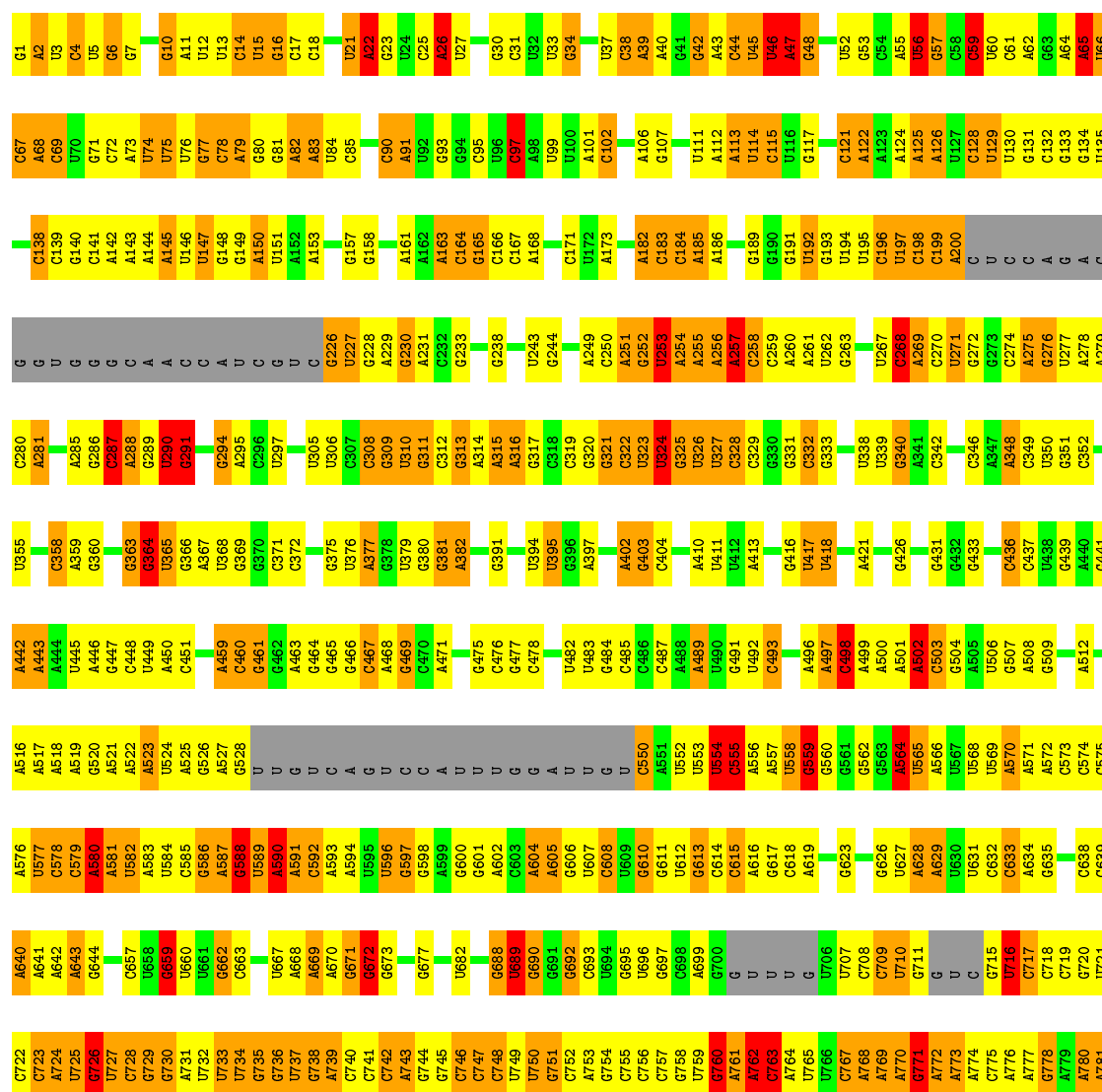
VAL
GLU
ALA
ALA
PRO
ALA
ALA
GLU
LYS
ALA
ALA
GLU

Chain 1:

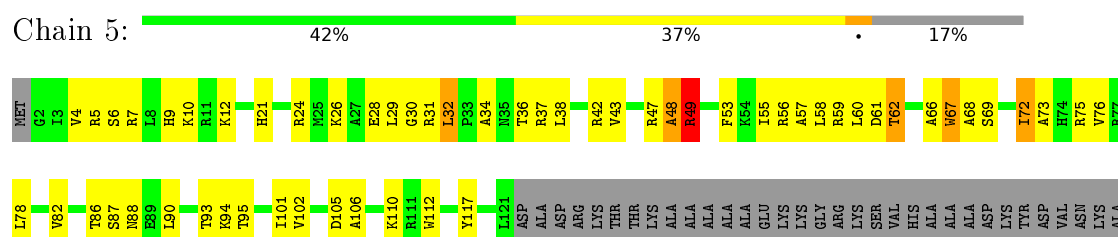
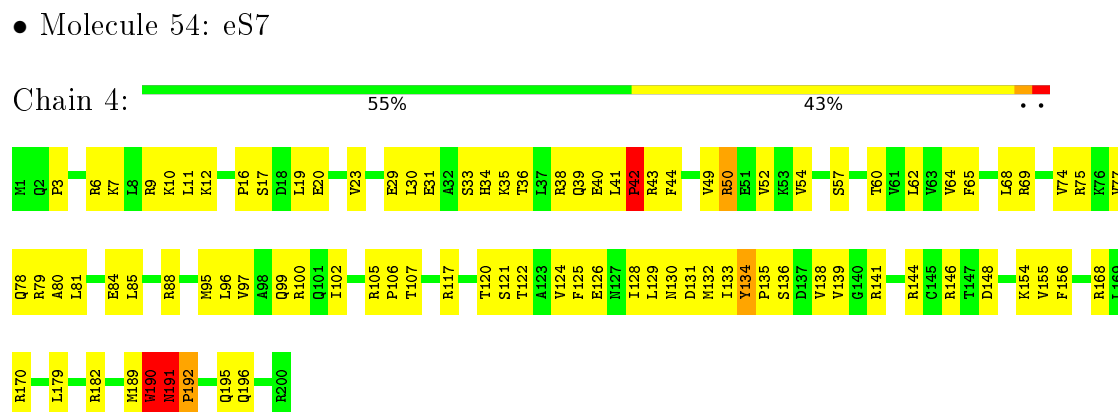
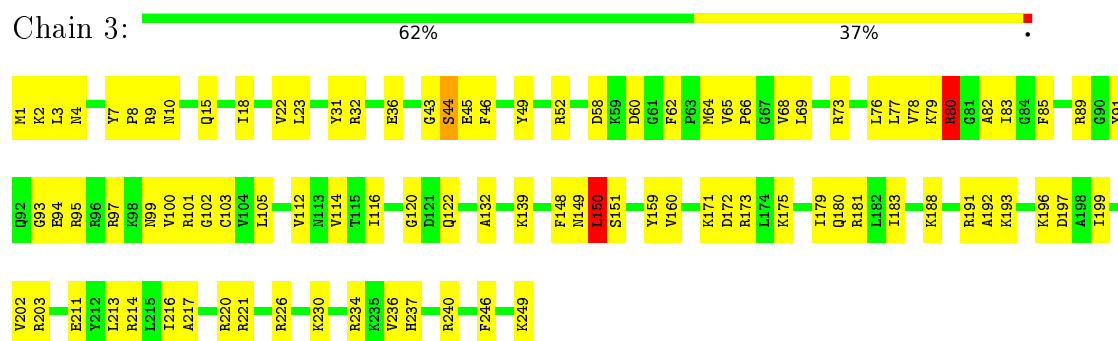
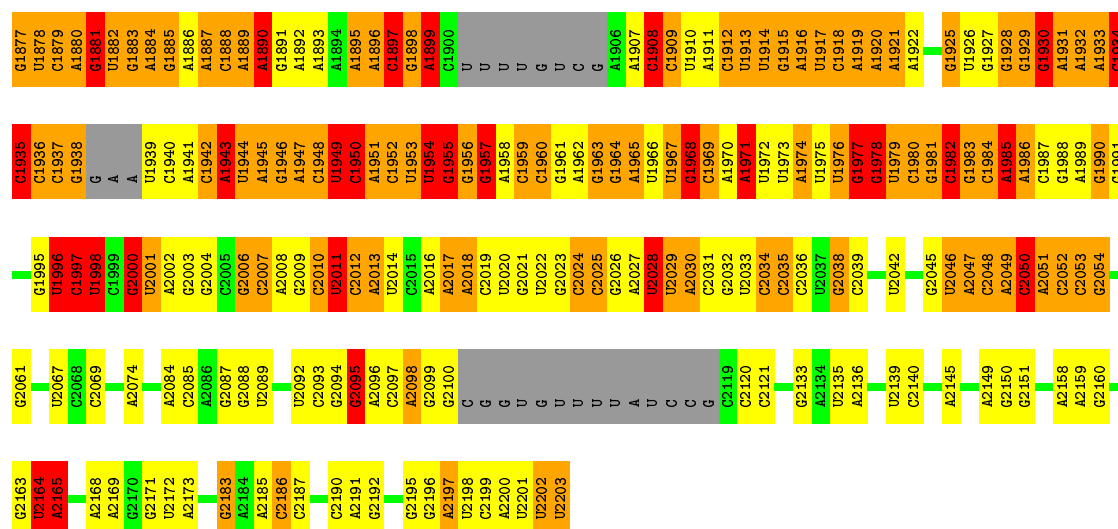


- Molecule 52: 18S rRNA

Chain 2:



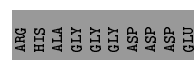
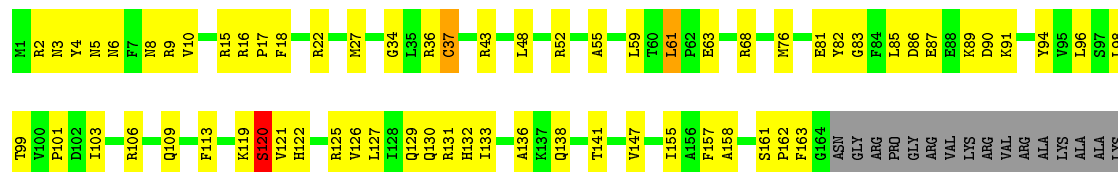
A1814	C1688	C1613	A1550	G1476	C1400	G1273	G1189	G1115	A	U	U935	C848	C782
A1815	A1689	G1617	C1551	G1476	G1401	A1274	C1190	U1119	G	C	U936	U849	A783
U1816	C1692	A1618	G1552	A1479	G1402	C1275	A1191	U1120	U	C	C937	G850	C784
U1818	G1693	A1619	G1553	A1479	G1403	U1278	U1192	U1121	C	C	U938	G851	G785
G1821	G1694	U1620	G1554	A1481	A1404	U1279	U1193	G1122	C	A	U939	U852	G786
G1822	C1697	G1621	A1556	U1489	U1411	A1280	U1194	G1123	C	U	U940	G853	G787
C1826	A1698	G1622	A1557	U1490	C1412	C1281	C1197	G1124	G	C	U941	A854	A788
A1827	A1698	U1623	C1558	U1490	A1413	A1282	A1198	U1129	U	C	U942	C855	G789
G1828	G1699	G1624	U1559	A1491	G1414	C1283	A1199	A1130	U	C	U944	U856	G791
C1829	U1700	G1625	U1560	A1492	C1415	U1291	G1200	U1131	A	A	U945	G792	G791
G1832	A1701	U1626	U1561	G1627	A1416	U1292	G1201	G1131	U	C	U946	A857	U793
C1833	G1702	G1627	A1562	A1496	C1417	A1287	U1287	G1132	G	C	U947	G866	U794
A1834	A1703	C1628	C1563	A1497	G	U1288	A1204	U1133	C	U	U948	A867	
U1835	A1704	A1629	A1564	G1500	U	A1289	U1206	G1137	C	C	U949	A870	U797
G1836	U1705	U1630	C1565	G1500	U	A1290	C1206	U1138	C	C	U950	A871	U
U1837	U1706	G1631	G1566	A1501	U	U1291	U1207	G1139	G	U	U951	A872	C
C1838	C1707	G1632	A1567	G1504	U	U1292	U1208	U1140	C	U	U952	C	C
U1839	A1708	C1633	U1568	U1504	U	G1293	A1213	G1141	C	U	U953	C	C
G1840	G1709	G1634	C1569	G1508	G	C1299	A1214	G1142	G	C	A954	A875	G
C1841	U1710	U1635	G1570	G1509	U	U	U1215	U1143	A	G	A955	G876	G
A1842	U1711	C1636	G1571	G1509	U	U	U1216	C1144	A	G	A956	U877	A
U1843	A1712	G1641	G1572	U1509	U	U	A1217	U1145	C	G	U957	U878	U
C1844	U1712	U1637	A1573	G1512	U	A	G1223	A1148	C	G	U958	A879	U
U1845	U1712	U1638	C1574	C1513	U	A	A1224	G1149	C	U	U959	U880	U
A1846	U1712	U1639	A1575	A1514	U	G	U1225	A1152	C	U	U960	U881	A
G1847	G1645	G1645	G1576	C1515	C	U	A1226	A1153	C	U	U961	U882	C
C1848	G1651	U1640	G1577	C1516	U	U	G1233	U1158	C	U	U962	G883	G
U1849	G1655	G1641	G1578	A1517	U	U	A1234	U1159	C	C	U963	A884	C
C1850	U1655	U1655	A1584	G1520	U	U	G1238	A1160	C	U	U964	C885	A
U1851	U1655	U1655	A1584	G1520	U	U	A1239	G1161	C	U	U965	U886	U
A1852	U1660	U1660	G1586	G1524	U	U	A1241	A1162	C	U	U966	U887	G
U1853	U1661	U1661	G1587	A1525	U	U	G1242	G1163	C	G	U967	G888	U
C1854	G1662	G1662	A1588	G1526	U	U	U1243	A1164	A	A	U968	A889	C
U1855	G1663	U1663	G1589	G1527	U	U	G1244	U1165	C	U	U969	A890	A
G1856	U1664	U1664	A1590	G1528	U	U	A1245	G1166	C	U	U970	A896	G
U1857	U1665	U1665	G1591	U1529	U	U	U1246	C1167	C	U	U971	G903	C
G1858	G1666	G1666	U1591	G1530	U	U	U1247	C1168	C	U	U972	G904	U
C1859	A1667	U1667	G1595	G1531	U	U	A1248	C1169	C	U	U973	A905	G
A1860	U1668	U1668	A1596	G1532	U	U	G1249	A1170	C	U	U974	U906	C
C1862	U1669	U1669	G1597	U1533	C	U	U1250	U1173	C	U	U975	A912	A
A1863	C1670	C1670	U1598	U1534	U	U	A1251	G1174	C	U	U976	G913	G
C1864	G1671	G1671	G1599	C1453	U	U	G1252	A1175	C	A	U977	A915	U
G1865	U1672	U1672	U1600	A1454	U	U	C1253	G1176	C	U	U978	G916	U
C1866	U1673	U1673	U1601	G1455	U	U	U1259	A1177	C	U	U979	C917	C
U1867	C1674	C1674	C1602	U1538	U	U	U1259	C1178	C	U	U980	A918	A
G1868	A1675	U1675	U1603	U1539	U	U	C1264	U1179	C	U	U981	G919	C
C1869	U1676	U1676	U1604	U1540	U	U	U1264	U1179	C	U	U982	C920	C
U1870	G1677	G1677	A1543	A1543	U	U	G1268	A1180	C	A	U983	A927	U
A1871	U1678	U1678	C1606	U1544	U	U	U1268	C1181	C	A	U984	A930	A
U1872	U1678	U1678	U1607	C1545	U	U	U1269	G1182	C	U	U985	C931	U
C1873	G1682	U1682	C1608	U1546	U	U	G1270	G1183	C	U	U986	C932	C
U1874	U1685	A1685	G1609	C1546	U	U	C	C1184	C	U	U987	U934	U
A1875	A1686	U1686	U1610	A1547	U	U	C1271	A1187	C	U	U988	U934	U
U1876	C1687	U1687	U1611	A1548	U	U	A1272	G1188	C	U	U989	U934	U
			U1612	C1549	U	U							





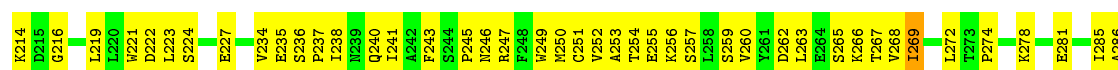
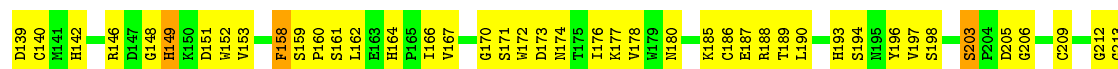
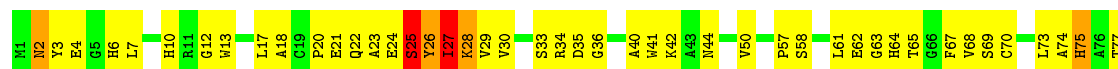
• Molecule 56: uS4

Chain 6: 52% 33% 14%



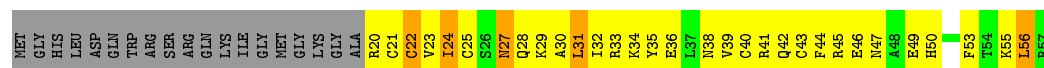
• Molecule 57: RACK1

Chain 7: 37% 59% 4%



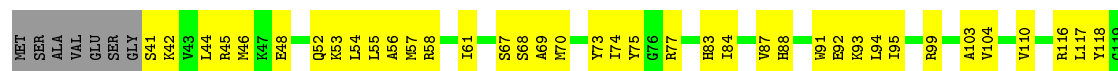
• Molecule 58: uS14

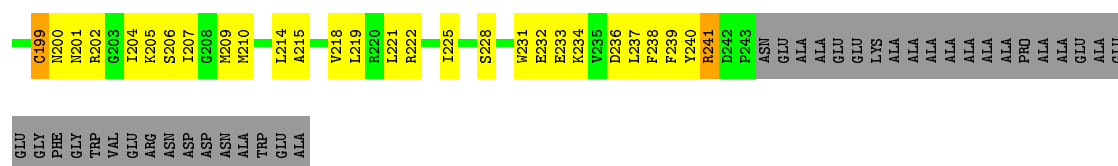
Chain 8: 12% 46% 9% 33%



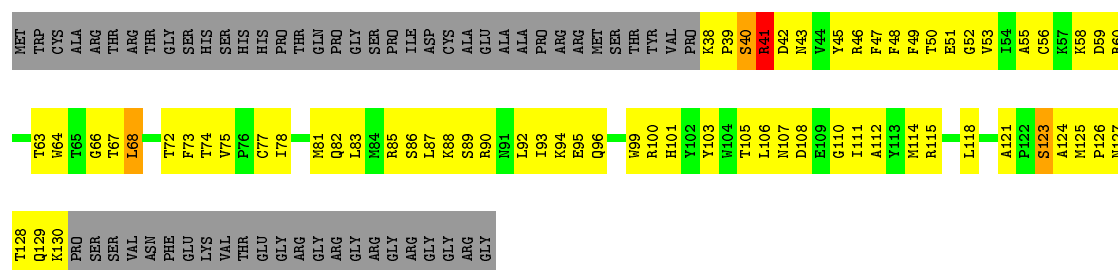
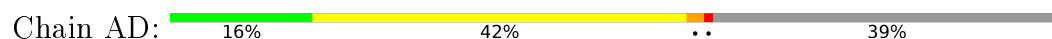
• Molecule 59: uS2

Chain AC: 40% 42% 17%

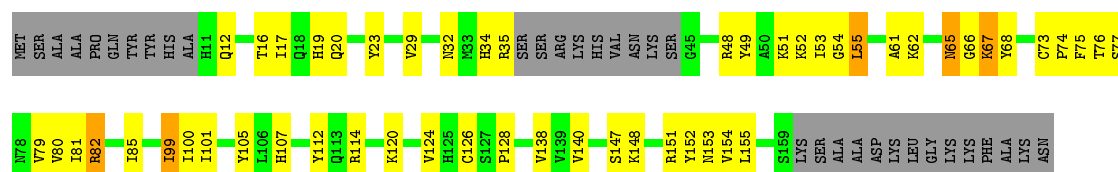




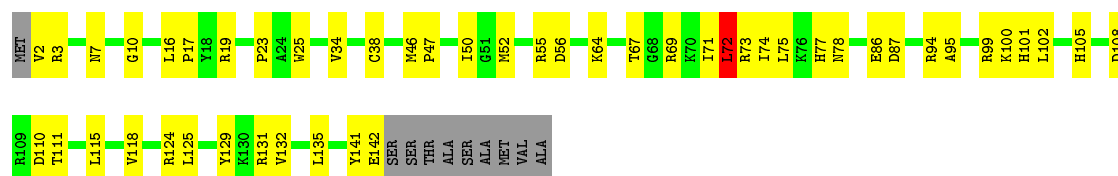
- Molecule 60: eS10



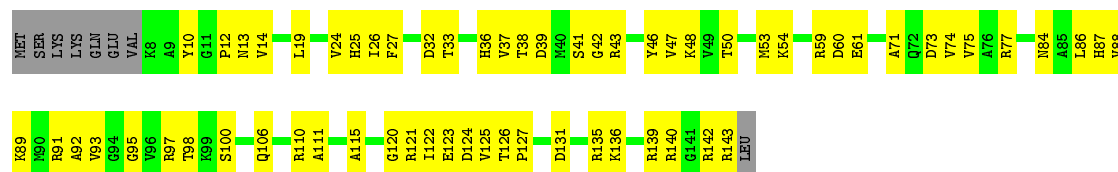
- Molecule 61: uS17



- Molecule 62: uS15

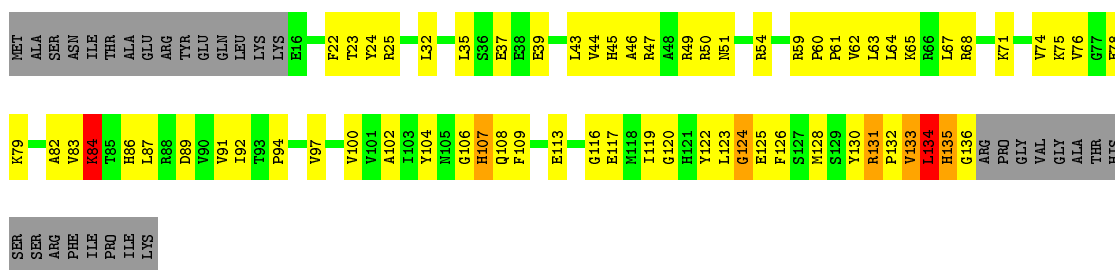


- Molecule 63: uS11



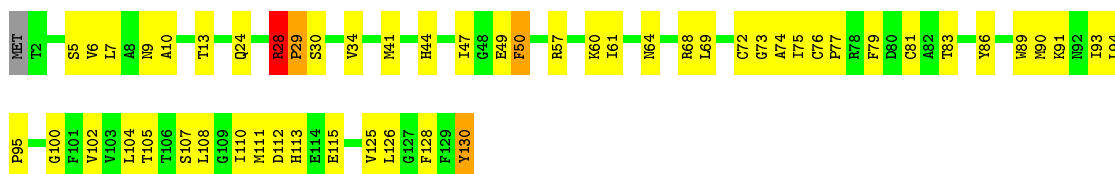
- Molecule 64: uS19





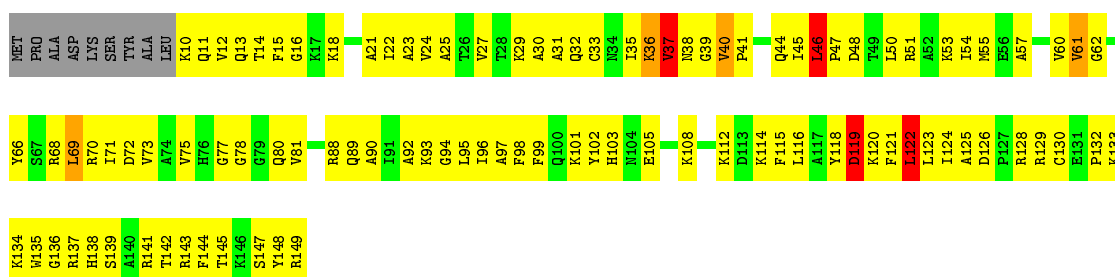
• Molecule 65: uS8

Chain AJ: 58% 38% ...



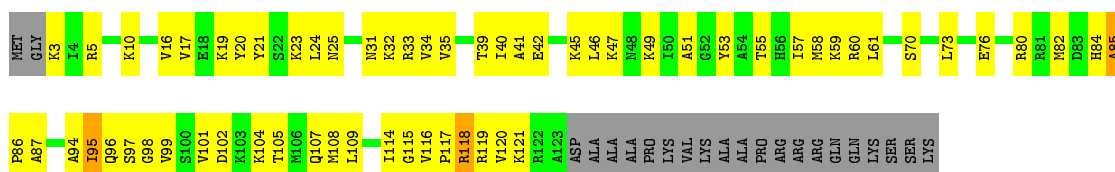
• Molecule 66: uS9

Chain AK: 27% 62% 6%



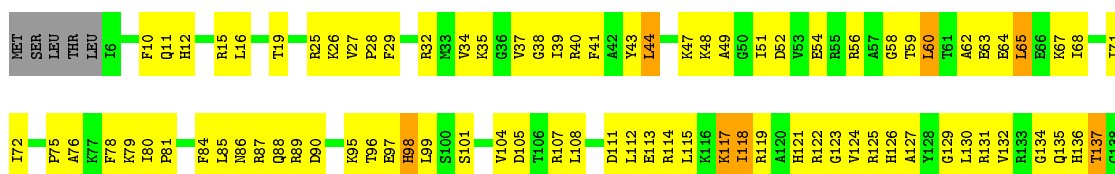
• Molecule 67: eS17

Chain AL: 41% 41% 15%



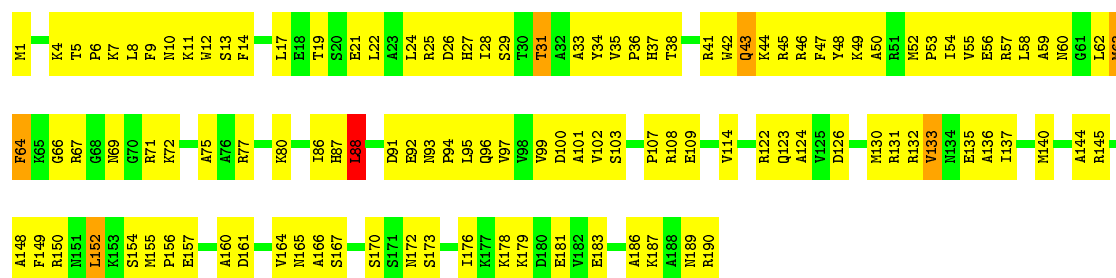
• Molecule 68: uS13

Chain AM: 31% 59% 6%



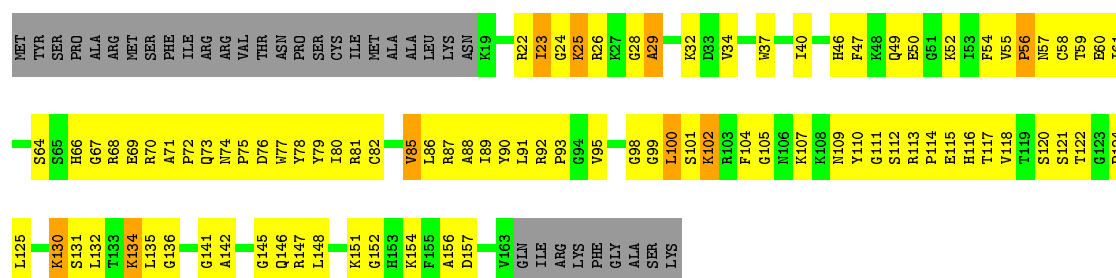
- Molecule 69: uS7

Chain AN:  38% 58%



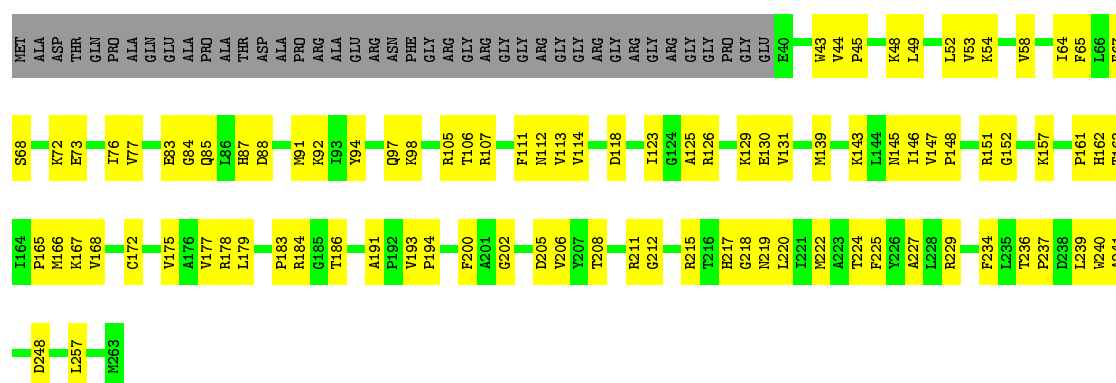
- Molecule 70: eS19

Chain AO: 



- Molecule 71: uS5

Chain AP: 



- Molecule 72: uS10

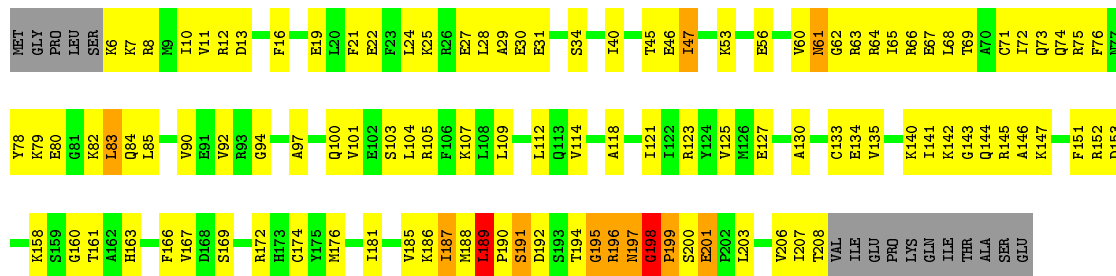
Chain AQ:  23% 65% 12%





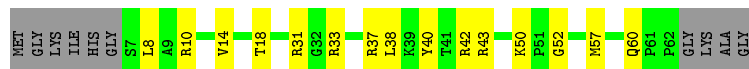
- Molecule 78: uS3

Chain AX:  42% 46% 5% • 7%



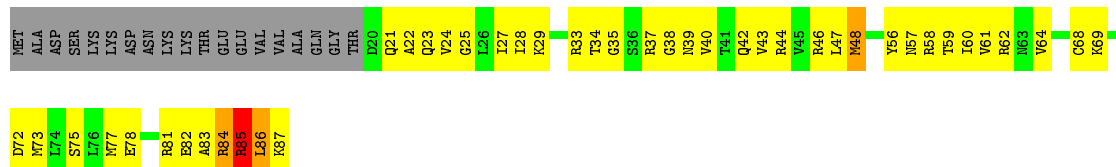
- Molecule 79: eS30

Chain AY:  62% 23% 15%



- Molecule 80: eS28

Chain AZ:  29% 45% • • 22%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	213108	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 ⓘ

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	1.03	0/38479	0.88	24/59984 (0.0%)
10	J	0.53	0/1737	0.62	0/2324
11	K	0.42	0/1362	0.56	0/1821
12	L	0.52	0/1463	0.60	2/1952 (0.1%)
13	M	0.59	0/1815	0.67	3/2436 (0.1%)
14	N	0.51	0/1355	0.66	3/1814 (0.2%)
15	O	0.65	2/1754 (0.1%)	0.71	5/2342 (0.2%)
16	P	0.61	0/1269	0.62	0/1700
17	Q	0.61	0/1490	0.60	0/2007
18	R	0.50	0/1665	0.54	0/2206
19	S	0.58	0/1290	0.71	2/1734 (0.1%)
2	B	1.05	0/25421	0.84	8/39614 (0.0%)
20	T	0.52	0/1013	0.61	1/1350 (0.1%)
21	U	0.64	0/1052	0.64	0/1417
22	V	0.50	0/978	0.58	0/1318
23	W	0.65	0/584	0.53	0/785
24	X	0.54	0/980	0.67	0/1308
25	Y	0.56	0/1100	0.57	0/1470
26	Z	0.57	0/1153	0.72	2/1541 (0.1%)
27	a	0.47	0/1157	0.65	2/1548 (0.1%)
28	b	0.41	0/565	0.62	1/754 (0.1%)
29	c	0.69	2/1961 (0.1%)	0.72	1/2630 (0.0%)
3	C	0.98	1/3855 (0.0%)	0.89	2/6002 (0.0%)
30	d	0.64	0/3250	0.69	4/4368 (0.1%)
31	e	0.57	0/730	0.77	3/988 (0.3%)
32	f	0.55	0/893	0.61	0/1196
33	g	0.57	0/1071	0.71	1/1432 (0.1%)
34	h	0.57	0/1030	0.62	0/1369
35	i	0.45	0/1067	0.59	1/1416 (0.1%)
36	j	0.63	0/1082	0.68	1/1454 (0.1%)
37	k	0.42	0/802	0.50	0/1073
38	l	0.64	1/688 (0.1%)	0.87	2/918 (0.2%)
39	m	0.63	0/724	0.66	0/964
4	D	0.93	0/2829	0.79	0/4405

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	n	0.54	0/614	0.58	1/818 (0.1%)
41	o	0.58	0/463	0.65	0/617
42	p	0.53	0/2874	0.67	3/3865 (0.1%)
43	q	0.61	0/431	0.66	1/572 (0.2%)
44	r	0.59	1/792 (0.1%)	0.69	2/1046 (0.2%)
45	s	0.49	0/2129	0.58	1/2846 (0.0%)
46	t	0.57	0/1074	0.78	5/1454 (0.3%)
47	u	0.57	0/1891	0.61	2/2531 (0.1%)
48	v	0.48	0/1878	0.57	0/2524
49	w	0.56	0/1504	0.64	0/2024
5	E	1.01	0/4004	0.83	1/6223 (0.0%)
50	0	0.70	0/1811	0.76	4/2438 (0.2%)
51	1	0.80	0/2076	0.78	1/2799 (0.0%)
52	2	1.66	86/43318 (0.2%)	1.27	315/67487 (0.5%)
53	3	0.66	1/2019 (0.0%)	0.77	3/2694 (0.1%)
54	4	0.76	0/1697	0.88	4/2276 (0.2%)
55	5	0.89	2/1494 (0.1%)	1.01	7/2000 (0.3%)
56	6	0.75	1/1389 (0.1%)	0.73	1/1866 (0.1%)
57	7	0.46	1/2454 (0.0%)	0.75	6/3337 (0.2%)
58	8	0.73	0/317	1.00	3/421 (0.7%)
59	AC	0.68	0/1656	0.69	0/2238
6	F	0.84	0/1686	0.86	1/2623 (0.0%)
60	AD	0.47	0/788	0.91	3/1064 (0.3%)
61	AE	0.98	0/1171	0.75	1/1570 (0.1%)
62	AG	0.83	0/1180	0.80	1/1581 (0.1%)
63	AH	0.78	0/1038	0.80	1/1392 (0.1%)
64	AI	1.11	1/1006 (0.1%)	0.94	8/1351 (0.6%)
65	AJ	0.94	2/1037 (0.2%)	0.89	1/1391 (0.1%)
66	AK	0.54	0/1128	0.82	3/1515 (0.2%)
67	AL	0.52	0/993	0.69	0/1322
68	AM	0.50	0/1206	0.88	2/1615 (0.1%)
69	AN	0.48	0/1516	0.75	2/2034 (0.1%)
7	G	1.11	0/4373	0.88	8/6817 (0.1%)
70	AO	0.51	0/1180	0.78	1/1585 (0.1%)
71	AP	0.80	0/1758	0.76	0/2380
72	AQ	0.51	0/817	0.75	0/1107
73	AR	0.67	0/639	0.72	0/866
74	AS	0.81	0/1134	0.89	3/1517 (0.2%)
75	AT	0.68	0/1054	0.70	0/1405
76	AV	0.69	0/845	0.76	0/1130
77	AW	1.25	2/658 (0.3%)	0.80	1/883 (0.1%)
78	AX	0.56	0/1616	0.83	6/2159 (0.3%)
79	AY	0.54	0/460	0.73	0/611

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
8	H	1.15	0/2230	0.88	2/3470 (0.1%)
80	AZ	0.60	1/528 (0.2%)	0.83	1/705 (0.1%)
9	I	0.60	1/1564 (0.1%)	0.75	2/2092 (0.1%)
All	All	1.06	105/215154 (0.0%)	0.92	475/315901 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
13	M	0	2
16	P	0	2
20	T	0	1
23	W	0	1
24	X	0	1
28	b	0	1
29	c	0	1
31	e	0	1
37	k	0	1
38	l	0	3
39	m	0	1
47	u	0	1
50	0	0	1
53	3	0	1
54	4	0	1
55	5	0	2
57	7	0	1
58	8	0	1
59	AC	0	3
61	AE	0	1
62	AG	0	3
64	AI	0	3
66	AK	0	1
67	AL	0	1
68	AM	0	7
69	AN	0	4
70	AO	0	6
72	AQ	0	1
75	AT	0	2
77	AW	0	1
78	AX	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	I	0	1
All	All	0	58

The worst 5 of 105 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	2	1864	C	N3-C4	80.83	1.90	1.33
52	2	1864	C	C2-N3	72.70	1.94	1.35
52	2	1864	C	N1-C6	69.47	1.78	1.37
52	2	1864	C	N1-C2	48.39	1.88	1.40
52	2	1864	C	C4-C5	48.22	1.81	1.43

The worst 5 of 475 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	2	971	U	O5'-P-OP2	-31.09	73.39	110.70
52	2	1954	U	P-O3'-C3'	28.04	153.35	119.70
52	2	1818	U	O5'-P-OP2	-26.60	78.78	110.70
52	2	1818	U	O5'-P-OP1	-22.31	83.92	110.70
52	2	971	U	O5'-P-OP1	-21.05	85.44	110.70

There are no chirality outliers.

5 of 58 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	I	180	THR	Peptide
13	M	132	ARG	Peptide
13	M	163	HIS	Peptide
16	P	36	ILE	Peptide
16	P	64	ASN	Peptide

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	34365	0	17292	454	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	22723	0	11462	217	0
3	C	3449	0	1745	81	0
4	D	2531	0	1283	26	0
5	E	3589	0	1818	22	0
6	F	1508	0	768	45	0
7	G	3911	0	1975	29	0
8	H	1996	0	1013	18	0
9	I	1539	0	1648	108	0
10	J	1704	0	1776	51	0
11	K	1339	0	1369	71	0
12	L	1435	0	1525	97	0
13	M	1780	0	1894	83	0
14	N	1336	0	1409	76	0
15	O	1714	0	1792	106	0
16	P	1245	0	1289	38	0
17	Q	1456	0	1498	57	0
18	R	1646	0	1749	85	0
19	S	1261	0	1317	53	0
20	T	997	0	1051	29	0
21	U	1035	0	1092	55	0
22	V	963	0	1032	26	0
23	W	563	0	577	10	0
24	X	965	0	1033	69	0
25	Y	1079	0	1148	28	0
26	Z	1126	0	1153	80	0
27	a	1140	0	1186	0	0
28	b	554	0	581	0	0
29	c	1921	0	1978	0	0
30	d	3183	0	3308	0	0
31	e	720	0	734	0	0
32	f	878	0	951	0	0
33	g	1050	0	1115	0	0
34	h	1014	0	1078	0	0
35	i	1056	0	1156	0	0
36	j	1060	0	1108	0	0
37	k	787	0	846	0	0
38	l	674	0	689	0	0
39	m	712	0	746	0	0
40	n	605	0	663	0	0
41	o	450	0	483	0	0
42	p	2825	0	2941	0	0
43	q	425	0	463	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	r	779	0	839	0	0
45	s	2094	0	2198	0	0
46	t	1054	0	1098	0	0
47	u	1857	0	1952	0	0
48	v	1850	0	1972	0	0
49	w	1484	0	1568	0	0
50	0	1786	0	1868	131	0
51	1	2037	0	2124	102	0
52	2	38724	0	19533	1772	0
53	3	1994	0	2134	103	0
54	4	1667	0	1782	111	0
55	5	1473	0	1559	131	0
56	6	1362	0	1416	74	0
57	7	2394	0	2312	226	0
58	8	314	0	323	75	0
59	AC	1622	0	1663	106	0
60	AD	767	0	758	105	0
61	AE	1148	0	1194	60	0
62	AG	1157	0	1230	46	0
63	AH	1023	0	1054	62	0
64	AI	984	0	1011	195	0
65	AJ	1020	0	1050	44	0
66	AK	1108	0	1167	178	0
67	AL	983	0	1054	87	0
68	AM	1186	0	1241	252	0
69	AN	1493	0	1538	159	0
70	AO	1150	0	1173	141	0
71	AP	1722	0	1768	81	0
72	AQ	807	0	851	106	0
73	AR	630	0	620	30	0
74	AS	1114	0	1170	77	0
75	AT	1033	0	1095	54	0
76	AV	828	0	874	49	0
77	AW	646	0	656	25	0
78	AX	1595	0	1662	171	0
79	AY	452	0	505	19	0
80	AZ	526	0	548	63	0
All	All	200172	0	148294	5673	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 20.

The worst 5 of 5673 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)
52:2:1864:C:C5	52:2:1864:C:C4	1.81	1.66
74:AS:27:TRP:CE3	74:AS:30:ALA:HB3	1.21	1.65
52:2:1863:A:H4'	64:AI:134:LEU:CD2	1.20	1.61
69:AN:62:LEU:HD22	69:AN:75:ALA:CB	1.23	1.60
52:2:1864:C:C2	64:AI:135:HIS:CG	1.90	1.57

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	
9	I	195/198 (98%)	180 (92%)	12 (6%)	3 (2%)	13	42
10	J	209/213 (98%)	193 (92%)	13 (6%)	3 (1%)	14	44
11	K	165/188 (88%)	152 (92%)	12 (7%)	1 (1%)	30	67
12	L	175/220 (80%)	159 (91%)	14 (8%)	2 (1%)	17	51
13	M	219/222 (99%)	212 (97%)	6 (3%)	1 (0%)	34	71
14	N	166/175 (95%)	153 (92%)	12 (7%)	1 (1%)	30	67
15	O	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
16	P	153/166 (92%)	145 (95%)	7 (5%)	1 (1%)	26	63
17	Q	176/179 (98%)	163 (93%)	11 (6%)	2 (1%)	17	51
18	R	194/245 (79%)	193 (100%)	1 (0%)	0	100	100
19	S	156/159 (98%)	144 (92%)	11 (7%)	1 (1%)	30	67
20	T	121/129 (94%)	116 (96%)	5 (4%)	0	100	100
21	U	135/139 (97%)	126 (93%)	9 (7%)	0	100	100
22	V	118/145 (81%)	106 (90%)	11 (9%)	1 (1%)	24	60
23	W	63/124 (51%)	61 (97%)	2 (3%)	0	100	100
24	X	118/143 (82%)	111 (94%)	5 (4%)	2 (2%)	11	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	Y	131/134 (98%)	124 (95%)	6 (5%)	1 (1%)	24	60
26	Z	142/145 (98%)	125 (88%)	14 (10%)	3 (2%)	9	32
27	a	144/147 (98%)	134 (93%)	9 (6%)	1 (1%)	26	63
28	b	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
29	c	251/260 (96%)	229 (91%)	20 (8%)	2 (1%)	24	60
30	d	397/419 (95%)	376 (95%)	20 (5%)	1 (0%)	46	79
31	e	92/104 (88%)	88 (96%)	4 (4%)	0	100	100
32	f	108/183 (59%)	102 (94%)	6 (6%)	0	100	100
33	g	127/133 (96%)	119 (94%)	8 (6%)	0	100	100
34	h	122/168 (73%)	117 (96%)	4 (3%)	1 (1%)	24	60
35	i	124/127 (98%)	117 (94%)	6 (5%)	1 (1%)	24	60
36	j	130/144 (90%)	119 (92%)	11 (8%)	0	100	100
37	k	97/105 (92%)	94 (97%)	3 (3%)	0	100	100
38	l	79/83 (95%)	72 (91%)	7 (9%)	0	100	100
39	m	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
40	n	73/83 (88%)	70 (96%)	3 (4%)	0	100	100
41	o	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
42	p	362/373 (97%)	340 (94%)	20 (6%)	2 (1%)	30	67
43	q	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
44	r	94/106 (89%)	85 (90%)	8 (8%)	1 (1%)	17	51
45	s	258/305 (85%)	246 (95%)	12 (5%)	0	100	100
46	t	133/195 (68%)	123 (92%)	8 (6%)	2 (2%)	13	42
47	u	226/252 (90%)	209 (92%)	16 (7%)	1 (0%)	39	74
48	v	228/348 (66%)	218 (96%)	10 (4%)	0	100	100
49	w	185/190 (97%)	173 (94%)	11 (6%)	1 (0%)	34	71
50	0	219/264 (83%)	208 (95%)	10 (5%)	1 (0%)	34	71
51	1	256/273 (94%)	231 (90%)	22 (9%)	3 (1%)	16	48
53	3	247/249 (99%)	236 (96%)	10 (4%)	1 (0%)	39	74
54	4	198/200 (99%)	183 (92%)	11 (6%)	4 (2%)	9	33
55	5	178/220 (81%)	160 (90%)	16 (9%)	2 (1%)	17	51
56	6	162/190 (85%)	151 (93%)	9 (6%)	2 (1%)	16	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	7	306/312 (98%)	275 (90%)	28 (9%)	3 (1%)	19	54
58	8	36/57 (63%)	30 (83%)	5 (14%)	1 (3%)	6	24
59	AC	201/246 (82%)	193 (96%)	8 (4%)	0	100	100
60	AD	91/153 (60%)	78 (86%)	11 (12%)	2 (2%)	8	31
61	AE	136/173 (79%)	131 (96%)	4 (3%)	1 (1%)	26	63
62	AG	139/151 (92%)	133 (96%)	6 (4%)	0	100	100
63	AH	134/144 (93%)	126 (94%)	8 (6%)	0	100	100
64	AI	119/152 (78%)	102 (86%)	17 (14%)	0	100	100
65	AJ	127/130 (98%)	120 (94%)	6 (5%)	1 (1%)	24	60
66	AK	138/149 (93%)	118 (86%)	16 (12%)	4 (3%)	6	23
67	AL	119/143 (83%)	108 (91%)	8 (7%)	3 (2%)	7	27
68	AM	146/153 (95%)	125 (86%)	21 (14%)	0	100	100
69	AN	188/190 (99%)	165 (88%)	21 (11%)	2 (1%)	17	51
70	AO	143/179 (80%)	114 (80%)	25 (18%)	4 (3%)	6	24
71	AP	222/265 (84%)	216 (97%)	6 (3%)	0	100	100
72	AQ	100/116 (86%)	86 (86%)	13 (13%)	1 (1%)	19	54
73	AR	81/164 (49%)	78 (96%)	3 (4%)	0	100	100
74	AS	140/143 (98%)	132 (94%)	5 (4%)	3 (2%)	9	32
75	AT	124/137 (90%)	117 (94%)	6 (5%)	1 (1%)	24	60
76	AV	102/112 (91%)	90 (88%)	8 (8%)	4 (4%)	4	15
77	AW	80/86 (93%)	76 (95%)	4 (5%)	0	100	100
78	AX	201/219 (92%)	179 (89%)	17 (8%)	5 (2%)	7	27
79	AY	54/66 (82%)	48 (89%)	6 (11%)	0	100	100
80	AZ	66/87 (76%)	60 (91%)	4 (6%)	2 (3%)	5	22
All	All	10774/12317 (88%)	9993 (93%)	696 (6%)	85 (1%)	29	60

5 of 85 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	J	142	GLU
10	J	145	VAL
12	L	21	SER
24	X	59	ALA
26	Z	114	HIS

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	
9	I	163/164 (99%)	158 (97%)	5 (3%)	47	82
10	J	178/179 (99%)	175 (98%)	3 (2%)	68	91
11	K	145/163 (89%)	144 (99%)	1 (1%)	88	97
12	L	152/182 (84%)	151 (99%)	1 (1%)	88	97
13	M	188/189 (100%)	187 (100%)	1 (0%)	92	98
14	N	139/144 (96%)	136 (98%)	3 (2%)	60	88
15	O	179/180 (99%)	178 (99%)	1 (1%)	90	97
16	P	133/144 (92%)	133 (100%)	0	100	100
17	Q	156/158 (99%)	156 (100%)	0	100	100
18	R	168/196 (86%)	166 (99%)	2 (1%)	78	94
19	S	132/133 (99%)	131 (99%)	1 (1%)	86	96
20	T	107/114 (94%)	107 (100%)	0	100	100
21	U	110/111 (99%)	110 (100%)	0	100	100
22	V	103/123 (84%)	103 (100%)	0	100	100
23	W	60/104 (58%)	59 (98%)	1 (2%)	68	91
24	X	103/121 (85%)	103 (100%)	0	100	100
25	Y	114/115 (99%)	113 (99%)	1 (1%)	84	96
26	Z	114/115 (99%)	114 (100%)	0	100	100
27	a	118/119 (99%)	116 (98%)	2 (2%)	68	91
28	b	57/58 (98%)	57 (100%)	0	100	100
29	c	198/204 (97%)	193 (98%)	5 (2%)	55	85
30	d	337/351 (96%)	336 (100%)	1 (0%)	94	99
31	e	82/90 (91%)	77 (94%)	5 (6%)	23	56
32	f	97/156 (62%)	97 (100%)	0	100	100
33	g	113/117 (97%)	111 (98%)	2 (2%)	66	90
34	h	107/145 (74%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	i	116/117 (99%)	116 (100%)	0	100	100
36	j	109/121 (90%)	107 (98%)	2 (2%)	66	90
37	k	81/87 (93%)	81 (100%)	0	100	100
38	l	69/70 (99%)	69 (100%)	0	100	100
39	m	73/74 (99%)	73 (100%)	0	100	100
40	n	68/74 (92%)	68 (100%)	0	100	100
41	o	46/47 (98%)	46 (100%)	0	100	100
42	p	295/302 (98%)	293 (99%)	2 (1%)	88	97
43	q	46/113 (41%)	46 (100%)	0	100	100
44	r	83/92 (90%)	80 (96%)	3 (4%)	42	78
45	s	209/242 (86%)	208 (100%)	1 (0%)	92	98
46	t	111/152 (73%)	110 (99%)	1 (1%)	84	96
47	u	190/209 (91%)	187 (98%)	3 (2%)	70	91
48	v	196/292 (67%)	196 (100%)	0	100	100
49	w	169/172 (98%)	168 (99%)	1 (1%)	90	97
50	0	194/222 (87%)	189 (97%)	5 (3%)	54	85
51	1	215/225 (96%)	212 (99%)	3 (1%)	74	93
53	3	208/208 (100%)	206 (99%)	2 (1%)	82	95
54	4	186/186 (100%)	185 (100%)	1 (0%)	92	98
55	5	149/176 (85%)	147 (99%)	2 (1%)	76	94
56	6	147/164 (90%)	145 (99%)	2 (1%)	74	93
57	7	263/266 (99%)	259 (98%)	4 (2%)	72	92
58	8	35/49 (71%)	35 (100%)	0	100	100
59	AC	177/202 (88%)	177 (100%)	0	100	100
60	AD	82/129 (64%)	81 (99%)	1 (1%)	78	94
61	AE	124/150 (83%)	122 (98%)	2 (2%)	70	91
62	AG	125/132 (95%)	125 (100%)	0	100	100
63	AH	105/113 (93%)	105 (100%)	0	100	100
64	AI	104/130 (80%)	102 (98%)	2 (2%)	65	89
65	AJ	110/111 (99%)	105 (96%)	5 (4%)	34	70
66	AK	113/120 (94%)	108 (96%)	5 (4%)	35	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	AL	107/123 (87%)	107 (100%)	0	100	100
68	AM	125/130 (96%)	121 (97%)	4 (3%)	46	81
69	AN	159/159 (100%)	158 (99%)	1 (1%)	90	97
70	AO	118/147 (80%)	118 (100%)	0	100	100
71	AP	184/209 (88%)	184 (100%)	0	100	100
72	AQ	94/104 (90%)	94 (100%)	0	100	100
73	AR	68/119 (57%)	68 (100%)	0	100	100
74	AS	115/116 (99%)	110 (96%)	5 (4%)	35	71
75	AT	111/120 (92%)	111 (100%)	0	100	100
76	AV	87/93 (94%)	86 (99%)	1 (1%)	80	95
77	AW	72/75 (96%)	71 (99%)	1 (1%)	74	93
78	AX	171/185 (92%)	167 (98%)	4 (2%)	58	87
79	AY	49/54 (91%)	49 (100%)	0	100	100
80	AZ	57/74 (77%)	54 (95%)	3 (5%)	28	63
All	All	9268/10330 (90%)	9167 (99%)	101 (1%)	81	95

5 of 101 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	u	224	MET
53	3	44	SER
77	AW	81	ARG
49	w	137	SER
50	0	134	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 137 such sidechains are listed below:

Mol	Chain	Res	Type
49	w	77	GLN
54	4	178	GLN
74	AS	77	ASN
50	0	102	GLN
51	1	142	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1591/1781 (89%)	282 (17%)	1 (0%)
2	B	1058/1465 (72%)	162 (15%)	7 (0%)
3	C	160/262 (61%)	24 (15%)	1 (0%)
4	D	118/120 (98%)	10 (8%)	0
5	E	163/213 (76%)	20 (12%)	0
52	2	1801/2205 (81%)	656 (36%)	162 (8%)
6	F	70/73 (95%)	16 (22%)	1 (1%)
7	G	182/183 (99%)	18 (9%)	1 (0%)
8	H	89/127 (70%)	13 (14%)	0
All	All	5232/6429 (81%)	1201 (22%)	173 (3%)

5 of 1201 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	G
1	A	20	G
1	A	24	A
1	A	28	G
1	A	38	A

5 of 173 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	2	885	C
52	2	1106	U
52	2	2000	G
52	2	887	U
52	2	935	U

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
77	AW	2
52	2	2
38	l	1
29	c	1
15	O	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	1972:U	O3'	1973:U	P	6.52
1	2	1954:U	O3'	1955:G	P	2.07
1	AW	79:GLY	C	80:TYR	N	1.68
1	l	66:TYR	C	67:LEU	N	1.18
1	O	50:MET	C	51:LEU	N	1.15