



## wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Feb 18, 2018 – 02:31 am GMT

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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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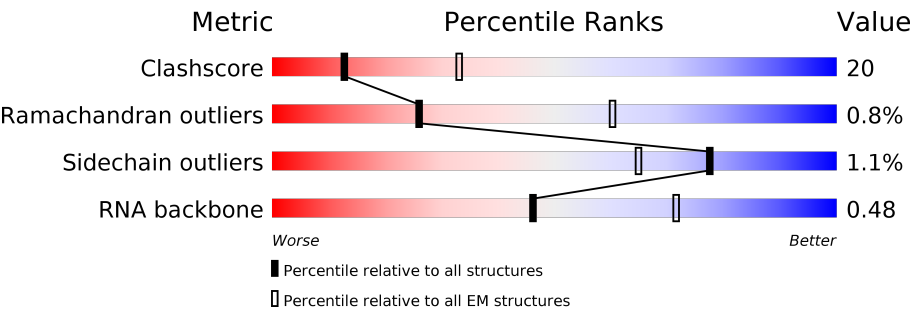
MolProbity : 4.02b-467  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30686

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 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	136279	1886
Ramachandran outliers	132675	1663
Sidechain outliers	132484	1531
RNA backbone	3744	458

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  $\geq 3$ , 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%


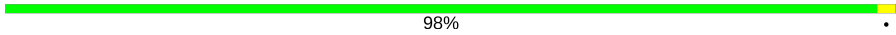

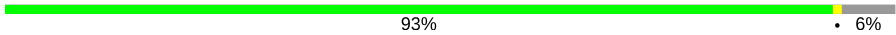
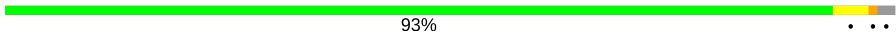
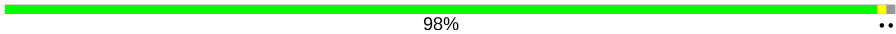

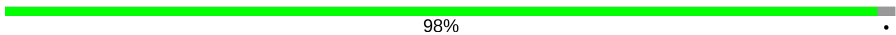
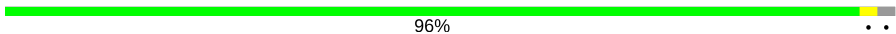






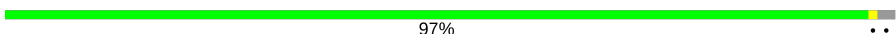









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Mol	Chain	Length	Quality of chain
9	I	198	
10	J	213	
11	K	188	
12	L	220	
13	M	222	
14	N	175	
15	O	204	
16	P	166	
17	Q	179	
18	R	245	
19	S	159	
20	T	129	
21	U	139	
22	V	145	
23	W	124	
24	X	143	
25	Y	134	
26	Z	145	
27	a	147	
28	b	70	
29	c	260	
30	d	419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






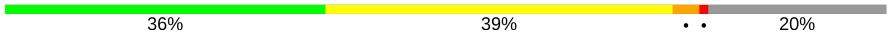

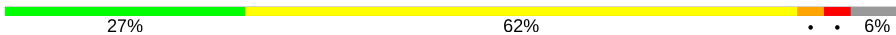
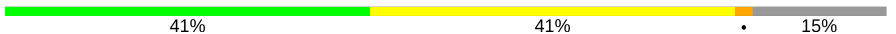
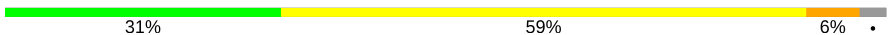
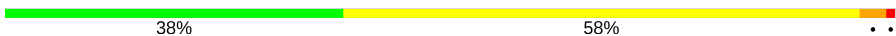
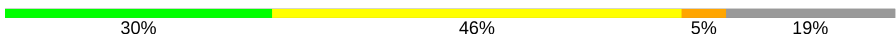









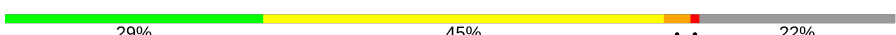
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Mol	Chain	Length	Quality of chain
34	h	168	
35	i	127	
36	j	144	
37	k	105	
38	l	83	
39	m	92	
40	n	83	
41	o	51	
42	p	373	
43	q	128	
44	r	106	
45	s	305	
46	t	195	
47	u	252	
48	v	348	
49	w	190	
50	0	264	
51	1	273	
52	2	2205	
53	3	249	
54	4	200	
55	5	220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

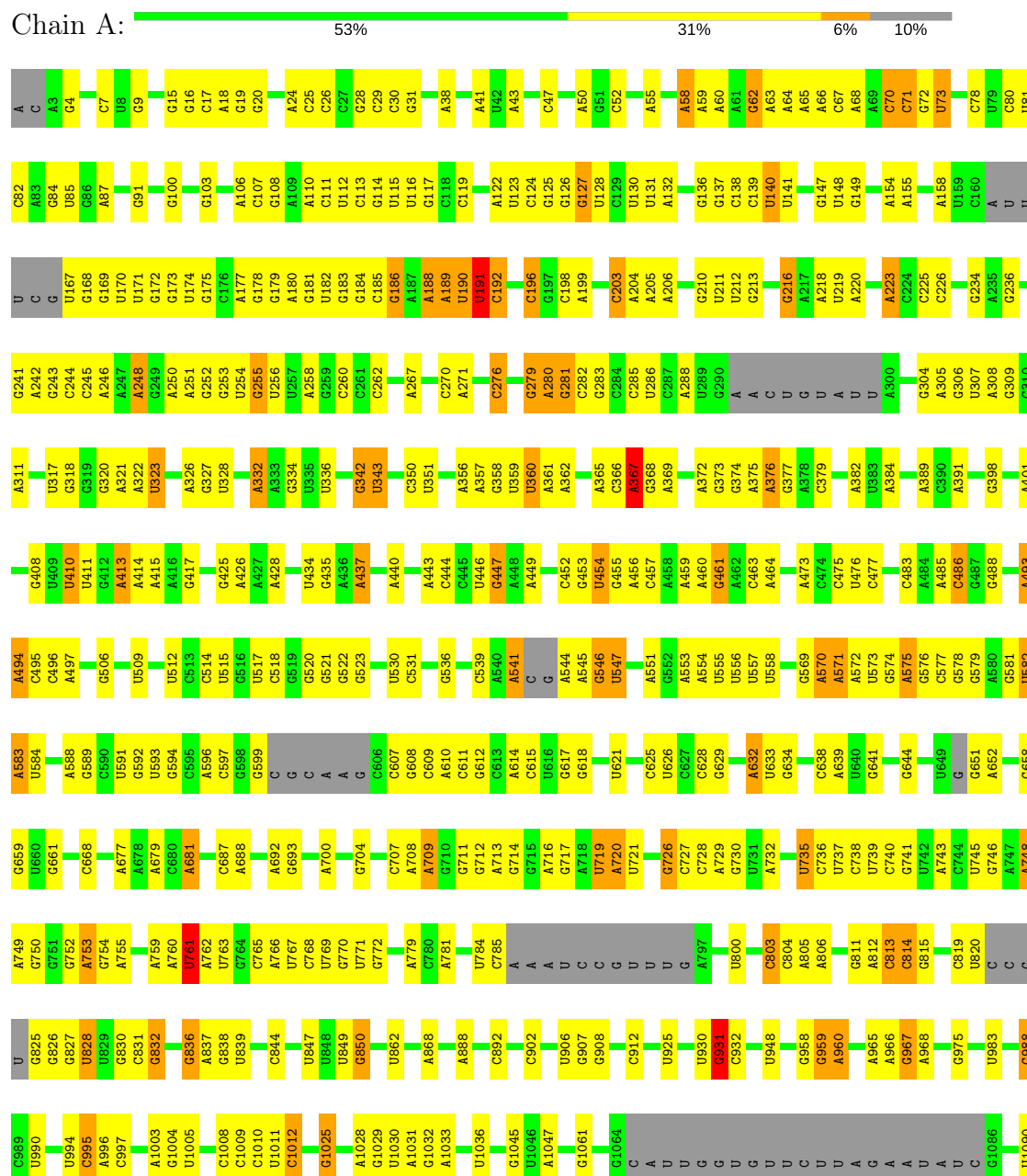
- Molecule 80 is a protein called eS28.

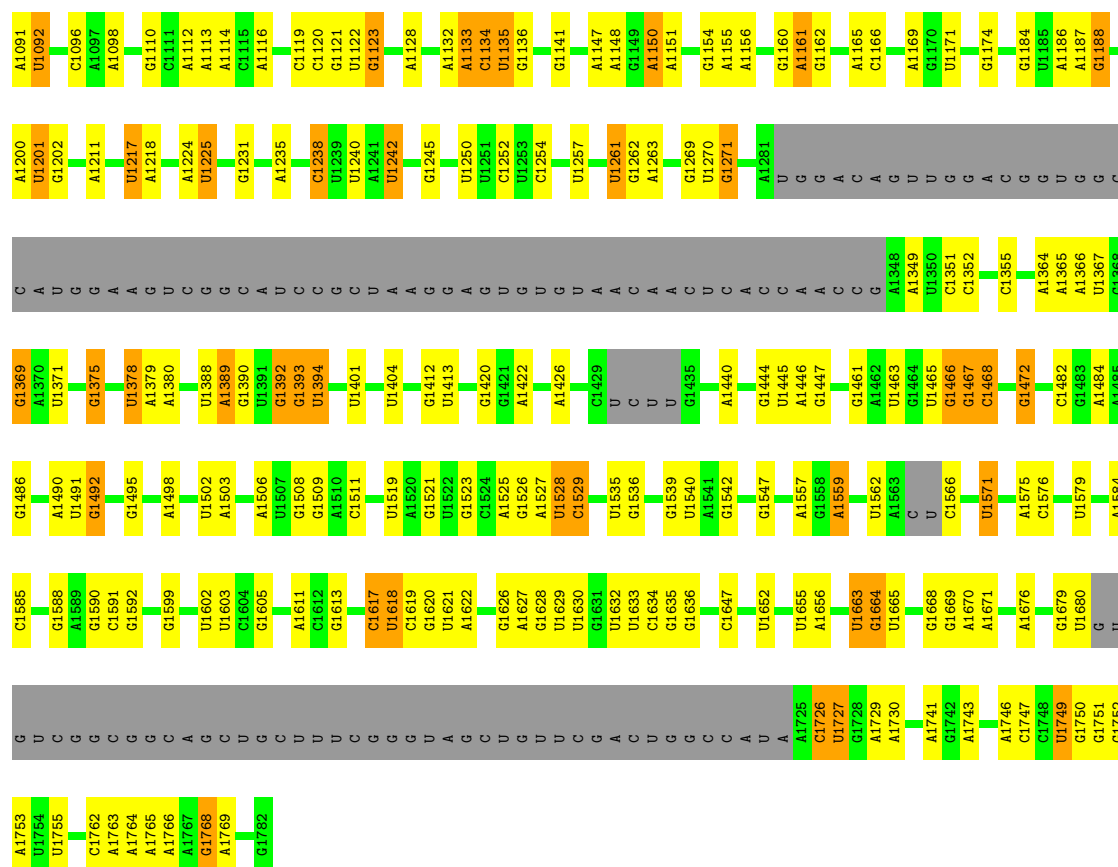
Mol	Chain	Residues	Atoms					AltConf	Trace
80	AZ	68	Total	C	N	O	S	0	0
			526	319	106	97	4		

### 3 Residue-property plots

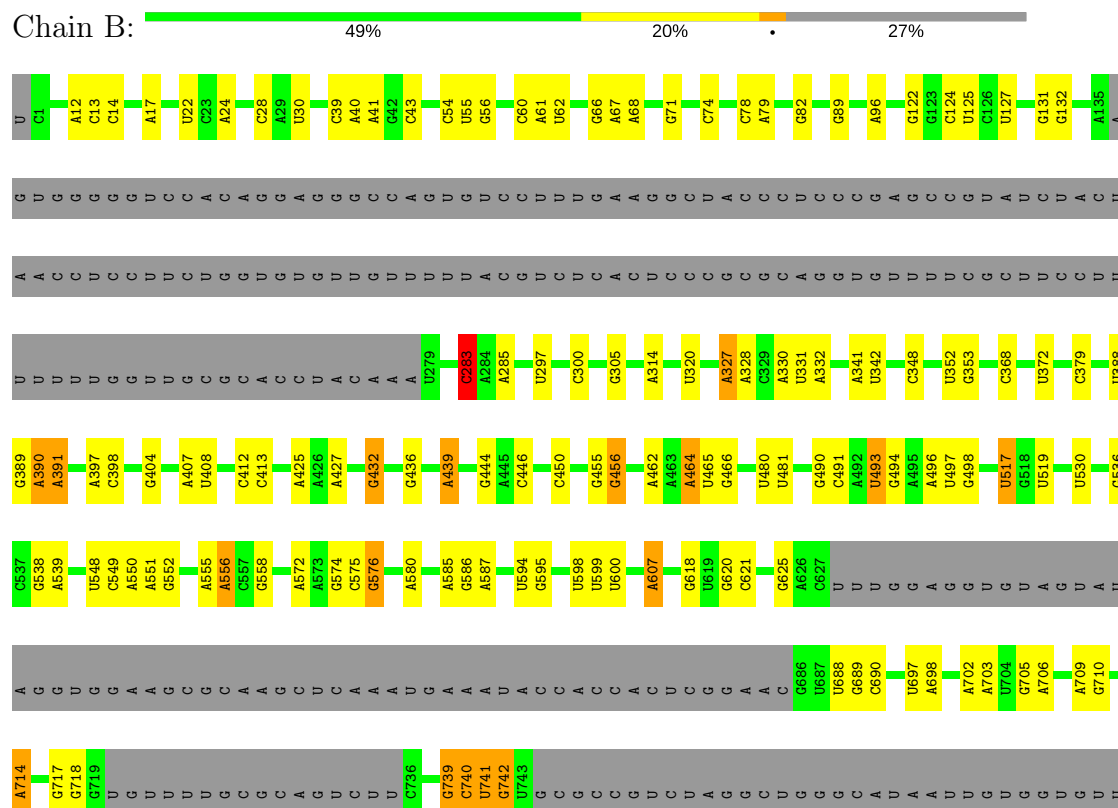
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according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

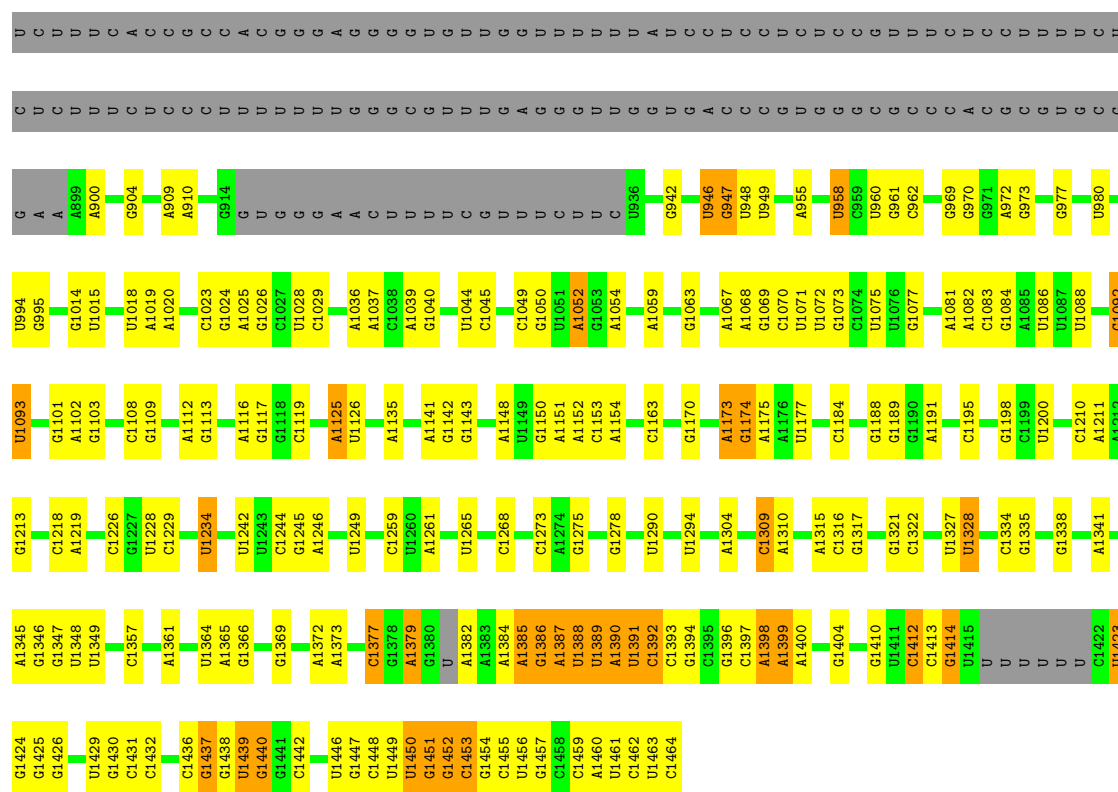
#### • Molecule 1: LSU-alpha





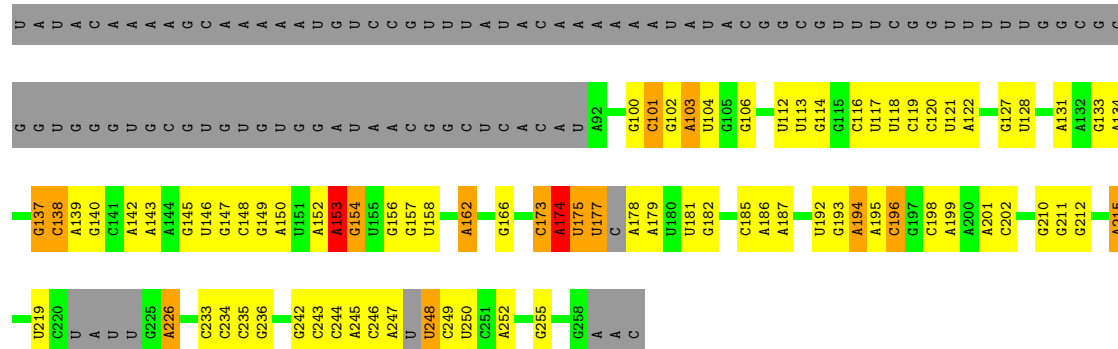
- Molecule 2: LSU-beta





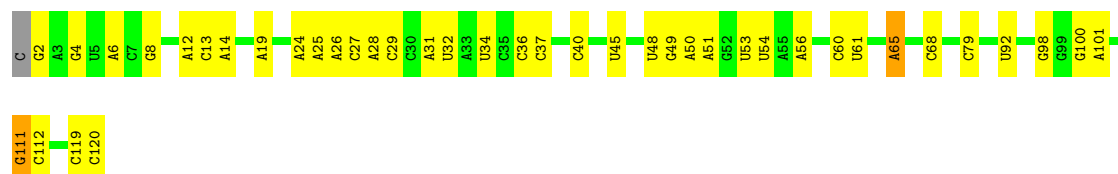
- Molecule 3: 5.8S rRNA

Chain C:



- Molecule 4: 5S rRNA

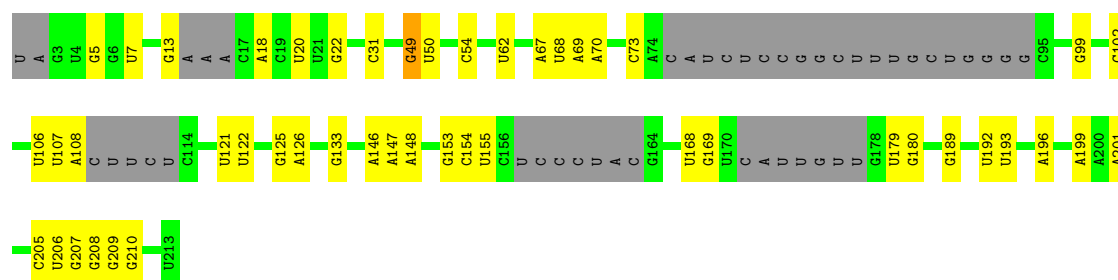
Chain D:



- Molecule 5: srRNA1

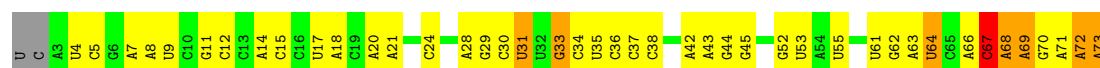
Chain E:





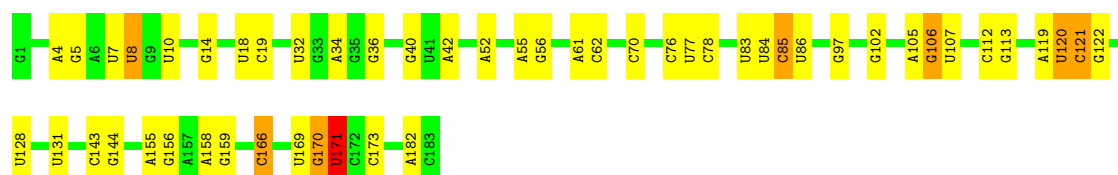
• Molecule 6: srRNA3

Chain F: 38% 48% 10% ..



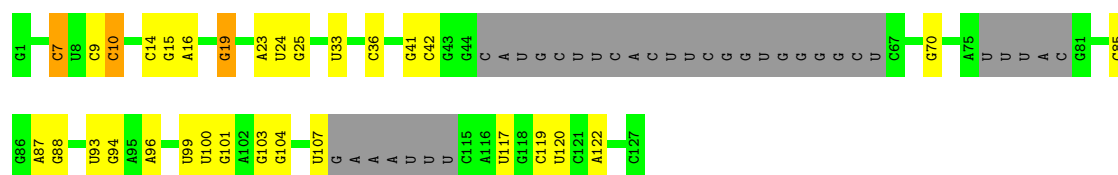
• Molecule 7: srRNA2

Chain G: 72% 23% ..



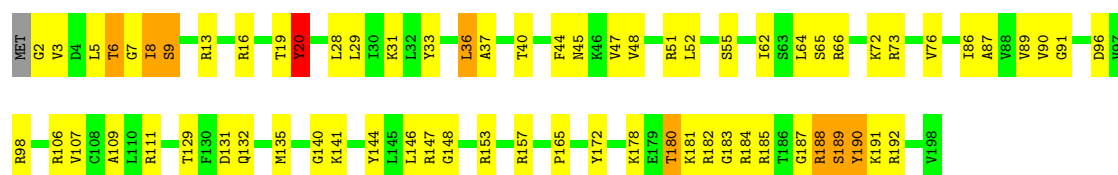
• Molecule 8: srRNA4

Chain H: 49% 22% 27% .



• Molecule 9: eL18

Chain I: 64% 31% ..



• Molecule 10: uL16

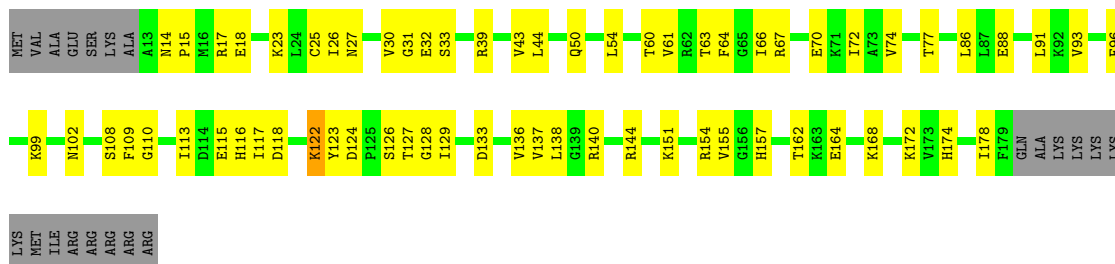
Chain J: 70% 27% ..





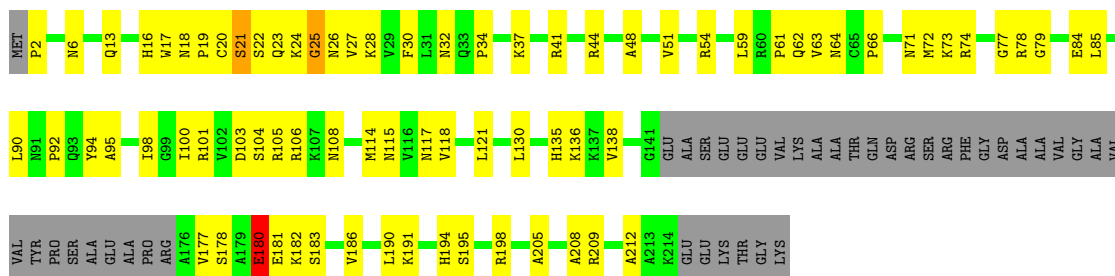
- Molecule 11: uL5

Chain K:  54% 34% 11%



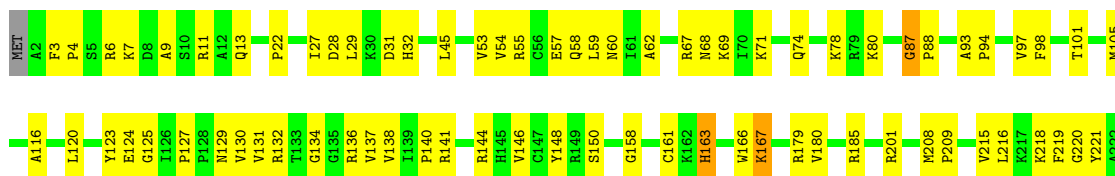
- Molecule 12: eL13

Chain L:  46% 34% • 19%



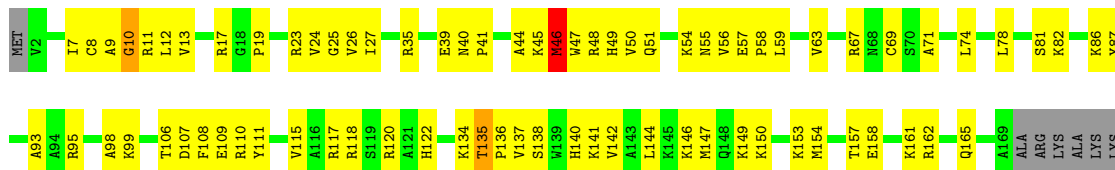
- Molecule 13: uL13

Chain M:  66% 32%



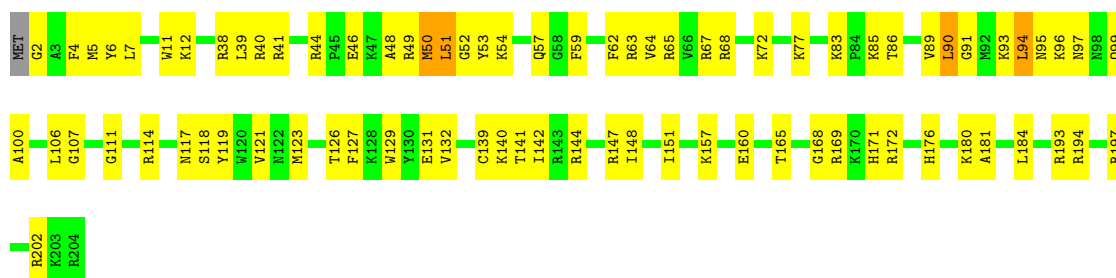
- Molecule 14: eL14

Chain N:  52% 42% ...

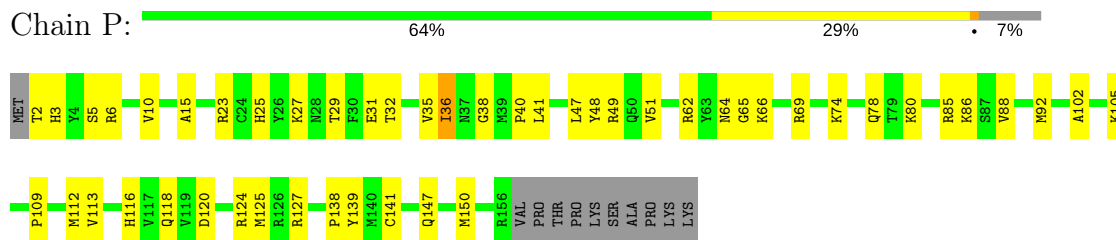


- Molecule 15: eL15

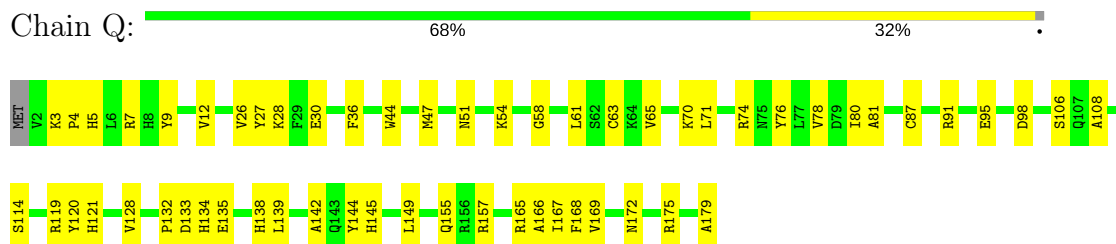
Chain 0:  60% 37% .



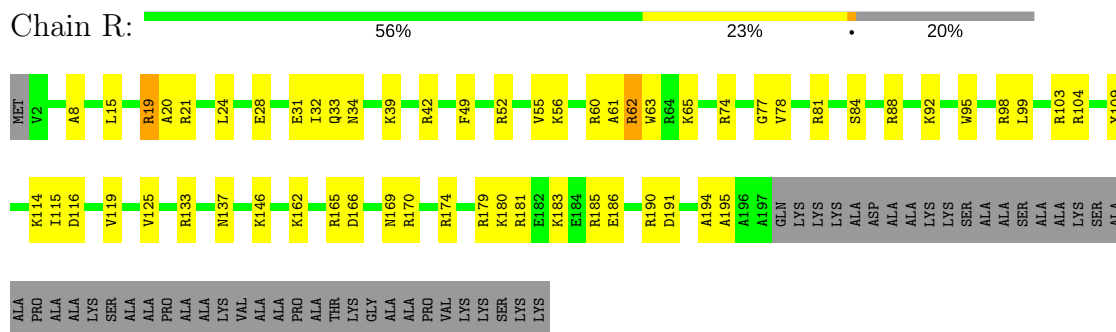
• Molecule 16: uL22



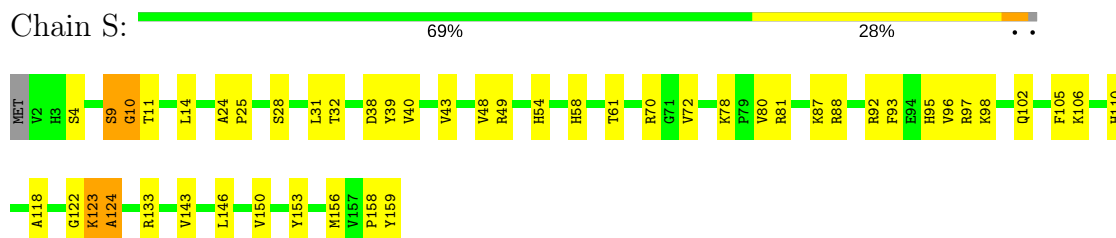
• Molecule 17: eL20



• Molecule 18: eL19

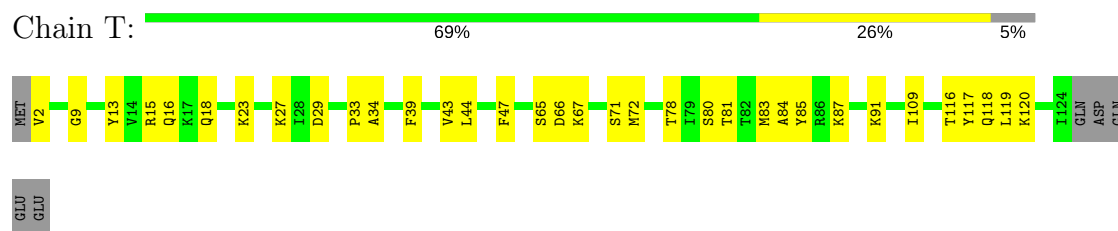


• Molecule 19: eL21

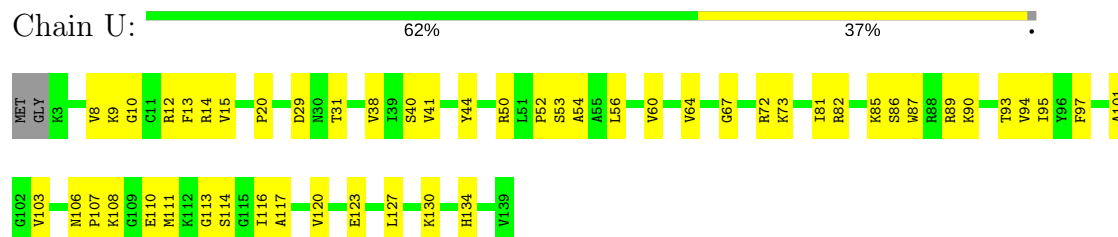




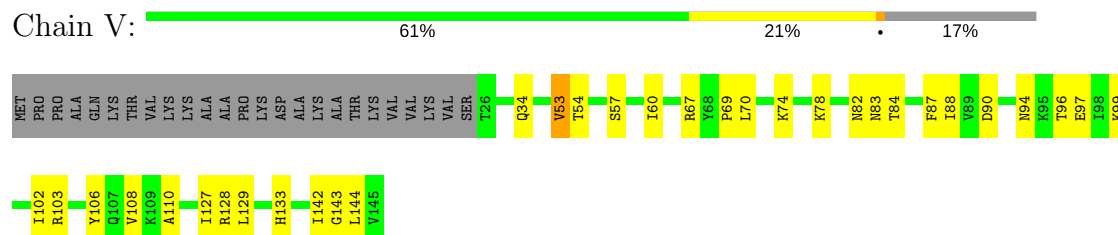
- Molecule 20: eL22



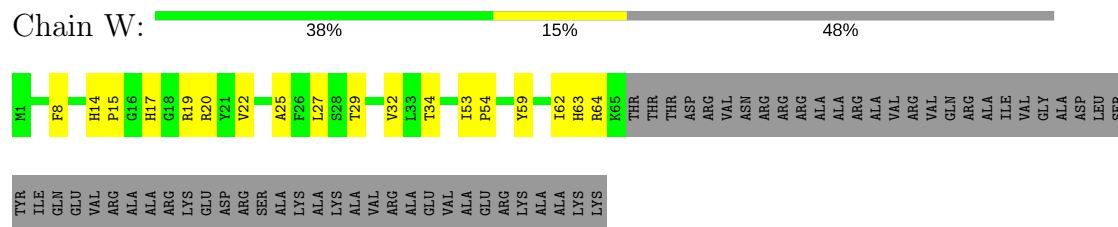
- Molecule 21: uL14



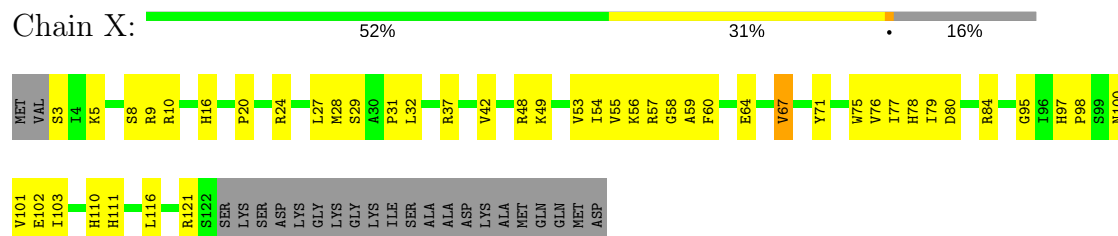
- Molecule 22: uL23



- Molecule 23: eL24



- Molecule 24: uL24



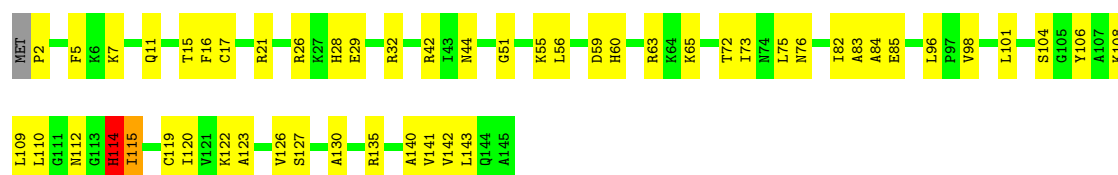
- Molecule 25: eL27





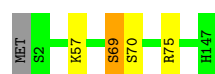
- Molecule 26: uL15

Chain Z: 63% 34% ...



- Molecule 27: eL28

Chain a: 97% ...



- Molecule 28: eL29

Chain b: 96% ..



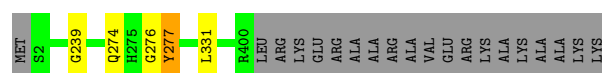
- Molecule 29: uL2

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%

MET LYS GLY LYS VAL LEU GLY LYS GLU LYS LYS LYS ALA ALA TLE ILE ASP ALA ARG LYS LYS ASP ALA GLU SER ARG LYS ASN ARG ASP ASP LYS ARG TRP LYS ARG VAL LEU ALA ASN MET ASP ASP GLU LYS ARG LYS LYS PHE HIS GLY VAL GLY ASN THR ALA LYS ASN SER ARG VAL

ARG GLY ALA THR ARG ALA SER LEU ARG LYS ARG THR GLY R74 Q183

- Molecule 33: eL32

Chain g:  95%

MET V2 G102 K129 L130 GLU SER ASN

- Molecule 34: eL34

Chain h:  73% 26%

MET S2 I63 K125 LYS SER LYS GLN SER LYS LYS GLU ALA ILE ALA LYS LYS ILE SER THR LYS THR VAL SER LYS LYS LYS ALA PRO ALA LYS LYS THR THR THR ARG GLN PRO VAL GLY SER LYS LEU VAL LYS LYS

- Molecule 35: uL29

Chain i:  98%

MET S2 G39 E42 I127

- Molecule 36: eL33

Chain j:  90% 8%

MET THR THR LYS VAL HIS SER GLN ARG SER LYS K43 L14 V126 I144

- Molecule 37: eL36

Chain k:  93% 6%

MET SER A3 A12 T101 LYS LYS HIS HIS

- Molecule 38: eL37

Chain l:  93%


MET T2 K3 G4 R65 Y66 R62 ALA

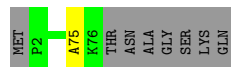
- Molecule 39: eL43

Chain m:  98%



- Molecule 40: eL38

Chain n:  89%



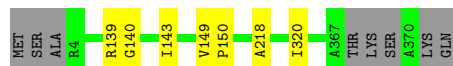
- Molecule 41: eL39

Chain o:  98%



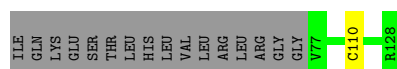
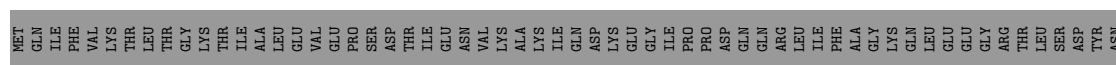
- Molecule 42: uL4

Chain p:  96%




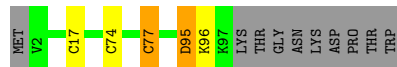
- Molecule 43: eL40

Chain q:  40%




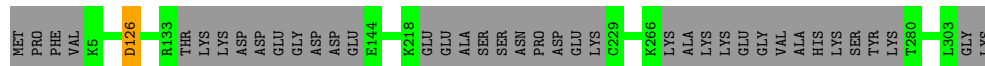
- Molecule 44: eL42

Chain r:  86%



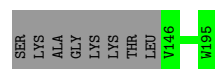
- Molecule 45: uL18

Chain s:  87%



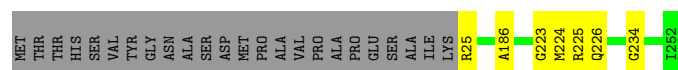
- Molecule 46: eL6

Chain t:  67% 2% 30%



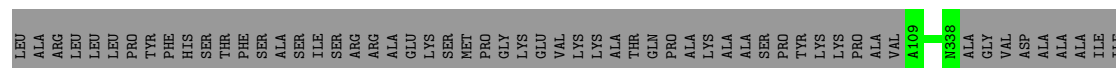
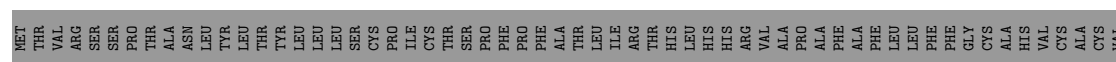
- Molecule 47: uL30

Chain u:  88% • 10%



- Molecule 48: eL8

Chain v:  66% 34%



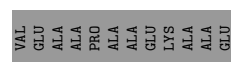
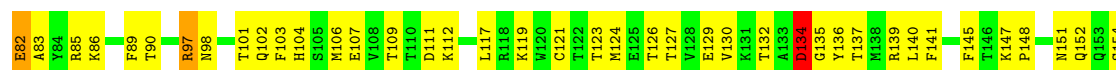
- Molecule 49: uL6

Chain w:  97%



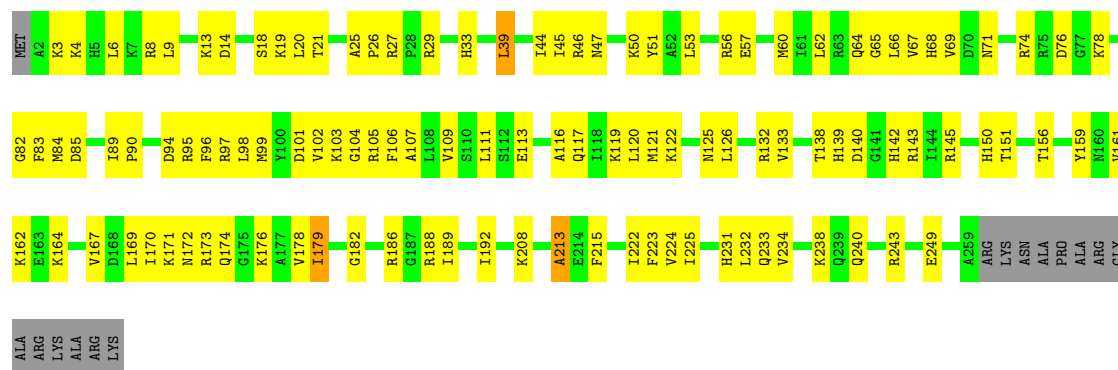
- Molecule 50: eS1

Chain 0: 



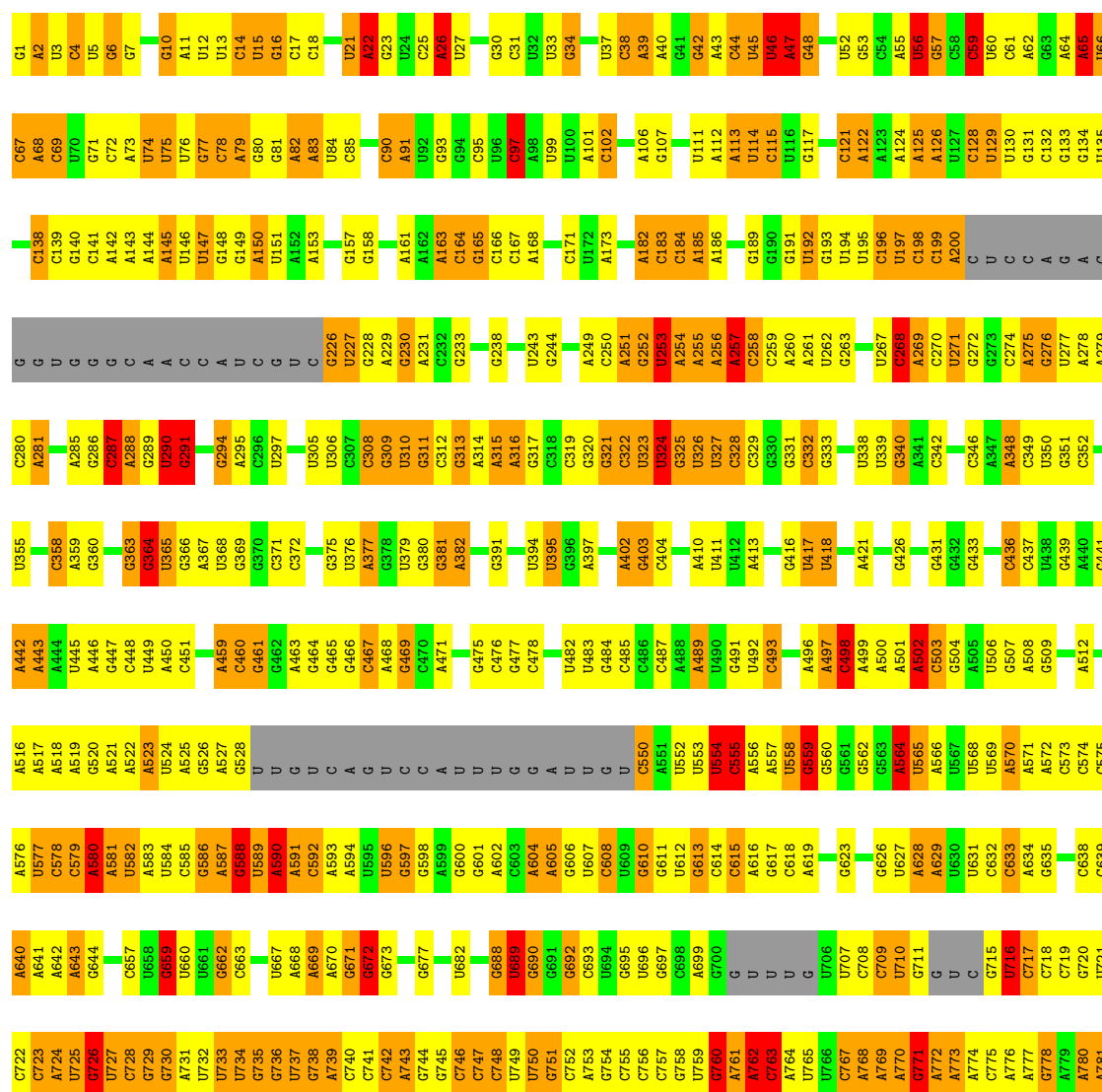
- Molecule 51: eS4

Chain 1:

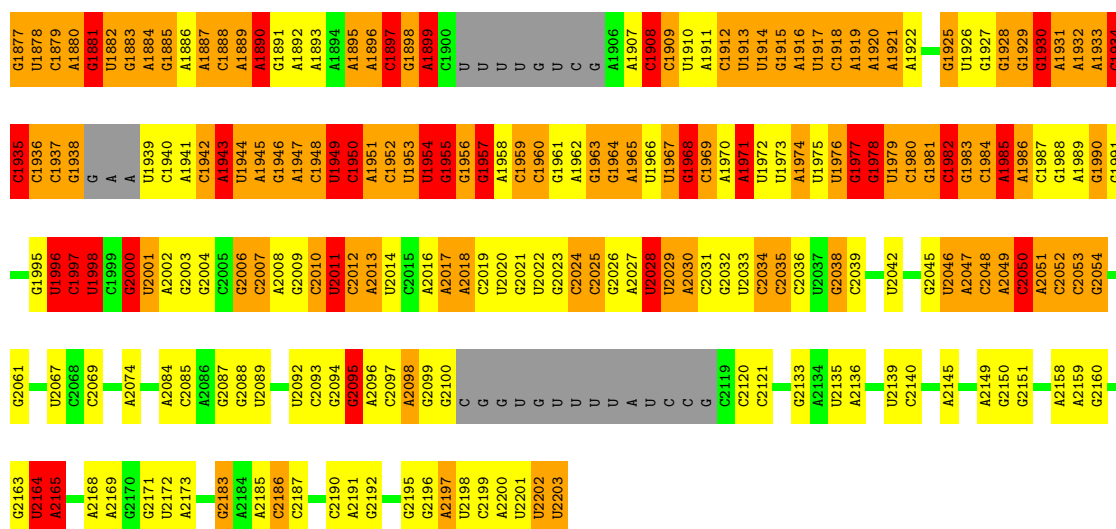


- Molecule 52: 18S rRNA

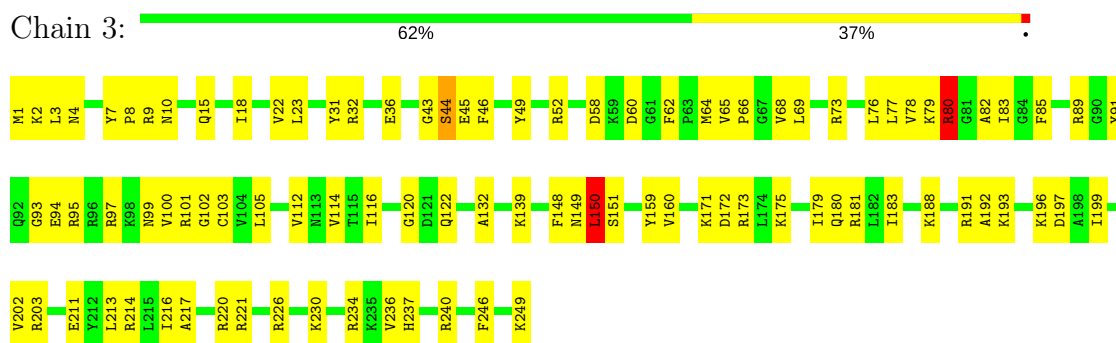
Chain 2:



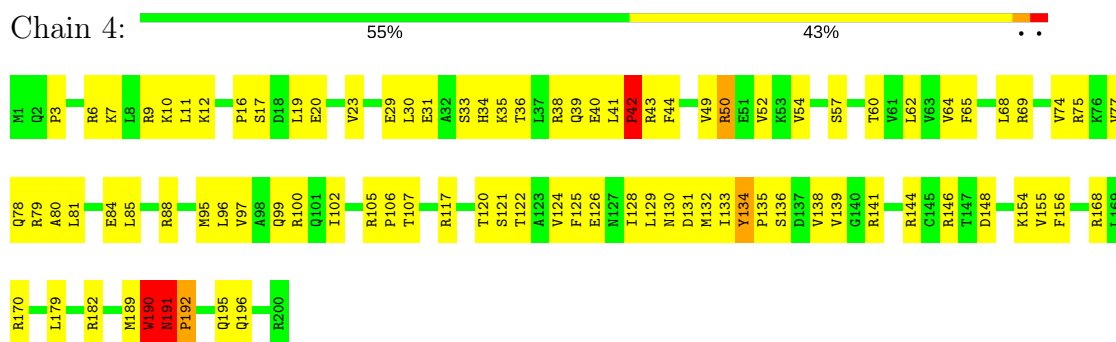
A1814	C1688	C1613	A1550	G1476	C1400	G1273	G1189	G1115	A	U	U835	C848	C782
A1815	A1689	G1617	C1551	G1476	G1401	A1274	C1190	U1119	G	C	U936	U849	A783
U1817	C1692	A1618	G1552	A1479	G1402	C1275	U1191	U1120	C	C	C937	G850	C784
U1818	G1693	A1619	G1554	G1480	G1404	C1278	U1193	C1121	U	A	G938	G785	G786
G1821	G1694	U1620	G1555	A1481	G1411	U1279	U1194	G1122	C	C	C940	G852	G787
G1822	C1697	G1621	A1556	U1489	U1412	A1280	A1280	G1123	G	C	U941	A788	A788
C1826	A1698	G1622	C1558	U1490	C1412	C1281	C1197	G1124	G	C	U942	C854	G789
A1827	G1699	U1623	A1559	A1413	C1413	A1282	A1198	A1129	U	C	U943	U855	U790
G1828	U1700	G1624	U1560	A1491	G1414	C1283	A1199	A1130	C	A	U944	A856	G791
C1829	A1701	G1625	U1561	A1492	C1415	U1287	G1200	A1131	C	A	U945	A857	G792
A1830	G1702	U1626	U1562	A1496	A1416	A1286	G1201	G1132	G	C	U947	G866	U793
G1831	A1703	G1627	C1563	A1497	C1417	U1287	U1287	U1133	C	U	G948	A867	U794
G1832	U1705	U1629	C1564	U1500	U	A1289	A1204	U1137	C	C	G949	A870	U797
U1833	U1706	U1630	A1565	G1500	U	A1290	C1205	G1137	C	C	U950	A871	U
G1834	C1707	G1631	G1566	A1501	U	U1291	U1207	G1138	G	G	U951	A872	C
U1835	A1708	G1632	U1567	U1504	U	U1292	U1208	G1139	C	U	U952	C	C
G1836	G1709	C1634	C1568	G1504	U	G1293	A1213	G1140	C	U	U953	U	U
U1837	U1710	G1635	C1569	U1508	G	C1299	A1214	G1141	G	C	A954	A875	A875
G1838	C1711	C1636	G1571	G1509	U	U	U1215	G1142	U	G	A955	G876	G876
A1839	U1712	U1637	G1572	U	U	U	U1216	G1143	A	G	A956	U877	U877
U1840	U	U1638	A1573	C1512	U	A	A1217	G1144	A	U	G957	A879	U
G1841	G1774	U1639	C1574	G1513	C1434	U	A1233	U1158	C	C	U958	U880	U
C1842	U1775	U1640	A1575	A1514	G1435	G	A1224	U1159	U	C	C960	U881	A
U1843	U1776	G1641	G1576	C1515	G1436	U	A1226	U1160	A	C	U961	U882	C
C1844	C1777	G1641	G1577	U1516	C	U	A1226	A1152	U	C	U962	G883	G
C1845	U	G1644	G1578	A1517	A1433	C	U1233	A1153	U	C	U963	A884	C
U1846	U1783	U1645	G1580	G1518	C1434	U	A1233	U1158	U	C	U964	C885	A
C1847	G1784	A	A1581	A1519	G1435	U	A1233	U1159	U	C	U965	U886	U
A1848	C1785	G1651	G1582	C1520	G1436	U	A1233	U1158	U	C	U966	U887	G
U1849	G1786	U1655	G1583	U1522	G1437	C	U1238	U1159	A	C	A967	G888	U
U1850	U1787	U1655	A1584	U1522	A1438	U	A1238	A1160	A	C	U968	U889	C
G1851	U	U1660	U1585	G1523	A1439	U	A1240	A1161	U	U	U969	A890	A
U1852	A1789	U1661	U1586	G1524	U	C	G1241	G1163	C	C	U970	A896	U
U1853	U1790	G1662	G1587	A1525	U1443	G	A1242	C1164	A	A	U971	C	C
C1854	U1791	G1663	A1588	G1526	U1444	G	U1243	G1165	C	A	A972	C	C
U1855	C1792	U1664	C1589	C1527	U1445	G	U1243	G1166	G	G	U973	G903	A
G1856	C1793	U1665	A1590	G1528	G1446	C	A1245	G1167	G	G	G974	G904	U
U1857	U1794	U1666	U1591	U1529	A1447	A	U1246	C1168	G	G	G975	A905	G
G1858	U1795	G1666	G1595	G1530	G1448	G	U1247	C1169	C	U	A976	U906	C
C1859	U1796	U1667	A1596	C1531	G1449	C	A1248	C1170	U	U	G977	A912	A
A1860	U1797	U1668	G1597	G1532	U1450	C	G1248	A1170	U	U	C978	G913	G
C1861	U1798	U1669	U1598	U1533	U1451	U	A1250	A1173	A	A	U	G914	C
U1862	C1670	C1671	U1599	U1534	A1452	U	A1250	G1174	G	G	G	A915	A
A1863	C1671	C1672	G1600	U1535	C1453	U	A1251	G1175	A	U	G	G916	U
C1864	G1672	U1673	U1601	U1536	A1454	A	C1252	A1176	G	G	C	C917	C
G1865	U1802	U1674	C1602	A1537	G1455	C	C1253	A1177	C	C	G	A918	A
C1866	G1803	C1674	U1603	U1538	U1456	C	U1259	C1178	A	A	A	G919	C836
G1867	C1804	A1675	U1604	U1539	C1459	C	U1259	C1179	U	U	C	C920	G837
C1868	C1805	A1676	U1605	U1540	C1459	G	C1264	U1179	U	U	C	A	U838
U1869	U1806	G1677	C1606	A1543	A1460	G	U1264	A1180	C	A	A	G927	G839
C1870	A1807	G1678	U1607	C1544	G1461	U	G1268	A1181	C	A	G	A	U
U1871	U1808	U1679	C1608	U1545	G1462	G	U1269	A1182	G	G	U	A300	C931
C1872	G1809	G1682	G1609	U1546	C1463	C	C1270	A1183	G	U	C	C932	U
G1873	U	U1685	A1610	A1547	G1464	C	C	C1184	G1111	U	G	U843	U844
U1874	A	U1686	A1611	A1548	G1465	C	C1271	A1187	A	C	C	G933	U845
A1875	C	C1687	U1612	U1612	A1467	G	A1272	G1188	G	U	U	U934	U845



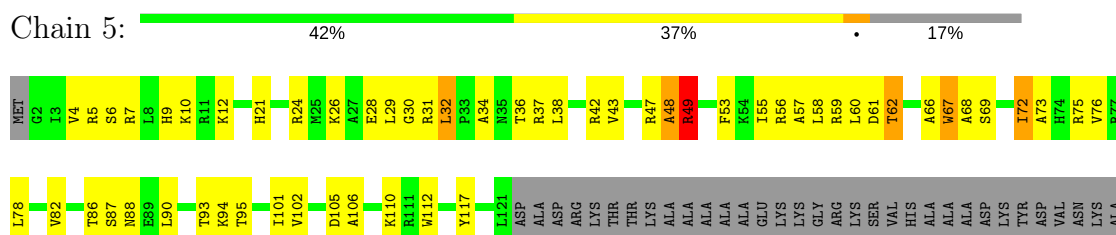
### • Molecule 53: eS6



### • Molecule 54: eS7



### • Molecule 55: eS8

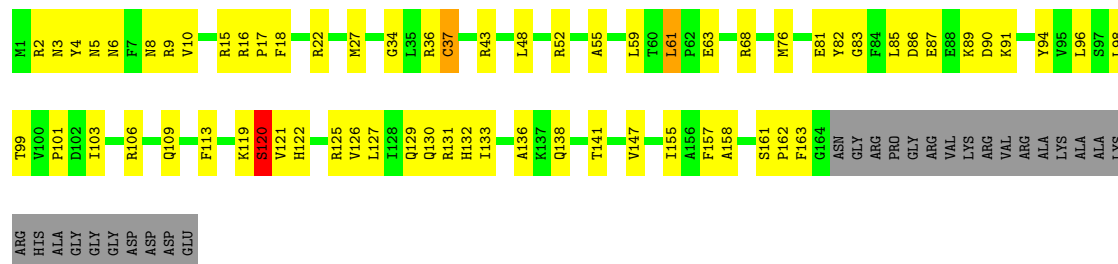






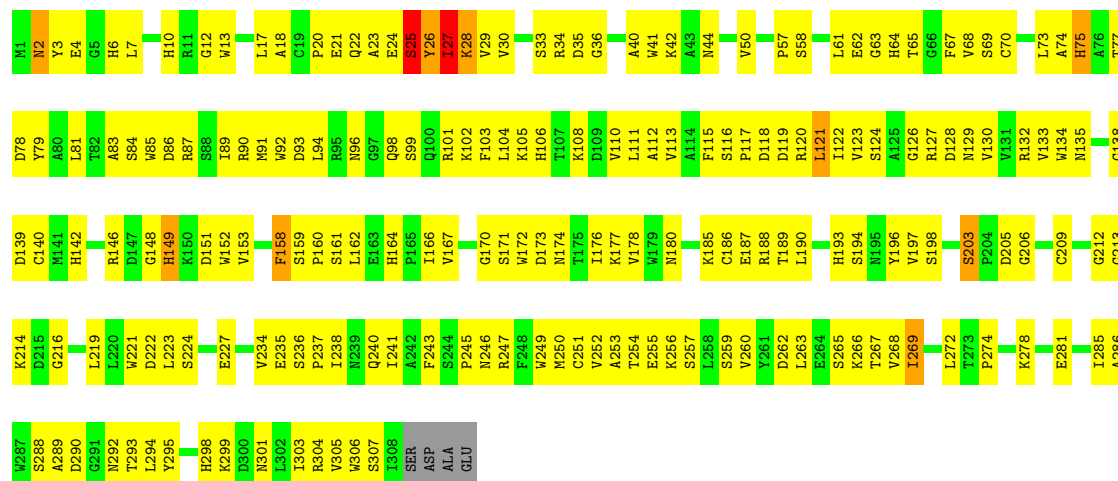
• Molecule 56: uS4

Chain 6: 52% 33% 14%



• Molecule 57: RACK1

Chain 7: 37% 59% 4%



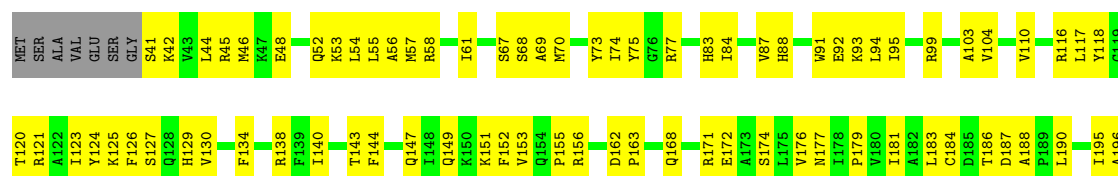
• Molecule 58: uS14

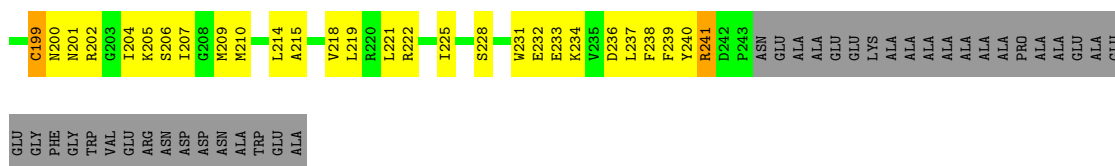
Chain 8: 12% 46% 9% 33%



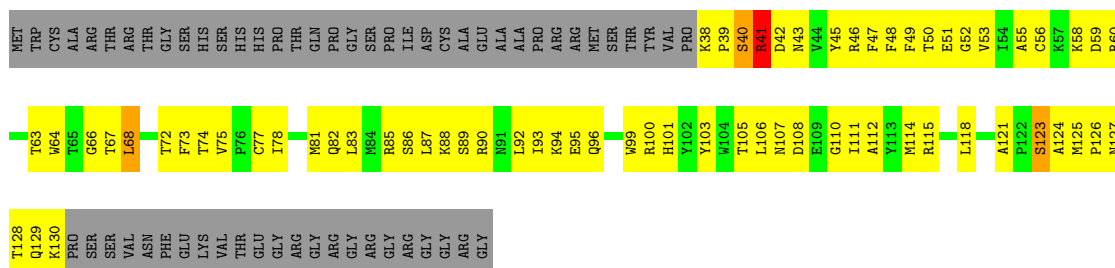
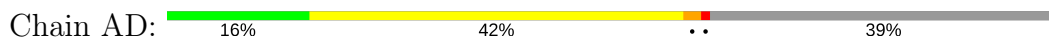
• Molecule 59: uS2

Chain AC: 40% 42% 17%

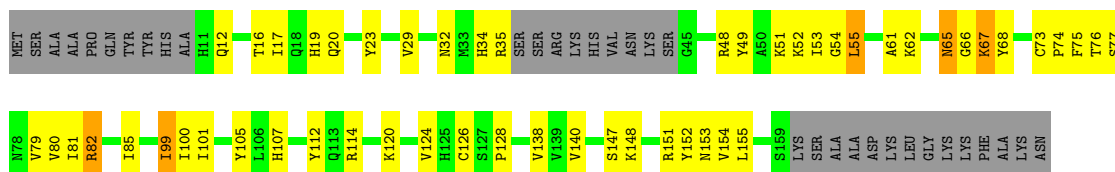




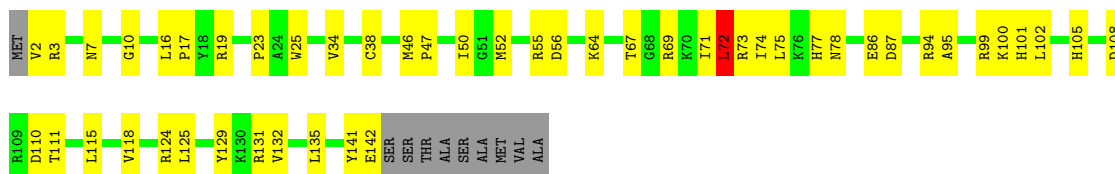
- Molecule 60: eS10



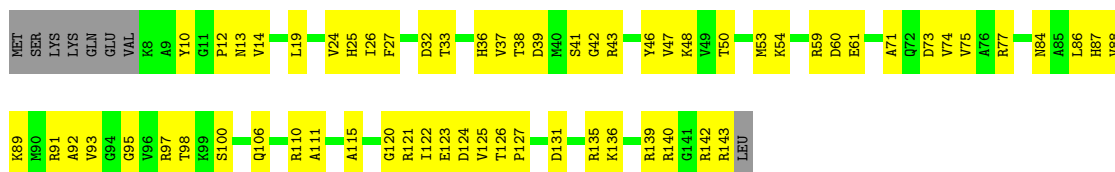
- Molecule 61: uS17



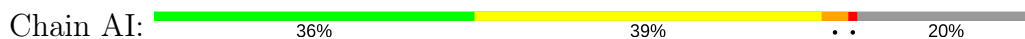
- Molecule 62: uS15

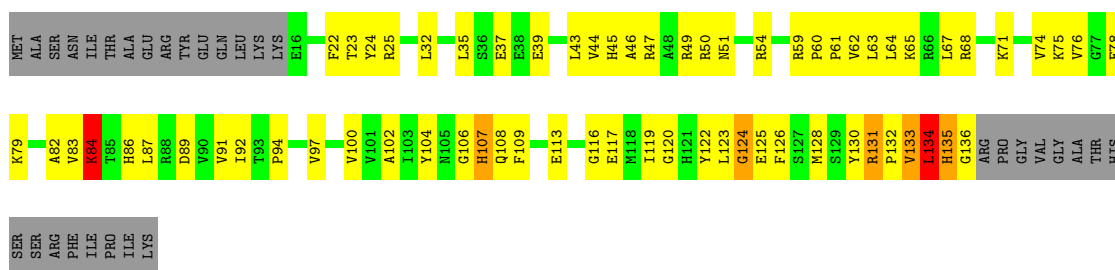


- Molecule 63: uS11



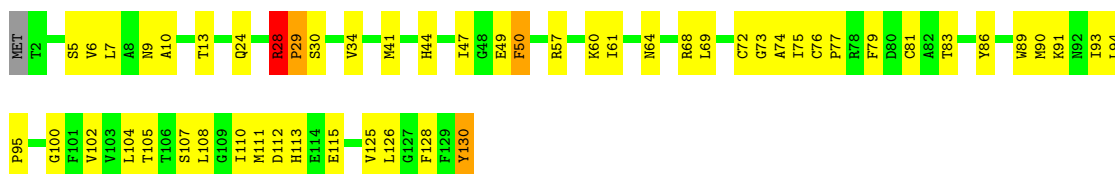
- Molecule 64: uS19





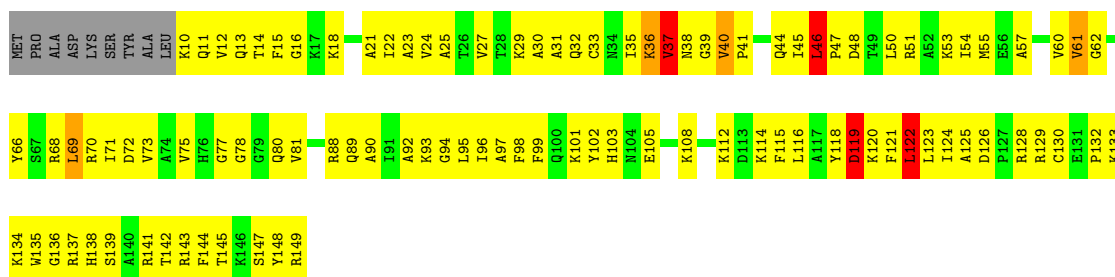
• Molecule 65: uS8

Chain AJ: 58% 38% ...



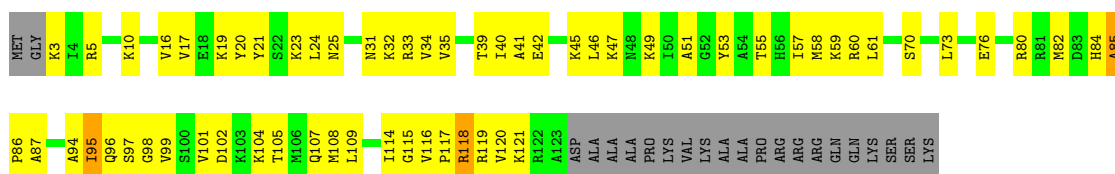
• Molecule 66: uS9

Chain AK: 27% 62% 6%



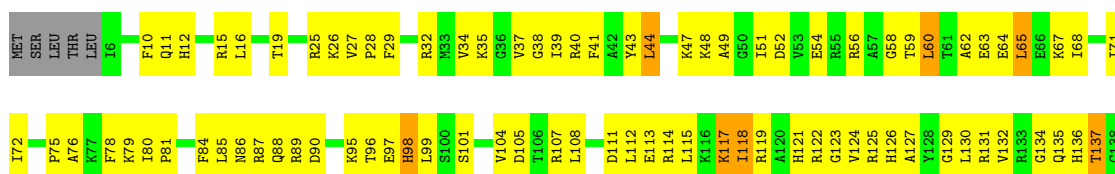
• Molecule 67: eS17

Chain AL: 41% 41% 15%



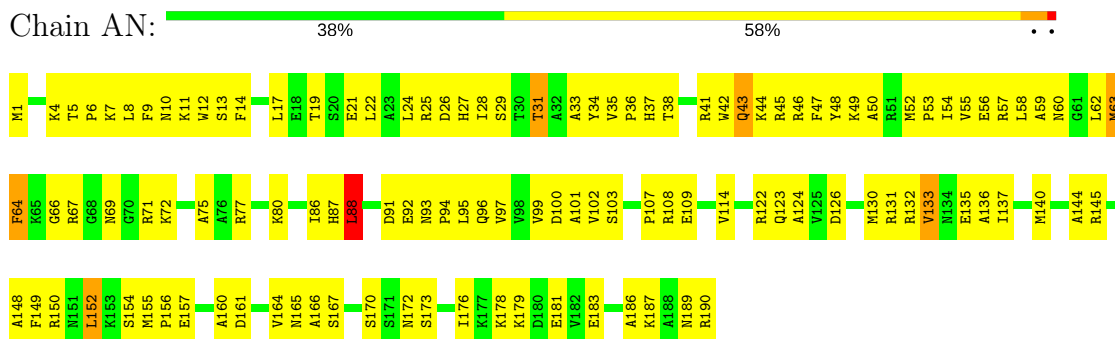
• Molecule 68: uS13

Chain AM: 31% 59% 6%



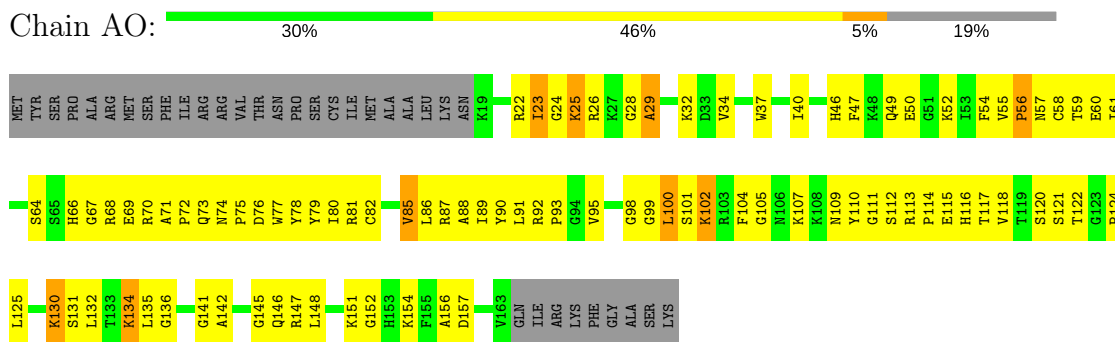
- Molecule 69: uS7

Chain AN:



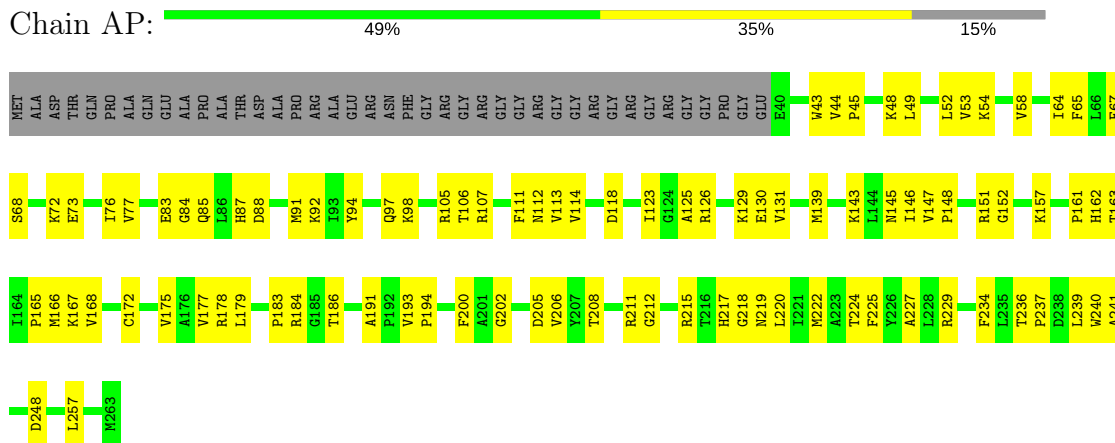
- Molecule 70: eS19

Chain AO:



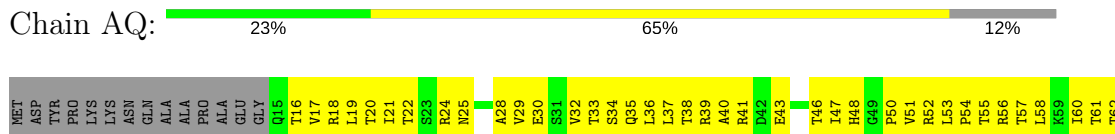
- Molecule 71: uS5

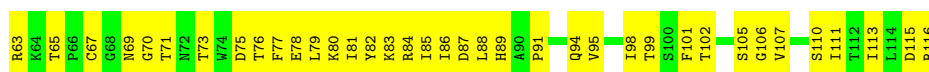
Chain AP:



- Molecule 72: uS10

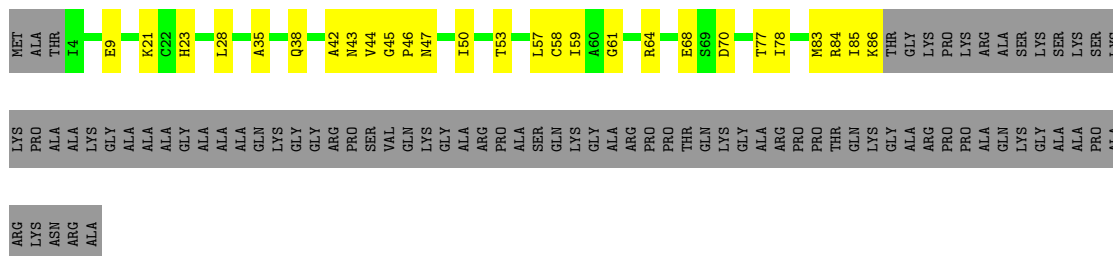
Chain AQ:





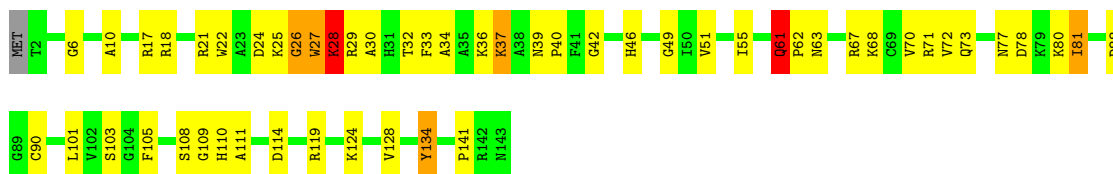
• Molecule 73: eS21

Chain AR: 34% 16% 49%



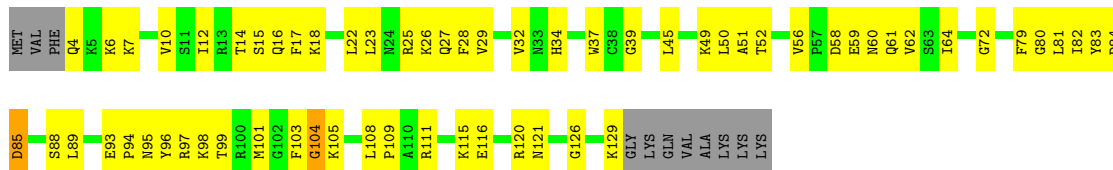
• Molecule 74: uS12

Chain AS: 62% 32%



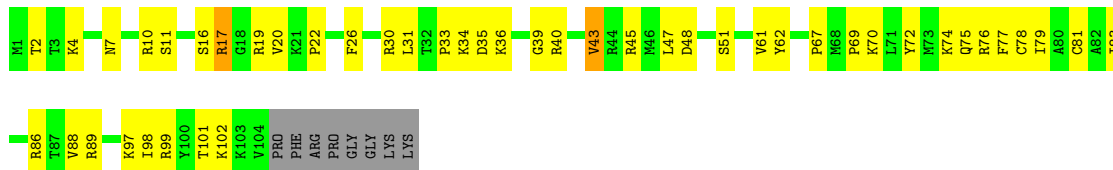
• Molecule 75: eS24

Chain AT: 46% 45% 8%



• Molecule 76: eS26

Chain AV: 52% 39% 7%



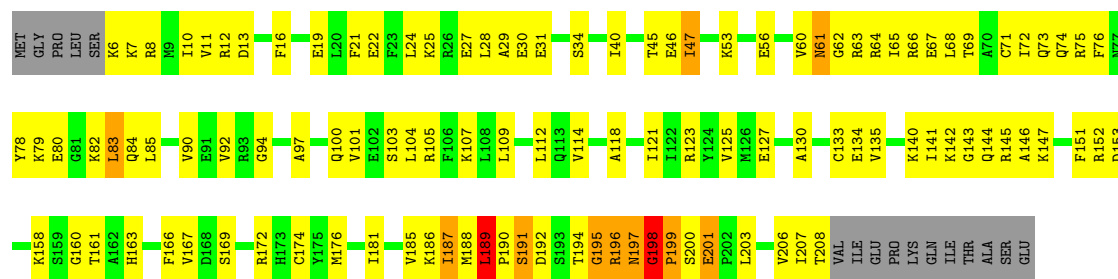
• Molecule 77: eS27

Chain AW: 64% 28% 5%



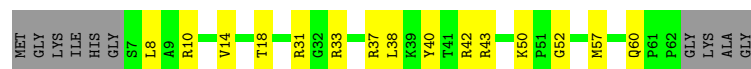
- Molecule 78: uS3

Chain AX: 



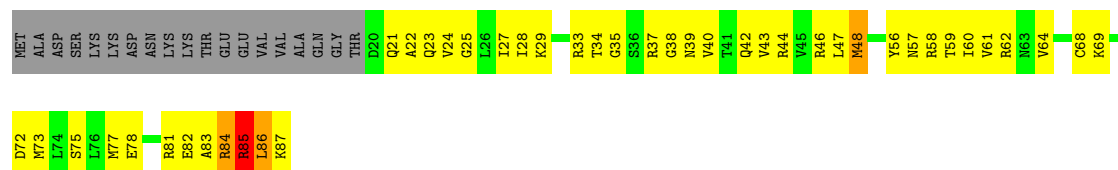
- Molecule 79: eS30

Chain AY: 



- Molecule 80: eS28

Chain AZ: 



## 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	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	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%)	11	37
10	J	209/213 (98%)	193 (92%)	13 (6%)	3 (1%)	12	39
11	K	165/188 (88%)	152 (92%)	12 (7%)	1 (1%)	27	61
12	L	175/220 (80%)	159 (91%)	14 (8%)	2 (1%)	16	46
13	M	219/222 (99%)	212 (97%)	6 (3%)	1 (0%)	31	65
14	N	166/175 (95%)	153 (92%)	12 (7%)	1 (1%)	27	61
15	O	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
16	P	153/166 (92%)	145 (95%)	7 (5%)	1 (1%)	24	58
17	Q	176/179 (98%)	163 (93%)	11 (6%)	2 (1%)	16	46
18	R	194/245 (79%)	193 (100%)	1 (0%)	0	100	100
19	S	156/159 (98%)	144 (92%)	11 (7%)	1 (1%)	27	61
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%)	21	54
23	W	63/124 (51%)	61 (97%)	2 (3%)	0	100	100
24	X	118/143 (82%)	111 (94%)	5 (4%)	2 (2%)	10	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	Y	131/134 (98%)	124 (95%)	6 (5%)	1 (1%)	21	54
26	Z	142/145 (98%)	125 (88%)	14 (10%)	3 (2%)	8	29
27	a	144/147 (98%)	134 (93%)	9 (6%)	1 (1%)	24	58
28	b	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
29	c	251/260 (96%)	229 (91%)	20 (8%)	2 (1%)	21	54
30	d	397/419 (95%)	376 (95%)	20 (5%)	1 (0%)	43	75
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%)	21	54
35	i	124/127 (98%)	117 (94%)	6 (5%)	1 (1%)	21	54
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%)	27	61
43	q	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
44	r	94/106 (89%)	85 (90%)	8 (8%)	1 (1%)	16	46
45	s	258/305 (85%)	246 (95%)	12 (5%)	0	100	100
46	t	133/195 (68%)	123 (92%)	8 (6%)	2 (2%)	11	37
47	u	226/252 (90%)	209 (92%)	16 (7%)	1 (0%)	36	69
48	v	228/348 (66%)	218 (96%)	10 (4%)	0	100	100
49	w	185/190 (97%)	173 (94%)	11 (6%)	1 (0%)	31	65
50	0	219/264 (83%)	208 (95%)	10 (5%)	1 (0%)	31	65
51	1	256/273 (94%)	231 (90%)	22 (9%)	3 (1%)	14	43
53	3	247/249 (99%)	236 (96%)	10 (4%)	1 (0%)	36	69
54	4	198/200 (99%)	183 (92%)	11 (6%)	4 (2%)	8	30
55	5	178/220 (81%)	160 (90%)	16 (9%)	2 (1%)	16	46
56	6	162/190 (85%)	151 (93%)	9 (6%)	2 (1%)	14	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	7	306/312 (98%)	275 (90%)	28 (9%)	3 (1%)	17	49
58	8	36/57 (63%)	30 (83%)	5 (14%)	1 (3%)	5	21
59	AC	201/246 (82%)	193 (96%)	8 (4%)	0	100	100
60	AD	91/153 (60%)	78 (86%)	11 (12%)	2 (2%)	7	27
61	AE	136/173 (79%)	131 (96%)	4 (3%)	1 (1%)	24	58
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%)	21	54
66	AK	138/149 (93%)	118 (86%)	16 (12%)	4 (3%)	5	20
67	AL	119/143 (83%)	108 (91%)	8 (7%)	3 (2%)	6	23
68	AM	146/153 (95%)	125 (86%)	21 (14%)	0	100	100
69	AN	188/190 (99%)	165 (88%)	21 (11%)	2 (1%)	16	46
70	AO	143/179 (80%)	114 (80%)	25 (18%)	4 (3%)	5	21
71	AP	222/265 (84%)	216 (97%)	6 (3%)	0	100	100
72	AQ	100/116 (86%)	86 (86%)	13 (13%)	1 (1%)	17	49
73	AR	81/164 (49%)	78 (96%)	3 (4%)	0	100	100
74	AS	140/143 (98%)	132 (94%)	5 (4%)	3 (2%)	8	29
75	AT	124/137 (90%)	117 (94%)	6 (5%)	1 (1%)	21	54
76	AV	102/112 (91%)	90 (88%)	8 (8%)	4 (4%)	3	13
77	AW	80/86 (93%)	76 (95%)	4 (5%)	0	100	100
78	AX	201/219 (92%)	179 (89%)	17 (8%)	5 (2%)	6	23
79	AY	54/66 (82%)	48 (89%)	6 (11%)	0	100	100
80	AZ	66/87 (76%)	60 (91%)	4 (6%)	2 (3%)	5	19
All	All	10774/12317 (88%)	9993 (93%)	696 (6%)	85 (1%)	26	54

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%)	43	77
10	J	178/179 (99%)	175 (98%)	3 (2%)	63	88
11	K	145/163 (89%)	144 (99%)	1 (1%)	85	96
12	L	152/182 (84%)	151 (99%)	1 (1%)	85	96
13	M	188/189 (100%)	187 (100%)	1 (0%)	90	97
14	N	139/144 (96%)	136 (98%)	3 (2%)	55	84
15	O	179/180 (99%)	178 (99%)	1 (1%)	87	96
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%)	74	92
19	S	132/133 (99%)	131 (99%)	1 (1%)	83	95
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%)	63	88
24	X	103/121 (85%)	103 (100%)	0	100	100
25	Y	114/115 (99%)	113 (99%)	1 (1%)	81	94
26	Z	114/115 (99%)	114 (100%)	0	100	100
27	a	118/119 (99%)	116 (98%)	2 (2%)	63	88
28	b	57/58 (98%)	57 (100%)	0	100	100
29	c	198/204 (97%)	193 (98%)	5 (2%)	50	81
30	d	337/351 (96%)	336 (100%)	1 (0%)	93	98
31	e	82/90 (91%)	77 (94%)	5 (6%)	20	51
32	f	97/156 (62%)	97 (100%)	0	100	100
33	g	113/117 (97%)	111 (98%)	2 (2%)	62	87
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%)	62	87
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%)	85	96
43	q	46/113 (41%)	46 (100%)	0	100	100
44	r	83/92 (90%)	80 (96%)	3 (4%)	38	73
45	s	209/242 (86%)	208 (100%)	1 (0%)	90	97
46	t	111/152 (73%)	110 (99%)	1 (1%)	81	94
47	u	190/209 (91%)	187 (98%)	3 (2%)	65	88
48	v	196/292 (67%)	196 (100%)	0	100	100
49	w	169/172 (98%)	168 (99%)	1 (1%)	87	96
50	0	194/222 (87%)	189 (97%)	5 (3%)	49	81
51	1	215/225 (96%)	212 (99%)	3 (1%)	69	90
53	3	208/208 (100%)	206 (99%)	2 (1%)	78	94
54	4	186/186 (100%)	185 (100%)	1 (0%)	90	97
55	5	149/176 (85%)	147 (99%)	2 (1%)	71	91
56	6	147/164 (90%)	145 (99%)	2 (1%)	69	90
57	7	263/266 (99%)	259 (98%)	4 (2%)	67	89
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%)	74	92
61	AE	124/150 (83%)	122 (98%)	2 (2%)	65	88
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%)	60	86
65	AJ	110/111 (99%)	105 (96%)	5 (4%)	30	64
66	AK	113/120 (94%)	108 (96%)	5 (4%)	31	65

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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%)	42	76
69	AN	159/159 (100%)	158 (99%)	1 (1%)	87	96
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%)	32	66
75	AT	111/120 (92%)	111 (100%)	0	100	100
76	AV	87/93 (94%)	86 (99%)	1 (1%)	76	93
77	AW	72/75 (96%)	71 (99%)	1 (1%)	69	90
78	AX	171/185 (92%)	167 (98%)	4 (2%)	53	83
79	AY	49/54 (91%)	49 (100%)	0	100	100
80	AZ	57/74 (77%)	54 (95%)	3 (5%)	25	58
All	All	9268/10330 (90%)	9167 (99%)	101 (1%)	77	93

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 [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](#)

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