



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:53 PM BST

PDB ID : 3JBP  
EMDB ID: : EMD-6454  
Title : Cryo-electron microscopy reconstruction of the Plasmodium falciparum 80S ribosome bound to E-tRNA  
Authors : Sun, M.; Li, W.; Blomqvist, K.; Das, S.; Hashem, Y.; Dvorin, J.D.; Frank, J.  
Deposited on : 2015-09-16  
Resolution : 6.70 Å(reported)  
Based on PDB ID : 3J79, 3J7A

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

---

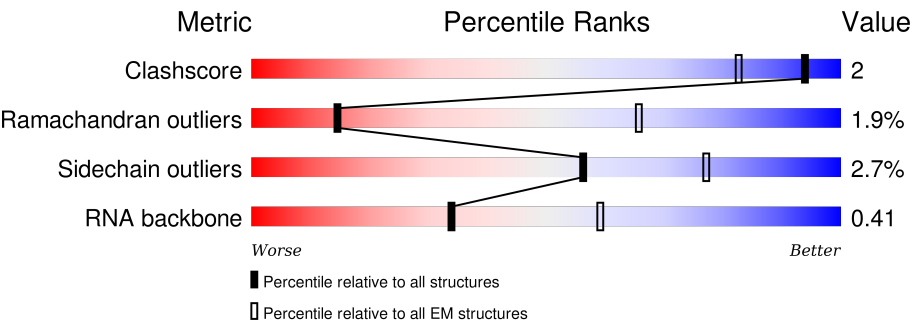
MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 6.70 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.













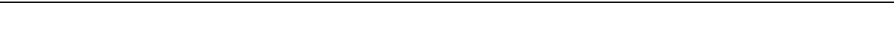

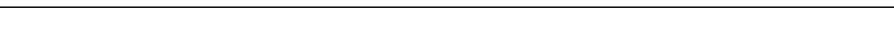
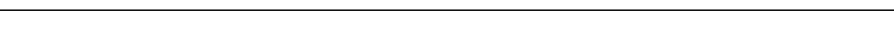











Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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  $\geq 3$ , 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	1608	<div><div>29%</div><div>44%</div><div>22%</div><div>5%</div></div>
2	7	74	<div><div>9%</div><div>41%</div><div>38%</div><div>12%</div></div>
3	D	209	<div><div>70%</div><div>25%</div></div>
4	E	185	<div><div>88%</div><div>11%</div></div>
5	G	224	<div><div>93%</div><div>7%</div></div>
6	I	189	<div><div>87%</div><div>5%</div><div>5%</div></div>
7	K	129	<div><div>90%</div><div>5%</div></div>
8	M	138	<div><div>94%</div><div>6%</div></div>

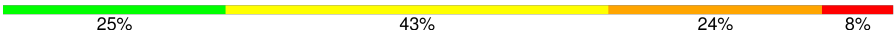
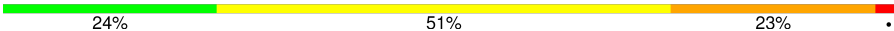
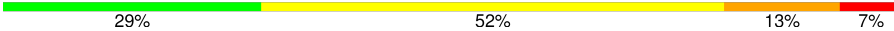








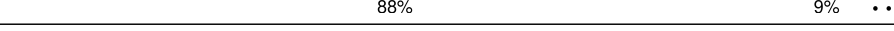




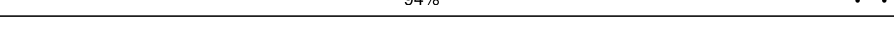

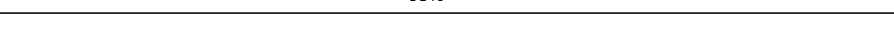
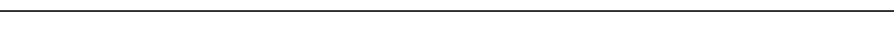

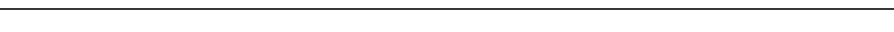
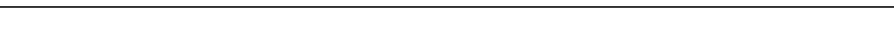


Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	W	108	
10	R	114	
11	O	79	
12	Y	154	
13	Z	72	
14	1	120	
15	2	68	
16	3	95	
17	4	76	
18	5	65	
19	6	43	
20	B	210	
21	F	257	
22	H	214	
23	J	188	
24	L	214	
25	N	98	
26	P	127	
27	Q	144	
28	S	128	
29	T	48	
30	U	149	
31	V	156	
32	X	103	
33	C	195	













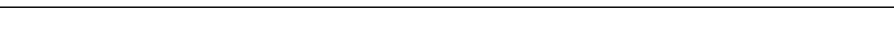



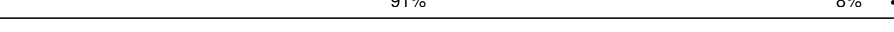


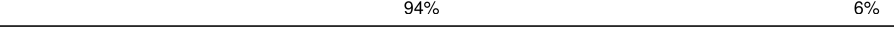
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	AA	3193	
35	AC	151	
36	AB	118	
37	AL	211	
38	A1	145	
39	A2	118	
40	A4	66	
41	A6	98	
42	A7	102	
43	AN	146	
44	A8	125	
45	A9	103	
46	Aa	106	
47	Ab	105	
48	Ad	76	
49	Ae	50	
50	Af	51	
51	AP	204	
52	Ah	85	
53	Ai	95	
54	AI	213	
55	AJ	244	
56	Ac	89	
57	AK	201	
58	AM	132	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	AS	186	 86% 12% .
60	AO	147	 89% 10% .
61	AQ	205	 80% 11% . 8%
62	AR	289	 77% 9% . 13%
63	AW	170	 88% 9% .
64	AY	101	 94% 5% .
65	AT	181	 91% 8% ..
66	AZ	121	 93% 5% .
67	A3	119	 92% 8% .
68	A5	223	 86% 11% .
69	AD	247	 89% 9% ..
70	AE	380	 89% 10% .
71	AF	390	 92% 7% .
72	AG	159	 70% 6% . 22%
73	AU	180	 88% 7% . .
74	AH	185	 91% 8% .
75	AV	155	 89% 10% .
76	Ag	37	 76% 16% 8%
77	AX	97	 94% 6%
78	A0	62	 92% 6% .

## 2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 193012 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1608	Total	C	N	O	P	0	0
			34207	15346	6106	11169	1586		

- Molecule 2 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	74	Total	C	N	O	P	0	0
			1571	702	275	521	73		

- Molecule 3 is a protein called 40S ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	157	Total	C	N	O	S	0	0
			1229	782	225	215	7		

- Molecule 4 is a protein called 40S ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	185	Total	C	N	O	S	0	0
			1515	962	290	261	2		

- Molecule 5 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	224	Total	C	N	O	S	0	0
			1758	1132	307	310	9		

- Molecule 6 is a protein called 40S ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	180	Total	C	N	O	S	0	0
			1424	893	263	258	10		

- Molecule 7 is a protein called 40S ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	129	Total	C	N	O	S	0	0
			1037	665	189	178	5		

- Molecule 8 is a protein called 40S ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	M	138	Total	C	N	O	S	0	0
			1099	704	200	194	1		

- Molecule 9 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	W	95	Total	C	N	O	S	0	0
			786	498	149	136	3		

- Molecule 10 is a protein called 40S ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	R	98	Total	C	N	O	S	0	0
			747	474	123	146	4		

- Molecule 11 is a protein called 40S ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	79	Total	C	N	O	S	0	0
			687	450	116	119	2		

- Molecule 12 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Y	154	Total	C	N	O	S	0	0
			1267	811	239	215	2		

- Molecule 13 is a protein called 40S ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Z	72	Total	C	N	O	S	0	0
			557	346	102	105	4		

- Molecule 14 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	1	120	Total	C	N	O	S	0	0
			986	632	189	163	2		

- Molecule 15 is a protein called 40S ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	2	41	Total	C	N	O		0	0
			321	208	56	57			

- Molecule 16 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	3	95	Total	C	N	O	S	0	0
			782	478	169	129	6		

- Molecule 17 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	4	76	Total	C	N	O	S	0	0
			586	368	102	107	9		

- Molecule 18 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	5	58	Total	C	N	O		0	0
			458	285	93	80			

- Molecule 19 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	6	43	Total	C	N	O		0	0
			346	213	75	58			

- Molecule 20 is a protein called 40S ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	B	210	Total	C	N	O	S	0	0
			1714	1097	301	304	12		

- Molecule 21 is a protein called 40S ribosomal protein eS4.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	F	257	Total	C	N	O	S	0	0
			2062	1320	377	357	8		

- Molecule 22 is a protein called 40S ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	H	204	Total	C	N	O	S	0	0
			1648	1045	313	284	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	158	ILE	-	INSERTION	UNP Q8IDR9
H	195	ASP	GLU	CONFLICT	UNP Q8IDR9

- Molecule 23 is a protein called 40S ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	J	188	Total	C	N	O	S	0	0
			1529	982	264	279	4		

- Molecule 24 is a protein called 40S ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L	171	Total	C	N	O	S	0	0
			1383	872	264	243	4		

- Molecule 25 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	N	98	Total	C	N	O	S	0	0
			772	484	135	148	5		

- Molecule 26 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	P	127	Total	C	N	O	S	0	0
			954	591	184	176	3		

- Molecule 27 is a protein called 40S ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Q	144	Total	C	N	O	S	0	0
			1129	712	222	193	2		

- Molecule 28 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	S	128	Total	C	N	O	S	0	0
			1047	657	205	181	4		

- Molecule 29 is a protein called 40S ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	T	48	Total	C	N	O	S	0	0
			405	252	85	64	4		

- Molecule 30 is a protein called 40S ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U	149	Total	C	N	O	S	0	0
			1202	769	220	210	3		

- Molecule 31 is a protein called 40S ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	V	146	Total	C	N	O	S	0	0
			1206	772	227	200	7		

- Molecule 32 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	96	Total	C	N	O	S	0	0
			777	497	137	139	4		

- Molecule 33 is a protein called 40S ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	C	195	Total	C	N	O	S	0	0
			1539	990	266	274	9		

- Molecule 34 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AA	3193	Total	C	N	O	P	0	0
			67884	30446	12054	22223	3161		

- Molecule 35 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AC	151	Total	C	N	O	P	0	0
			3215	1444	589	1034	148		

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	118	Total	C	N	O	P	0	0
			2522	1128	461	816	117		

- Molecule 37 is a protein called 60S ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AL	211	Total	C	N	O	S	0	0
			1757	1116	346	291	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL	19	HIS	ARG	CONFLICT	UNP Q8IAX6
AL	20	ARG	HIS	CONFLICT	UNP Q8IAX6
AL	201	CYS	ARG	CONFLICT	UNP Q8IAX6

- Molecule 38 is a protein called 60S ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 39 is a protein called 60S ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A2	104	Total	C	N	O	S	0	0
			831	529	151	148	3		

- Molecule 40 is a protein called 60S ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 41 is a protein called 60S ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A6	98	Total	C	N	O	S	0	0
			741	462	132	140	7		

- Molecule 42 is a protein called 60S ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	A7	96	Total	C	N	O	S	0	0
			794	508	151	130	5		

- Molecule 43 is a protein called 60S ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AN	146	Total	C	N	O	S	0	0
			1202	781	210	205	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AN	?	-	LYS	DELETION	UNP Q8ILE8

- Molecule 44 is a protein called 60S ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	A8	125	Total	C	N	O	S	0	0
			1037	660	206	164	7		

- Molecule 45 is a protein called 60S ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	A9	103	Total	C	N	O	S	0	0
			845	543	163	136	3		

- Molecule 46 is a protein called 60S ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Aa	106	Total	C	N	O	S	0	0
			859	530	184	139	6		

- Molecule 47 is a protein called 60S ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ab	95	Total	C	N	O	S	0	0
			757	477	150	130			

- Molecule 48 is a protein called 60S ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ad	72	Total	C	N	O	S	0	0
			604	395	107	100	2		

- Molecule 49 is a protein called 60S ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ae	43	Total	C	N	O	S	0	0
			388	243	92	52	1		

- Molecule 50 is a protein called 60S ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Af	51	Total	C	N	O	S	0	0
			414	255	87	67	5		

- Molecule 51 is a protein called 60S ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AP	204	Total	C	N	O	S	0	0
			1697	1075	351	267	4		

- Molecule 52 is a protein called 60S ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ah	85	Total	C	N	O	S	0	0
			659	417	127	108	7		

- Molecule 53 is a protein called 60S ribosomal protein eL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ai	95	Total	C	N	O	S	0	0
			779	490	152	128	9		

- Molecule 54 is a protein called 60S ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AI	207	Total	C	N	O	S	0	0
			1685	1096	298	286	5		

- Molecule 55 is a protein called 60S ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AJ	222	Total	C	N	O	S	0	0
			1813	1174	323	309	7		

- Molecule 56 is a protein called 60S ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ac	89	Total	C	N	O	S	0	0
			710	441	150	114	5		

- Molecule 57 is a protein called 60S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AK	201	Total	C	N	O	S	0	0
			1660	1064	311	277	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AK	109	ALA	TYR	CONFLICT	UNP Q8IJZ7

- Molecule 58 is a protein called 60S ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AM	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

- Molecule 59 is a protein called 60S ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AS	186	Total	C	N	O	S	0	0
			1503	958	299	241	5		

- Molecule 60 is a protein called 60S ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AO	147	Total	C	N	O	S	0	0
			1172	747	232	189	4		

- Molecule 61 is a protein called 60S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AQ	189	Total	C	N	O	S	0	0
			1545	984	291	262	8		

- Molecule 62 is a protein called 60S ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AR	252	Total	C	N	O	S	0	0
			2050	1300	385	359	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	?	-	LYS	DELETION	UNP Q8ILL3

- Molecule 63 is a protein called 60S ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AW	170	Total	C	N	O	S	0	0
			1319	824	266	222	7		

- Molecule 64 is a protein called 60S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AY	101	Total	C	N	O	S	0	0
			797	502	144	145	6		

- Molecule 65 is a protein called 60S ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AT	181	Total	C	N	O	S	0	0
			1509	952	309	244	4		

- Molecule 66 is a protein called 60S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	121	Total	C	N	O	S	0	0
			1001	626	206	166	3		

- Molecule 67 is a protein called 60S ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	A3	119	Total	C	N	O	S	0	0
			995	635	194	164	2		

- Molecule 68 is a protein called 60S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	A5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 69 is a protein called 60S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AD	247	Total	C	N	O	S	0	0
			1867	1166	374	318	9		

- Molecule 70 is a protein called 60S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AE	380	Total	C	N	O	S	0	0
			3062	1948	575	522	17		

- Molecule 71 is a protein called 60S ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AF	390	Total	C	N	O	S	0	0
			3095	1962	594	528	11		

- Molecule 72 is a protein called 60S ribosomal protein uL5.



Mol	Chain	Residues	Atoms					AltConf	Trace
72	AG	124	Total	C	N	O	S	0	0
			1011	636	197	172	6		

- Molecule 73 is a protein called 60S ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AU	180	Total	C	N	O	S	0	0
			1497	946	289	255	7		

- Molecule 74 is a protein called 60S ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AH	185	Total	C	N	O	S	0	0
			1476	950	264	256	6		

- Molecule 75 is a protein called 60S ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AV	155	Total	C	N	O	S	0	0
			1276	814	241	215	6		

- Molecule 76 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ag	37	Total	C	N	O	S	0	0
			343	210	86	45	2		

- Molecule 77 is a protein called 60S ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AX	97	Total	C	N	O	S	0	0
			825	548	135	140	2		

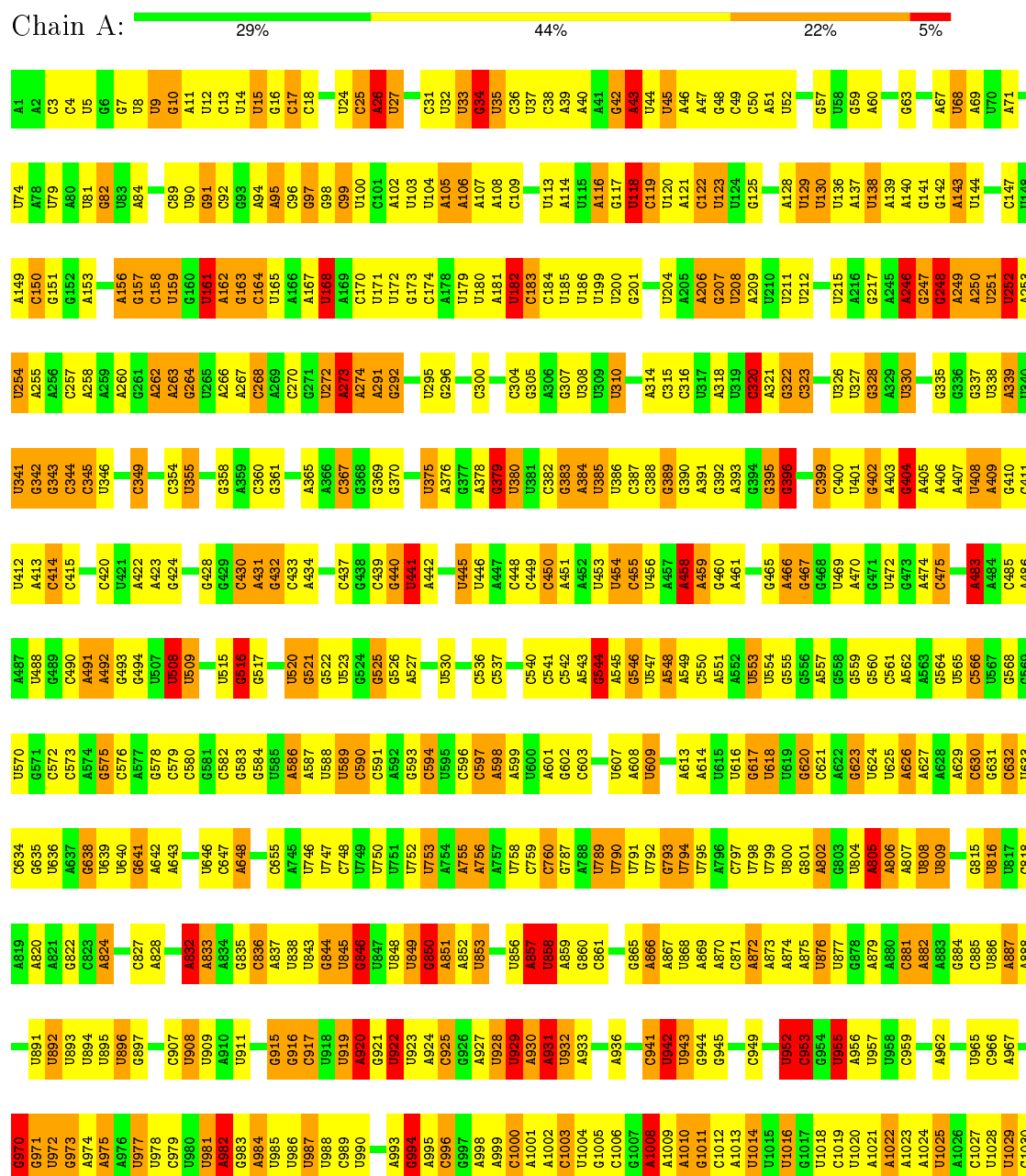
- Molecule 78 is a protein called 60S ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	A0	62	Total	C	N	O	S	0	0
			522	336	97	88	1		

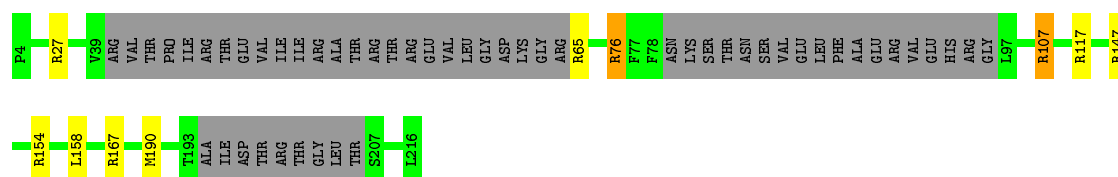
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: 18S ribosomal RNA







- Molecule 4: 40S ribosomal protein uS4

Chain E: 88% 11%



- Molecule 5: 40S ribosomal protein uS5

Chain G: 93% 7%



- Molecule 6: 40S ribosomal protein uS7

Chain I: 87% 5% 5%



- Molecule 7: 40S ribosomal protein uS8

Chain K: 90% 5% 5%



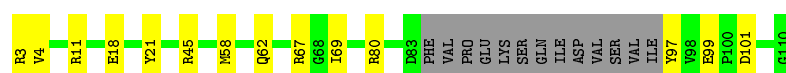
- Molecule 8: 40S ribosomal protein uS9

Chain M: 94% 6%



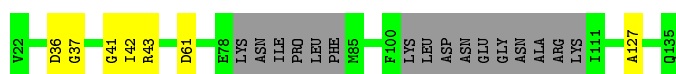
- Molecule 9: 40S ribosomal protein eS17

Chain W: 75% 13% 12%

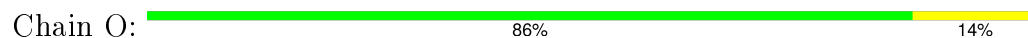


- Molecule 10: 40S ribosomal protein eS12

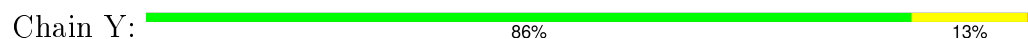
Chain R: 80% 6% 14%



- Molecule 11: 40S ribosomal protein eS10



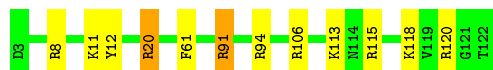
- Molecule 12: 40S ribosomal protein eS19



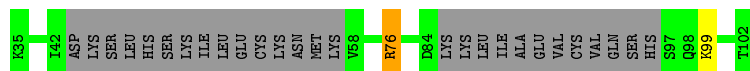
- Molecule 13: 40S ribosomal protein eS21



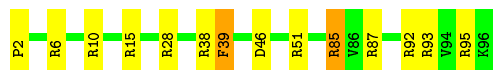
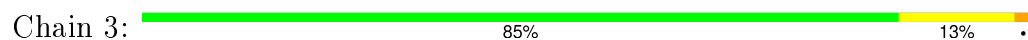
- Molecule 14: 40S ribosomal protein eS24



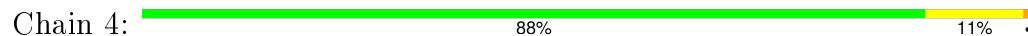
- Molecule 15: 40S ribosomal protein eS25



- Molecule 16: 40S ribosomal protein eS26

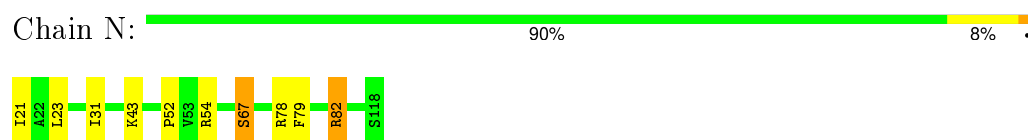


- Molecule 17: 40S ribosomal protein eS27

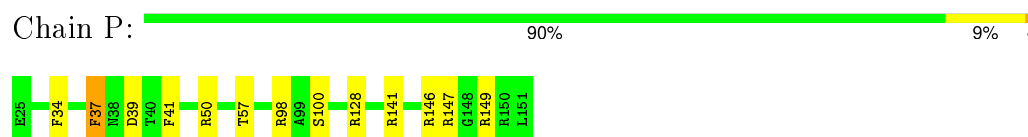


- |     |     |     |     |     |     |     |     |     |     |     |     |      |      |      |      |      |      |      |      |      |     |     |      |      |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|-----|-----|------|------|------|
| ASP | GLU | THR | THR | LYS | THR | TYR | GLY | VAL | ILE | LYS | LYS | I162 | I168 | D169 | F176 | R188 | E201 | G202 | R210 | D213 | LYS | LYS | K216 | K217 | N218 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|-----|-----|------|------|------|

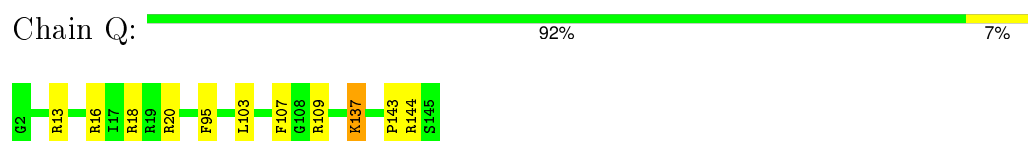
- Molecule 25: 40S ribosomal protein uS10



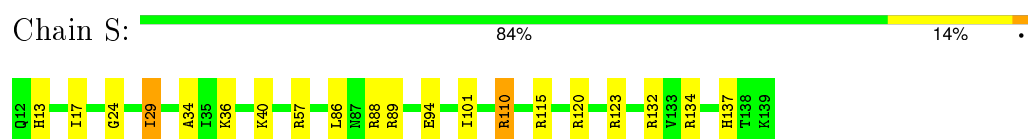
- Molecule 26: 40S ribosomal protein uS11



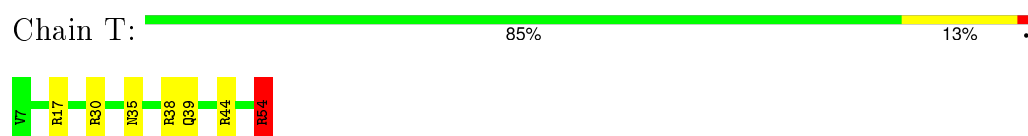
- Molecule 27: 40S ribosomal protein uS12



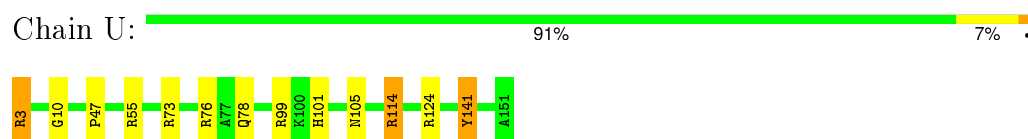
- Molecule 28: 40S ribosomal protein uS13



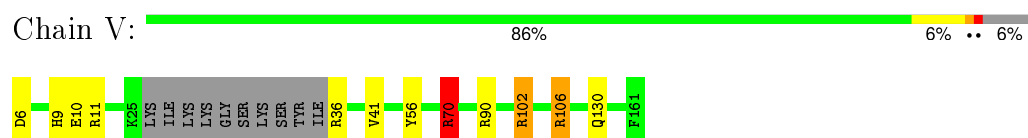
- Molecule 29: 40S ribosomal protein uS14




- Molecule 30: 40S ribosomal protein uS15

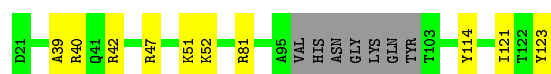


- Molecule 31: 40S ribosomal protein uS17




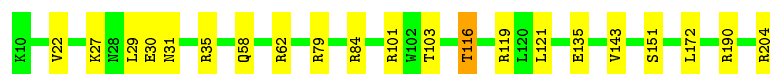
- Molecule 32: 40S ribosomal protein uS19

Chain X: 



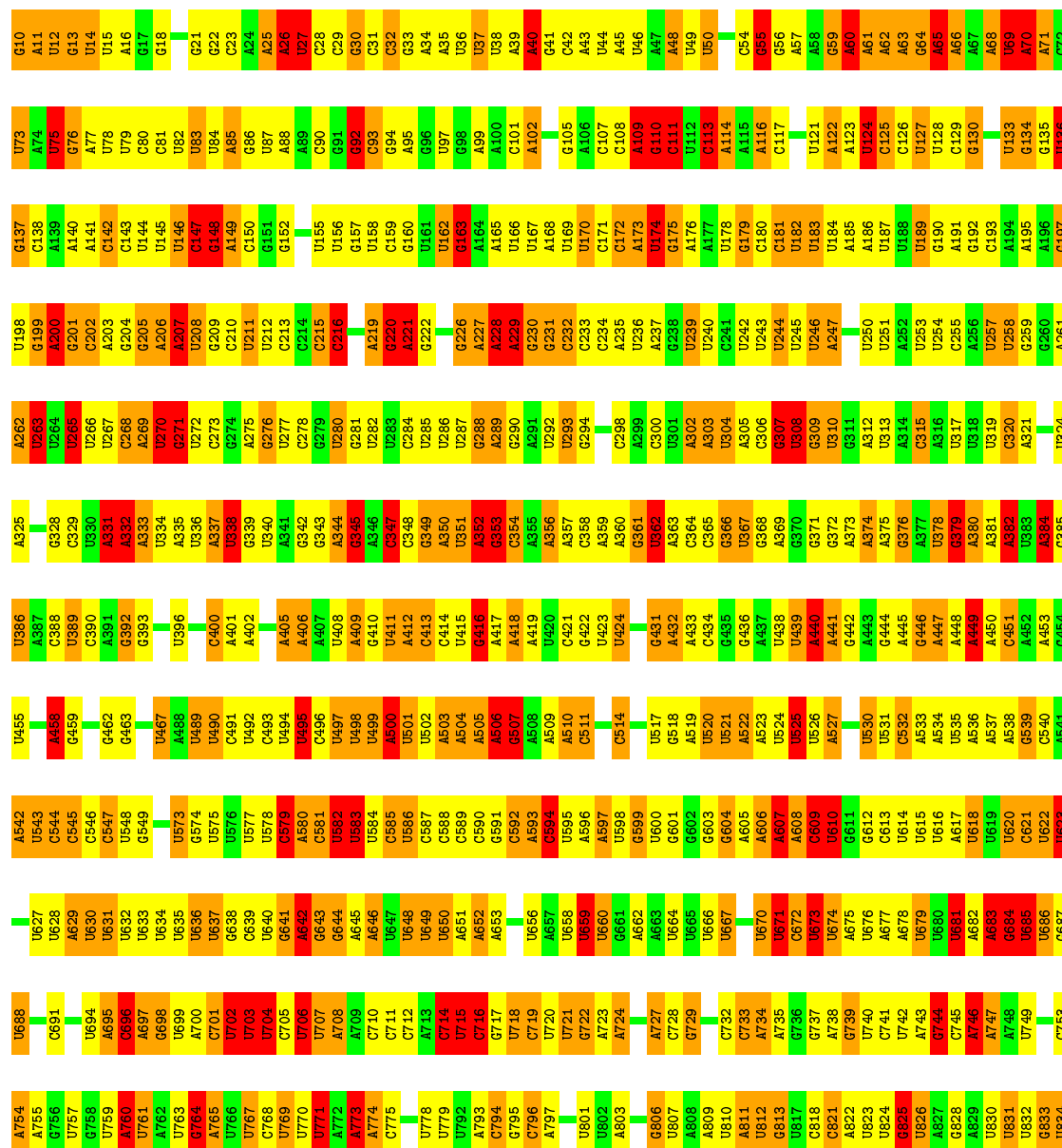
- Molecule 33: 40S ribosomal protein uS2

Chain C: 



- Molecule 34: 28S ribosomal RNA

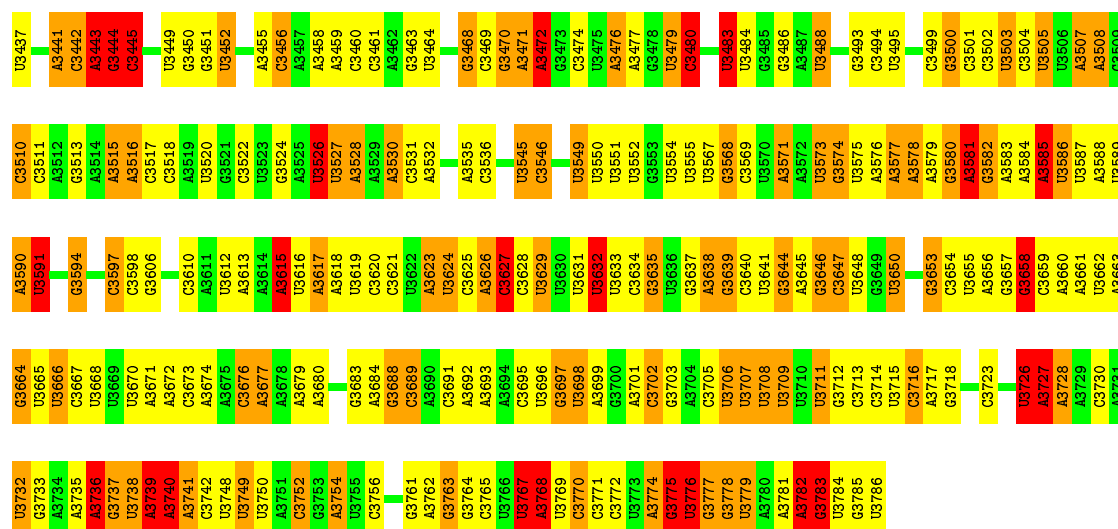
Chain AA: 





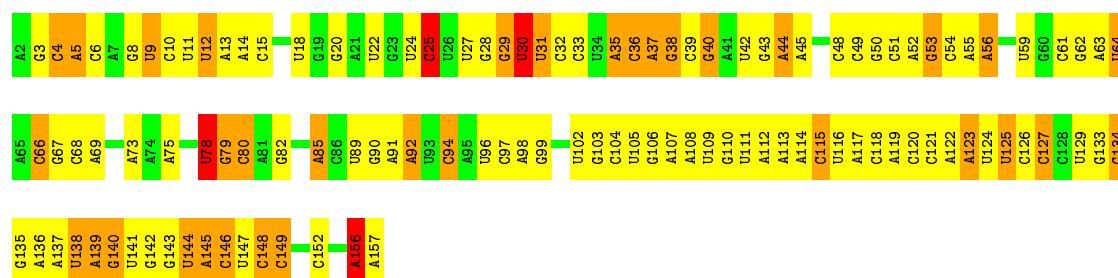
U1973	C1866	U1800	A1732	U1661	G1593	A1522	G1447	A1318	U1252	C1192	C1112	G1048	A984	C921	G885
U1974	U1867	G1662	G1733	G1663	A1594	A1523	G1448	U1319	U1253	C1193	C1113	C1049	G985	C922	C886
A1975	U1868	A1663	G1734	A1664	A1595	U1524	G1449	G1320	G1254	G1193	A1114	C1050	G986	C923	C887
A1976	C1804	A1664	G1735	A1665	G1596	C1525	G1450	A1321	G1255	G1194	G1115	C1051	U987	G924	C888
U1977	A1871	A1805	A1736	A1666	U1597	G1526	A1451	U1324	U1256	A1196	U1116	U1053	G988	A925	C889
U1978	A1872	A1806	A1737	A1667	A1598	G1529	U1452	C1325	A1257	A1197	U1117	U1054	A989	A926	A860
C1979	C1807	C1807	A1738	A1667	G1599	G1530	U1453	C1326	U1258	U1198	A1118	A1055	U990	A927	C861
G1980	U1808	G1668	C1739	G1668	C1600	G1531	U1454	C1327	G1259	A1199	G1119	G1056	A991	G928	U862
U1981	U1809	A1669	A1740	A1669	A1601	U1534	U1456	A1328	G1260	A1200	C1120	U1057	C992	G929	G865
A1982	G1741	U1670	G1742	U1671	A1602	U1535	G1457	U1329	A1263	U1201	G1121	U1058	G993	U931	C866
U1983	G1742	C1603	G1743	G1672	C1604	G1536	A1458	A1330	A1264	C1202	U1123	G1060	A995	U932	G869
A1984	U1743	U1604	U1744	A1673	A1605	U1536	U1459	A1331	C1265	A1203	U1124	U1061	C996	U933	A869
U1985	U1745	C1675	G1746	C1676	U1606	G1537	A1460	A1332	U1266	A1204	A1125	U1062	G997	G934	C870
A1986	C1746	C1677	G1747	C1677	U1607	U1538	C1461	A1333	C1269	U1205	U1126	U1063	U998	A935	U873
U1987	U1748	C1678	U1749	C1679	G1608	A1540	C1462	A1334	C1270	U1206	U1130	U1064	G999	A936	A874
A1988	U1819	U1679	G1750	C1680	G1613	G1541	C1466	U1336	U1272	U1207	U1131	U1065	A1001	U938	C875
U1989	A1820	C1681	C1751	C1681	A1614	A1542	C1467	G1337	G1273	U1208	G1132	U1066	A1002	U939	C876
G2000	U1821	G1682	C1752	G1682	G1615	C1543	U1468	U1338	G1276	A1210	U1004	C1068	A1003	G941	U879
G2001	A1822	A1683	G1753	A1683	A1616	A1548	A1473	G1340	A1277	U1211	G1135	C1069	G942	G948	A880
G2002	C1823	A1684	G1754	A1684	C1617	U1549	A1474	G1341	A1278	U1212	A1136	A1070	G943	G943	A881
G2003	A1824	C1685	G1755	C1685	C1618	A1550	U1475	U1342	U1279	U1213	C1139	A1071	G944	G945	G882
U2004	C1825	G1686	U1756	G1686	U1619	C1551	A1476	U1343	G1280	A1214	A1140	A1072	G946	U1008	C883
A2005	U1826	G1687	G1757	C1687	G1620	C1552	U1477	C1344	C1281	A1215	G1141	G1073	U947	U1009	A884
G2008	C1827	A1688	C1758	G1688	G1621	U1553	A1478	U1345	U1282	U1217	G1143	U1075	G949	G949	A885
A2009	G1828	U1689	U1760	C1689	A1625	G1554	U1479	A1346	C1283	U1218	C1154	C1076	A948	A948	A888
G2010	A1829	A1690	G1761	A1690	A1626	U1555	G1480	U1347	A1284	U1219	U1156	U1077	G950	G950	U889
U2011	C1830	G1691	A1762	G1691	C1627	G1556	A1481	U1415	U1285	A1220	C1014	C1018	A951	A951	G890
G2012	A1831	C1692	G1770	A1692	U1628	A1555	U1482	U1416	U1286	A1221	U1157	U1079	U952	U952	C891
U2013	U1832	G1693	U1771	G1693	G1630	G1556	A1484	U1417	A1287	U1222	G1158	C1080	U953	U953	U892
C2014	A1833	C1694	U1766	A1694	A1631	U1560	U1485	A1418	C1288	U1223	A1159	A1081	G954	G954	U893
U2015	G1834	A1695	U1767	A1695	A1632	C1561	U1486	A1419	G1289	U1224	C1160	A1082	A955	A955	U894
G2016	U1835	A1696	A1768	A1696	G1633	G1564	U1487	C1420	C1290	A1225	C1161	A1084	A956	A956	A895
U2017	G1836	A1697	U1769	A1697	G1634	U1565	U1488	U1421	U1291	A1226	U1164	U1085	G957	G957	U896
G2018	U1837	G1698	G1770	A1698	G1635	G1566	U1489	A1422	G1294	A1229	U1165	C1086	U958	U958	U897
A2019	U1838	A1699	U1771	G1699	A1636	A1567	U1490	C1423	U1295	A1230	C1166	G1087	U959	U959	G898
A2020	U1839	U1700	G1772	U1701	G1637	A1568	U1491	C1424	U1296	A1231	U1167	C1088	C963	C963	A899
A2021	C1840	G1702	U1773	G1702	G1640	A1569	U1492	C1425	U1297	A1232	U1168	A1091	G964	G964	U901
A2022	U1841	U1703	U1774	U1703	G1641	A1570	U1493	U1427	A1298	A1233	C1169	A1092	A965	A965	A902
G2030	U1842	U1704	A1775	A1704	G1642	C1572	U1494	G1428	G1299	A1234	A1170	A1093	A966	A966	G903
C2033	G1843	A1705	U1782	A1705	U1643	C1573	A1501	A1429	G1300	A1235	C1171	U1094	G967	G967	G904
G2034	C1844	U1706	G1783	U1706	U1644	C1574	G1502	A1430	U1301	U1236	C1172	G1095	G968	G968	A905
C2035	A1845	G1784	U1784	G1784	U1645	C1575	A1503	A1431	C1302	C1237	U1173	C1030	U969	U969	G906
C2036	U1846	U1785	U1785	U1785	U1646	U1576	A1504	A1432	C1303	C1238	C1174	G1031	C970	C970	C907
U2037	U1847	A1786	U1786	A1786	U1647	A1577	C1505	G1433	C1304	A1239	C1175	A1032	U971	U971	A908
U2041	U1848	U1787	C1787	U1787	U1648	G1578	U1507	G1434	U1305	A1240	C1176	A1000	G972	G972	U909
G2068	A1851	C1788	U1788	A1788	U1649	C1579	U1508	A1436	A1306	G1241	A1177	A1101	A973	A973	A910
C2069	C1852	G1712	U1789	U1789	U1650	G1583	U1509	U1437	A1307	U1242	A1178	U1102	U974	U974	U911
U2070	U1853	C1723	U1790	C1723	C1651	A1584	U1510	G1438	C1308	G1243	U1179	A1103	G975	G975	U912
U2071	G1854	G1724	U1791	U1791	U1652	U1585	U1511	U1439	U1309	G1244	C1183	U1104	A976	A976	U913
U2072	U1855	U1725	U1792	U1725	C1654	C1586	A1512	C1440	A1310	G1245	U1184	A1105	G977	G977	G914
U2073	A1856	C1726	U1793	A1726	U1655	U1587	U1513	G1441	U1311	C1246	A1185	A1106	G978	G978	G915
A2075	U1857	U1727	U1794	U1727	G1656	U1588	U1514	C1442	U1312	G1247	U1186	U1107	U1041	U1041	U916
U2076	C1861	C1728	U1795	C1728	U1657	G1589	U1515	U1443	C1313	A1248	A1187	U1108	A980	A980	A917
U2077	U1861	A1729	U1796	A1729	G1658	G1590	U1516	U1444	G1314	U1249	U1188	U1109	G981	G981	G918
A2079	U1862	U1730	U1797	U1730	U1660	U1591	U1517	A1445	C1315	U1251	A1189	U1110	C982	C982	G919
	C1865	A1731	U1799	A1731	U1661	G1592	U1518	A1446			G1189	A1111	A1047	A1047	A920

A3373	G3302	C3240	A3172	U3109	C3046	U2977	A2834	G2705	C2639	A2572	A2506	A2442	U2148	C2080
A3374	U3303	U3241	G3173	A3110	U3047	A2978	G2835	A2706	U2640	A2573	A2507	G2443	A2149	U2081
A3375	G3304	C3242	G3174	U3111	U3048	U2979	G2836	G2707	C2643	A2574	C2508	C2444		C2082
A3376	A3305	C3243	G3175	U3112	U3049	U2980	G2837	G2708	C2643	U2575	U2509	A2445	A2152	U2083
A3377	G3306	C3244	A3176	U3113	U3050	A2981	A2838	U2709	U2644	C2576	U2510	U2446	A2153	U2084
A3378	C3307	U3245	G3114	G3115	U3051	A2982	U2883	U2710		C2577	G2514		A2154	
A3379	U3308	A3246	C3180	C3115	U3052	G2983	G2884	U2711	G2647	C2578	U2515	U2449	A2155	C2089
U3380	G3309	U3247	U3181	G3116	G3053	G2984	A2885	A2712	G2648	U2579	A2516	G2450	A2156	U2090
A3381		C3248	A3117	A3117	A3054	C2985	A2886	C2713	A2649	C2580	U2517	U2221	G2157	U2091
A3382	U3312	A3249	G3183	A3118	U3055	U2986	U2887	U2714		G2581	A2517	A2386	U2158	G2092
A3383	U3313		C3184	A3119	U3056	G2987	U2888	C2715	C2652	U2582	U2518	A2387	A2159	U2093
G3384	U3314	G3253	U3185	U3120	U3057	U2988	U2889	U2716	C2653	C2583	U2519	U2388	A2160	U2094
U3385	A3315	G3254	U3186	G3121	U3058	G2990	C2916		A2654	C2520	G2520	G2389	G2161	A2095
A3386	G3316	A3255	G3187	A3122	U3059	U2991	C2917	C2720	C2655	A2521	C2456	U2390	U2162	G2096
U3387	C3317	C3256	U3188	C3123		C2992	C2918		A2656	U2587	C2457			A2097
U3388	G3318	G3257	G3189	G3124	U3062	C2993	C2919	G2723	G2657	A2588	A2458	A2393		G2098
G3389	C3319	C3258	G3190	U3125	U3063	A2994	A2920	C2724	C2658	A2589	C2459	C2394	G2166	C2099
U3390	U3320	A3259	C3184	A3126	U3064	U2995	U2925		C2659	U2590	A2460	U2395	G2167	
G3391	U3321	G3260	A3127	A3127	C3065	A2996	A2926	U2727	A2660	U2591	A2526	A2461	A2168	A2102
A3392	C3322	A3261	G3193	A3128	A3066	G2997	U2927	G2728	A2661	A2592	C2463	C2463	A2169	C2103
C3393	G3323	C3262	C3194	U3130	G3067	C2998	U2928	G2730	G2662	G2593	G2464	U2402	U2170	C2104
A3394	U3324	G3263	A3195	A3131	A3068	C2999			G2664	U2594	G2465	U2402	U2171	A2105
G3395	G3325	U3264		A3132	A3069	A3000	A2932		A2665	A2596	G2466	A2404	G2172	A2106
	A3326	C3265	G3198	C3132	C3070	G3001	C2933	G2734	A2666	C2597	U2467	A2404	G2173	C2107
A3396	U3327	U3266	C3199	U3133	A3071	G3002	A2934	G2735	C2667	C2598	U2468	A2405	C2175	A2108
A3397	G3328	C3267	G3200	U3134	A3072	C3003		A2736						A2109
A3400	C3329	A3268	C3201	A3135	G3073		C2938	C2737	G2668	C2599	C2472	G2408	A2177	C2110
A3401	A3330	A3269	U3202	C3136	U3074	C3005	C2939	U2738	C2669	C2600	C2473	G2409	A2178	C2111
A3402	G3331	G3270	C3203	U3137	A3075				G2670	C2601	C2474	G2410	C2113	C2112
A3403	G3332	A3271	G3204	A3138	C3076	A3008	G2942	G2744	U2673	U2602	C2541	C2411	U2180	C2113
A3404	U3333	U3272	U3205	C3139			U2943	G2745	A2674	G2604	G2542	A2412	A2181	U2115
U3405	U3334	G3273		U3140	A3079	A3013	G2944	U2746	U2675	A2605	G2543	A2413	A2182	C2116
U3406	A3335	U3274	C3208	G3141	A3080	C3014	G2945	G2747	G2674	C2606	G2544	G2414	G2183	C2117
G3407	G3336	C3275	C3209	U3142	C3081	A3015	G2946	U2748	C2675	A2607	U2545	G2415	U2184	G2118
G3408	U3337	G3276	A3210	G3143		G3016	G2947	U2802	C2676	G2607		G2416	C2185	
U3409	U3338	C3277	C3211	C3144	A3084	A3017	U2948	A2803		G2608	A2481		C2186	C2121
A3410	G3339	A3278	G3212	A3145	G3085	A3018	G2949	C2804	U2679	U2611	A2548	U2482	G2187	U2122
C3411		U3279	U2213	U3146	A3086	A3019	U2950	U2805	U2680	U2612	A2549	U2483	G2188	C2123
G3412	U3340	U3280		A3147	A3087	U3020	U2951	U2806	U2681	U2613	C2550	U2484	U2189	C2124
A3413	C3343	G3281	C3216	U3148	C3088	C3021	G2952	U2807	C2682	A2614	U2551	C2421	A2190	C2125
A3414	C3344	U3282		A3149	C3089	U3022	G2953	U2808	A2683	C2615	U2553	C2422	C2191	A2126
A3415		U3283	U3219		G3090	C3023	A2954	A2809	U2684	C2615	G2554	C2423	U2192	G2127
G3416	C3347	A3284	U3220	G3153	U3091	U3024	C2955	A2810	C2685	G2618	A2555	C2424	U2193	G2128
G3417	U3348	U3221	G3222	G3155	G3092	U3025	U2956	A2811	C2686		C2556	U2425	C2194	
U3418	A3350	C3286		G3156	G3093	G3026	G2957	G2812				U2426		
U3419	U3351	C3287	C3225	C3157	C3094	U3027	G2958	U2813	G2689	U2621	U2557	A2491		A2131
A3421	G3352	G3289	C3226	U3158	C3095	A3028	G2959	U2814	A2690	C2622	C2558	G2492	G2197	A2132
G3422	A3353	C3290		G3159	U3096	G3029	G2960	G2815		C2623	U2559	U2493	A2198	C2133
		U3291	C3229	A3160	U3098	A3030	C2961	U2816	G2693	C2624	C2560	G2494	A2199	A2134
	U3356	A3292		A3161	C3099	C3031	U2962	U2817	A2694	A2625	U2561	C2495	A2200	G2135
U3427	U3357	A3293	G3230		C3099	U3032	A2967		A2695	U2562	U2496	A2432	A2201	C2136
U3428	U3358	C3294	A3231	G3164	G3100	A3033	U2968	C2821	G2696	U2627	U2497	U2433	G2202	C2137
C3429	A3359	U3232	U3101	U3165	A3101	A3034	C2969	U2822	A2697	G2628	A2564	U2498	U2138	U2139
G3430	G3360	G3233	G3233	U3166	U3102	A3035	U2970	U2823	C2698	U2629	U2565	U2499	A2204	C2139
A3431	U3361	U3234	U3234	A3167	C3103	A3036	G2971	G2824	C2699	C2630	A2500	A2436	U2205	U2140
A3432	U3362	C3235	C3235	G3236	C3104	G3037	U2972	U2825	C2700	U2567	A2501	A2437	U2206	G2141
C3433	A3363	G3236		C3168	U3105	G3038	U2973	C2826	U2701	A2566	U2502	A2438	G2207	
A3434	U3364	G3237	U3237	C3169	U3106	U3038	A2974		G2702	C2569	G2503	C2439	C2208	A2145
U3435	A3365	U3107	U3107	A3044	U3107	A3044	A2975	A2832	U2703	C2570	U2504	A2440	C2209	A2146
U3436		C3301	U3239	G3045	A3108	G3045	A2976	U2833	U2704		C2505		U2210	A2147



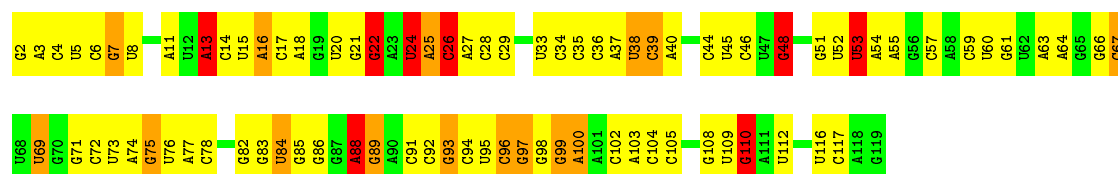
- Molecule 35: 5.8S ribosomal RNA

Chain AC: 24% 51% 23% .



- Molecule 36: 5S ribosomal RNA

Chain AB: 29% 52% 13% 7%



- Molecule 37: 60S ribosomal protein eL13

Chain AL: 92% 7% .



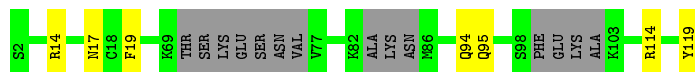
- Molecule 38: 60S ribosomal protein eL27

Chain A1: 89% 8% .



- Molecule 39: 60S ribosomal protein eL28

Chain A2: 82% 6% 12%



- Molecule 40: 60S ribosomal protein eL29

Chain A4: 86% 8% 5%



- Molecule 41: 60S ribosomal protein eL30

Chain A6: 90% 8% ..



- Molecule 42: 60S ribosomal protein eL31

Chain A7: 86% 8% 6%



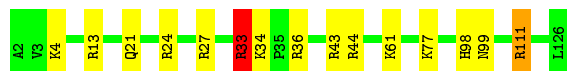
- Molecule 43: 60S ribosomal protein eL14

Chain AN: 90% 8% ..



- Molecule 44: 60S ribosomal protein eL32

Chain A8: 88% 10% ..

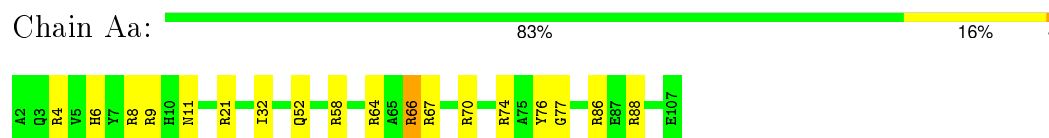


- Molecule 45: 60S ribosomal protein eL33

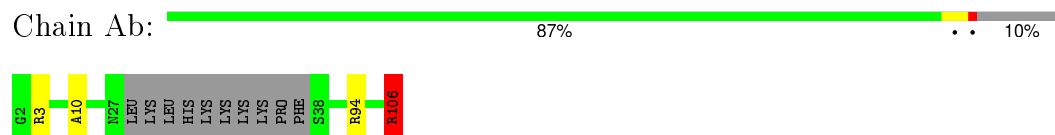
Chain A9: 88% 9% ..



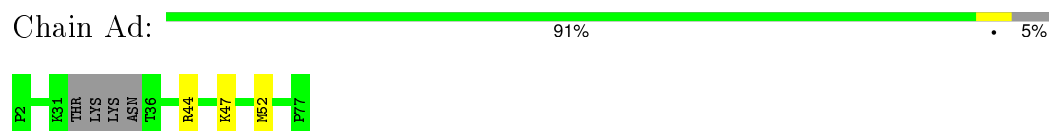
- Molecule 46: 60S ribosomal protein eL34



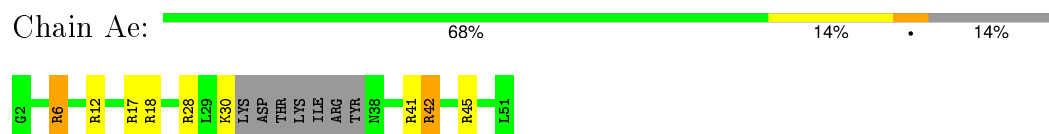
- Molecule 47: 60S ribosomal protein eL36



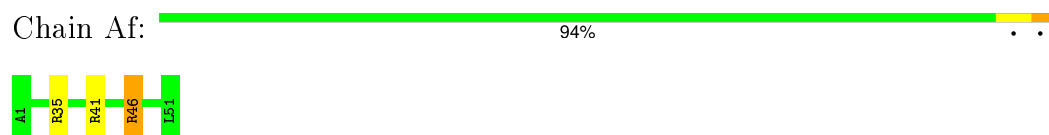
- Molecule 48: 60S ribosomal protein eL38



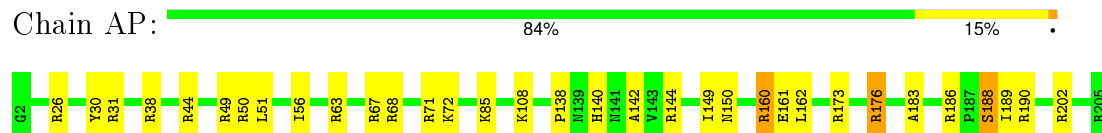
- Molecule 49: 60S ribosomal protein eL39



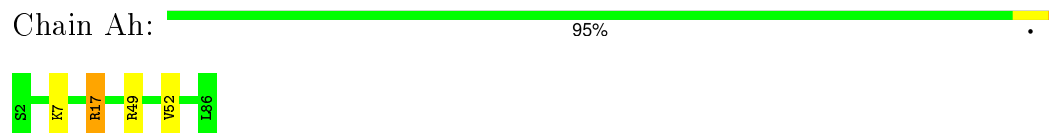
- Molecule 50: 60S ribosomal protein eL40



- Molecule 51: 60S ribosomal protein eL15

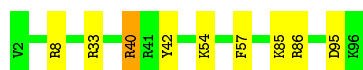


- Molecule 52: 60S ribosomal protein eL43



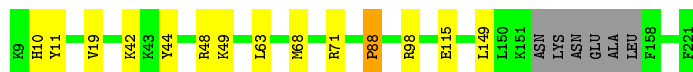
- Molecule 53: 60S ribosomal protein eL44

Chain Ai:  91% 8%

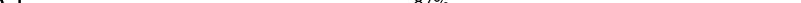


- Molecule 54: 60S ribosomal protein eL6

Chain AI:  91% 6% .




- Molecule 55: 60S ribosomal protein eL8

Chain AJ:  87% 9%



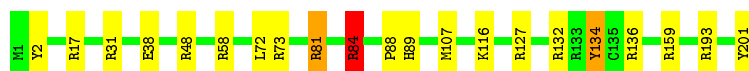
- Molecule 56: 60S ribosomal protein eL37

Chain Ac: 



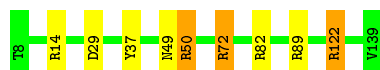
- Molecule 57: 60S ribosomal protein uL13

Chain AK:  90% 9%

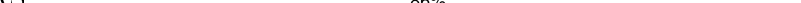


- Molecule 58: 60S ribosomal protein uL14

Chain AM:  93% 5%



- Molecule 59: 60S ribosomal protein eL18

Chain AS:  86% 12%



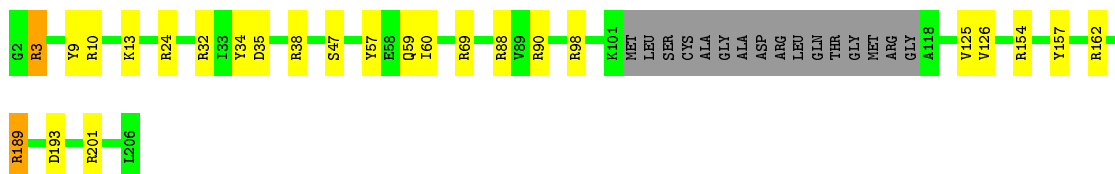
- Molecule 60: 60S ribosomal protein uL15

Chain AO:  89% 10%



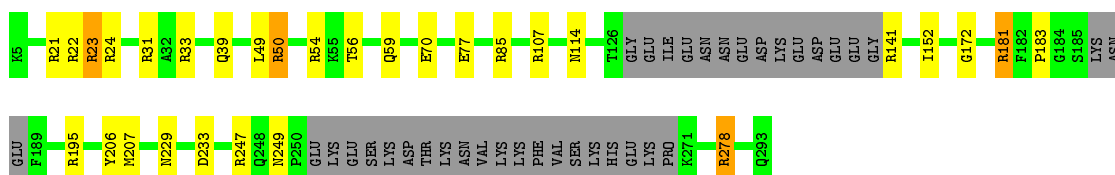
- Molecule 61: 60S ribosomal protein uL16

Chain AQ: 80% 11% 8%



- Molecule 62: 60S ribosomal protein uL18

Chain AR: 77% 9% 13%



- Molecule 63: 60S ribosomal protein uL22

Chain AW: 88% 9% 3%



- Molecule 64: 60S ribosomal protein uL23

Chain AY: 94% 5% 1%



- Molecule 65: 60S ribosomal protein eL19

Chain AT: 91% 8% 1%



- Molecule 66: 60S ribosomal protein uL24

Chain AZ: 93% 5% 2%




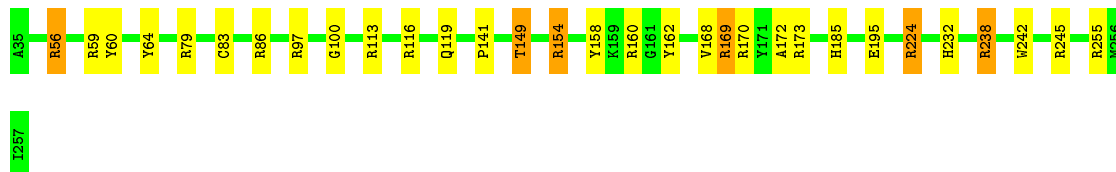
- Molecule 67: 60S ribosomal protein uL29

Chain A3:  92% 8%



- Molecule 68: 60S ribosomal protein uL30

Chain A5:  86% 11%



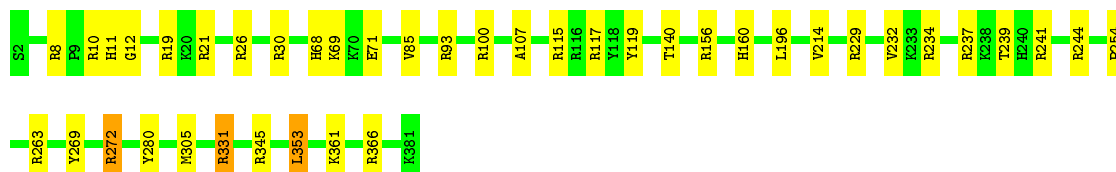
- Molecule 69: 60S ribosomal protein uL2

Chain AD:  89% 9%



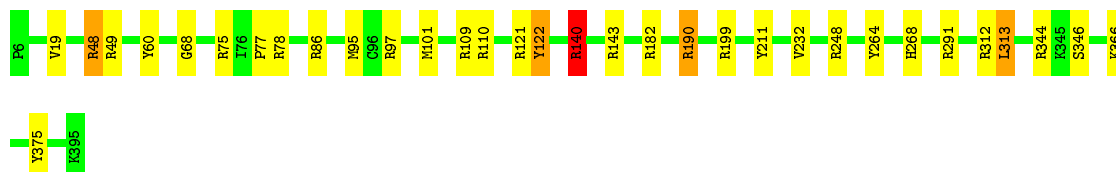
- Molecule 70: 60S ribosomal protein uL3

Chain AE:  89% 10%



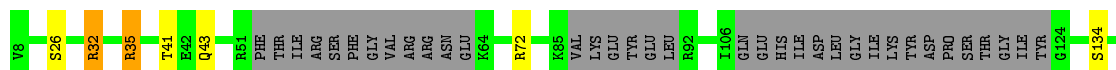
- Molecule 71: 60S ribosomal protein uL4

Chain AF:  92% 7%



- Molecule 72: 60S ribosomal protein uL5

Chain AG:  70% 6% 22%







- Molecule 73: 60S ribosomal protein eL20

Chain AU: 88% 7% . .



- Molecule 74: 60S ribosomal protein uL6

Chain AH: 91% 8% .



- Molecule 75: 60S ribosomal protein eL21

Chain AV: 89% 10% .



- Molecule 76: 60S ribosomal protein eL41

Chain Ag: 76% 16% 8%



- Molecule 77: 60S ribosomal protein eL22

Chain AX: 94% 6%



- Molecule 78: 60S ribosomal protein eL24

Chain A0: 92% 6% .



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	96732	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Each micrograph	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	25	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	23000	Depositor
Image detector	GATAN K2 (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	1.23	26/38275 (0.1%)	1.58	870/59596 (1.5%)
10	R	0.74	0/755	1.06	0/1013
11	O	0.72	0/706	1.03	3/950 (0.3%)
12	Y	0.70	0/1295	1.18	9/1742 (0.5%)
13	Z	0.70	0/565	1.08	2/758 (0.3%)
14	1	0.70	0/999	1.17	11/1321 (0.8%)
15	2	0.75	0/324	0.98	1/435 (0.2%)
16	3	0.71	0/794	1.24	10/1055 (0.9%)
17	4	0.68	0/597	1.09	0/801
18	5	0.75	0/459	1.33	9/606 (1.5%)
19	6	0.73	0/349	1.24	3/458 (0.7%)
2	7	1.23	4/1754 (0.2%)	1.79	69/2732 (2.5%)
20	B	0.65	0/1738	1.11	9/2321 (0.4%)
21	F	0.67	0/2098	1.14	11/2819 (0.4%)
22	H	0.67	0/1665	1.10	5/2210 (0.2%)
23	J	0.68	0/1545	1.07	7/2064 (0.3%)
24	L	0.71	0/1407	1.23	16/1879 (0.9%)
25	N	0.70	0/780	1.24	7/1053 (0.7%)
26	P	0.70	0/966	1.23	8/1295 (0.6%)
27	Q	0.69	0/1149	1.25	11/1532 (0.7%)
28	S	0.65	0/1063	1.27	11/1425 (0.8%)
29	T	0.73	0/412	1.25	6/544 (1.1%)
3	D	0.75	0/1241	1.13	10/1652 (0.6%)
30	U	0.67	0/1223	1.14	9/1634 (0.6%)
31	V	0.71	0/1233	1.10	4/1645 (0.2%)
32	X	0.71	0/788	1.18	7/1050 (0.7%)
33	C	0.67	0/1570	1.08	4/2129 (0.2%)
34	AA	1.30	70/75947 (0.1%)	1.59	1892/118255 (1.6%)
35	AC	1.30	7/3599 (0.2%)	1.55	88/5603 (1.6%)
36	AB	1.27	2/2823 (0.1%)	1.52	57/4400 (1.3%)
37	AL	0.67	0/1789	1.14	9/2381 (0.4%)
38	A1	0.68	0/1151	1.02	1/1531 (0.1%)
39	A2	0.72	0/840	1.01	3/1114 (0.3%)
4	E	0.70	0/1539	1.16	13/2055 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
40	A4	0.66	0/564	1.01	3/737 (0.4%)
41	A6	0.69	0/749	0.99	2/1001 (0.2%)
42	A7	0.70	0/806	1.14	3/1073 (0.3%)
43	AN	0.69	0/1218	1.12	6/1621 (0.4%)
44	A8	0.70	0/1054	1.24	10/1399 (0.7%)
45	A9	0.72	0/865	1.20	7/1160 (0.6%)
46	Aa	0.68	0/872	1.26	11/1161 (0.9%)
47	Ab	0.71	0/763	1.13	5/1008 (0.5%)
48	Ad	0.72	0/612	1.09	2/812 (0.2%)
49	Ae	0.75	0/396	1.41	6/521 (1.2%)
5	G	0.70	0/1800	1.01	5/2429 (0.2%)
50	Af	0.67	0/419	1.16	3/556 (0.5%)
51	AP	0.69	0/1735	1.31	21/2320 (0.9%)
52	Ah	0.68	0/668	1.13	2/887 (0.2%)
53	Ai	0.67	0/789	1.16	6/1032 (0.6%)
54	AI	0.66	0/1708	1.04	6/2274 (0.3%)
55	AJ	0.67	0/1840	1.03	3/2456 (0.1%)
56	Ac	0.72	0/723	1.29	8/951 (0.8%)
57	AK	0.67	0/1690	1.15	13/2260 (0.6%)
58	AM	0.68	0/1012	1.15	5/1363 (0.4%)
59	AS	0.69	0/1531	1.24	17/2040 (0.8%)
6	I	0.69	0/1443	1.22	15/1936 (0.8%)
60	AO	0.66	0/1199	1.18	10/1597 (0.6%)
61	AQ	0.73	0/1580	1.21	16/2113 (0.8%)
62	AR	0.68	0/2079	1.16	20/2777 (0.7%)
63	AW	0.68	0/1244	1.22	12/1663 (0.7%)
64	AY	0.67	0/806	1.15	5/1074 (0.5%)
65	AT	0.66	0/1525	1.17	15/2016 (0.7%)
66	AZ	0.68	0/1013	1.17	9/1339 (0.7%)
67	A3	0.65	0/1005	1.09	8/1329 (0.6%)
68	A5	0.70	0/1917	1.25	22/2562 (0.9%)
69	AD	0.68	0/1902	1.19	17/2544 (0.7%)
7	K	0.70	0/1054	1.15	10/1411 (0.7%)
70	AE	0.68	0/3130	1.16	25/4195 (0.6%)
71	AF	0.68	0/3145	1.16	23/4205 (0.5%)
72	AG	0.73	0/1021	1.19	9/1349 (0.7%)
73	AU	0.70	0/1527	1.18	15/2043 (0.7%)
74	AH	0.69	0/1501	1.17	10/2025 (0.5%)
75	AV	0.68	0/1301	1.20	11/1732 (0.6%)
76	Ag	0.74	0/348	1.57	8/448 (1.8%)
77	AX	0.72	0/842	1.06	3/1125 (0.3%)
78	A0	0.73	0/534	1.12	4/711 (0.6%)
8	M	0.71	0/1114	1.12	4/1487 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 2$	RMSZ	$\# Z  > 2$
9	W	0.71	0/793	1.18	4/1053 (0.4%)
All	All	1.07	109/207275 (0.1%)	1.44	3594/303853 (1.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	231
11	O	0	1
12	Y	0	6
14	1	0	2
15	2	0	1
16	3	0	2
17	4	0	3
19	6	0	2
2	7	0	18
20	B	0	4
21	F	0	5
22	H	0	3
23	J	0	5
24	L	0	3
25	N	0	1
26	P	0	3
27	Q	0	2
29	T	0	1
3	D	0	1
30	U	0	2
31	V	0	6
32	X	0	1
33	C	0	6
34	AA	1	546
35	AC	0	19
36	AB	0	14
37	AL	0	5
38	A1	0	1
39	A2	0	1
4	E	0	6
40	A4	0	2
41	A6	0	4
42	A7	0	1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	#Chirality outliers	#Planarity outliers
43	AN	0	3
44	A8	0	2
45	A9	0	2
46	Aa	0	4
47	Ab	0	1
49	Ae	0	5
5	G	0	4
50	Af	0	2
51	AP	0	6
52	Ah	0	2
53	Ai	0	3
54	AI	0	2
55	AJ	0	2
56	Ac	0	3
57	AK	0	5
58	AM	0	5
59	AS	0	8
6	I	0	4
60	AO	0	3
61	AQ	0	4
62	AR	0	4
63	AW	0	6
64	AY	0	1
65	AT	0	6
66	AZ	0	4
67	A3	0	1
68	A5	0	7
69	AD	0	6
7	K	0	2
70	AE	0	4
71	AF	0	6
72	AG	0	3
73	AU	0	7
74	AH	0	3
75	AV	0	5
76	Ag	0	2
77	AX	0	1
78	A0	0	2
8	M	0	1
9	W	0	3
All	All	1	1052

The worst 5 of 109 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	AA	2552	A	N9-C4	-8.94	1.32	1.37
2	7	74	A	C4'-C3'	8.62	1.62	1.53
34	AA	275	A	O3'-P	-7.93	1.51	1.61
34	AA	3122	A	N9-C4	-7.49	1.33	1.37
1	A	2055	A	N9-C4	-7.09	1.33	1.37

The worst 5 of 3594 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	3632	U	P-O5'-C5'	19.68	152.39	120.90
34	AA	257	U	P-O3'-C3'	18.75	142.20	119.70
34	AA	181	C	P-O3'-C3'	15.57	138.38	119.70
34	AA	3018	A	P-O3'-C3'	15.30	138.06	119.70
2	7	74	A	C5'-C4'-O4'	-14.85	91.28	109.10

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
34	AA	3018	A	C3'

5 of 1052 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	14	U	Sidechain
1	A	15	U	Sidechain
1	A	5	U	Sidechain
1	A	8	U	Sidechain
1	A	9	U	Sidechain

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	34207	0	17266	123	0
2	7	1571	0	797	12	0
3	D	1229	0	1311	0	0
4	E	1515	0	1605	2	0
5	G	1758	0	1811	1	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	I	1424	0	1471	0	0
7	K	1037	0	1099	2	0
8	M	1099	0	1183	1	0
9	W	786	0	858	1	0
10	R	747	0	754	0	0
11	O	687	0	695	0	0
12	Y	1267	0	1316	1	0
13	Z	557	0	558	0	0
14	1	986	0	1076	0	0
15	2	321	0	338	0	0
16	3	782	0	820	0	0
17	4	586	0	604	1	0
18	5	458	0	496	0	0
19	6	346	0	381	0	0
20	B	1714	0	1838	0	0
21	F	2062	0	2200	3	0
22	H	1648	0	1803	0	0
23	J	1529	0	1680	0	0
24	L	1383	0	1434	3	0
25	N	772	0	813	1	0
26	P	954	0	997	0	0
27	Q	1129	0	1196	0	0
28	S	1047	0	1101	2	0
29	T	405	0	419	0	0
30	U	1202	0	1299	1	0
31	V	1206	0	1239	1	0
32	X	777	0	832	1	0
33	C	1539	0	1600	1	0
34	AA	67884	0	34244	322	0
35	AC	3215	0	1633	8	0
36	AB	2522	0	1275	9	0
37	AL	1757	0	1888	0	0
38	A1	1134	0	1245	2	0
39	A2	831	0	887	1	0
40	A4	555	0	599	4	0
41	A6	741	0	763	1	0
42	A7	794	0	869	2	0
43	AN	1202	0	1316	2	0
44	A8	1037	0	1139	2	0
45	A9	845	0	886	3	0
46	Aa	859	0	912	0	0
47	Ab	757	0	842	0	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	Ad	604	0	686	0	0
49	Ae	388	0	421	0	0
50	Af	414	0	452	0	0
51	AP	1697	0	1802	2	0
52	Ah	659	0	727	0	0
53	Ai	779	0	861	0	0
54	AI	1685	0	1849	0	0
55	AJ	1813	0	1985	1	0
56	Ac	710	0	761	0	0
57	AK	1660	0	1785	2	0
58	AM	996	0	1044	0	0
59	AS	1503	0	1636	1	0
60	AO	1172	0	1230	3	0
61	AQ	1545	0	1582	0	0
62	AR	2050	0	2140	1	0
63	AW	1319	0	1304	1	0
64	AY	797	0	850	0	0
65	AT	1509	0	1682	0	0
66	AZ	1001	0	1099	0	0
67	A3	995	0	1121	0	0
68	A5	1879	0	2005	3	0
69	AD	1867	0	1964	4	0
70	AE	3062	0	3205	5	0
71	AF	3095	0	3333	1	0
72	AG	1011	0	1073	1	0
73	AU	1497	0	1556	2	0
74	AH	1476	0	1574	2	0
75	AV	1276	0	1355	0	0
76	Ag	343	0	388	0	0
77	AX	825	0	882	0	0
78	A0	522	0	539	0	0
All	All	193012	0	144279	522	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 2.

The worst 5 of 522 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)
70:AE:353:LEU:H	70:AE:353:LEU:HD23	1.55	0.71
34:AA:3632:U:H3	34:AA:3653:G:H1	1.42	0.65

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:123:A:H3'	34:AA:124:U:H5''	1.81	0.62
34:AA:744:G:H1	34:AA:915:G:H1	1.47	0.62
34:AA:642:A:C6	34:AA:684:G:C8	2.89	0.61

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	
3	D	149/209 (71%)	142 (95%)	7 (5%)	0	100	100
4	E	183/185 (99%)	171 (93%)	11 (6%)	1 (0%)	34	77
5	G	222/224 (99%)	204 (92%)	16 (7%)	2 (1%)	21	67
6	I	176/189 (93%)	165 (94%)	9 (5%)	2 (1%)	17	63
7	K	127/129 (98%)	113 (89%)	9 (7%)	5 (4%)	4	36
8	M	136/138 (99%)	125 (92%)	9 (7%)	2 (2%)	13	57
9	W	91/108 (84%)	82 (90%)	6 (7%)	3 (3%)	5	40
10	R	92/114 (81%)	80 (87%)	7 (8%)	5 (5%)	2	29
11	O	77/79 (98%)	69 (90%)	5 (6%)	3 (4%)	4	36
12	Y	152/154 (99%)	145 (95%)	4 (3%)	3 (2%)	9	51
13	Z	70/72 (97%)	64 (91%)	5 (7%)	1 (1%)	14	58
14	1	118/120 (98%)	112 (95%)	5 (4%)	1 (1%)	24	69
15	2	35/68 (52%)	33 (94%)	2 (6%)	0	100	100
16	3	93/95 (98%)	82 (88%)	10 (11%)	1 (1%)	17	63
17	4	74/76 (97%)	62 (84%)	8 (11%)	4 (5%)	2	29
18	5	54/65 (83%)	53 (98%)	1 (2%)	0	100	100
19	6	41/43 (95%)	33 (80%)	7 (17%)	1 (2%)	7	47

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	B	208/210 (99%)	189 (91%)	11 (5%)	8 (4%)	4	37
21	F	255/257 (99%)	232 (91%)	18 (7%)	5 (2%)	9	51
22	H	200/214 (94%)	187 (94%)	10 (5%)	3 (2%)	13	57
23	J	186/188 (99%)	169 (91%)	9 (5%)	8 (4%)	3	34
24	L	165/214 (77%)	146 (88%)	14 (8%)	5 (3%)	5	42
25	N	96/98 (98%)	90 (94%)	4 (4%)	2 (2%)	9	50
26	P	125/127 (98%)	109 (87%)	13 (10%)	3 (2%)	7	47
27	Q	142/144 (99%)	127 (89%)	13 (9%)	2 (1%)	14	58
28	S	126/128 (98%)	107 (85%)	12 (10%)	7 (6%)	2	28
29	T	46/48 (96%)	45 (98%)	1 (2%)	0	100	100
30	U	147/149 (99%)	141 (96%)	4 (3%)	2 (1%)	14	58
31	V	142/156 (91%)	128 (90%)	11 (8%)	3 (2%)	9	50
32	X	92/103 (89%)	78 (85%)	11 (12%)	3 (3%)	5	40
33	C	193/195 (99%)	171 (89%)	17 (9%)	5 (3%)	7	45
37	AL	209/211 (99%)	191 (91%)	14 (7%)	4 (2%)	10	52
38	A1	136/145 (94%)	125 (92%)	8 (6%)	3 (2%)	8	49
39	A2	96/118 (81%)	90 (94%)	4 (4%)	2 (2%)	9	50
40	A4	64/66 (97%)	60 (94%)	1 (2%)	3 (5%)	3	32
41	A6	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
42	A7	92/102 (90%)	87 (95%)	5 (5%)	0	100	100
43	AN	144/146 (99%)	137 (95%)	5 (4%)	2 (1%)	14	58
44	A8	123/125 (98%)	102 (83%)	21 (17%)	0	100	100
45	A9	101/103 (98%)	92 (91%)	7 (7%)	2 (2%)	9	51
46	Aa	104/106 (98%)	96 (92%)	6 (6%)	2 (2%)	10	52
47	Ab	91/105 (87%)	85 (93%)	5 (6%)	1 (1%)	17	63
48	Ad	68/76 (90%)	65 (96%)	3 (4%)	0	100	100
49	Ae	39/50 (78%)	36 (92%)	3 (8%)	0	100	100
50	Af	49/51 (96%)	43 (88%)	6 (12%)	0	100	100
51	AP	202/204 (99%)	187 (93%)	7 (4%)	8 (4%)	4	35
52	Ah	83/85 (98%)	78 (94%)	4 (5%)	1 (1%)	16	61
53	Ai	93/95 (98%)	87 (94%)	4 (4%)	2 (2%)	8	49

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	AI	203/213 (95%)	183 (90%)	17 (8%)	3 (2%)	13	57
55	AJ	216/244 (88%)	202 (94%)	12 (6%)	2 (1%)	21	67
56	Ac	87/89 (98%)	76 (87%)	7 (8%)	4 (5%)	3	32
57	AK	199/201 (99%)	192 (96%)	5 (2%)	2 (1%)	19	65
58	AM	130/132 (98%)	123 (95%)	7 (5%)	0	100	100
59	AS	184/186 (99%)	168 (91%)	14 (8%)	2 (1%)	17	63
60	AO	145/147 (99%)	132 (91%)	12 (8%)	1 (1%)	26	71
61	AQ	185/205 (90%)	161 (87%)	19 (10%)	5 (3%)	6	45
62	AR	244/289 (84%)	224 (92%)	13 (5%)	7 (3%)	6	43
63	AW	149/170 (88%)	133 (89%)	10 (7%)	6 (4%)	4	35
64	AY	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	19	65
65	AT	179/181 (99%)	171 (96%)	5 (3%)	3 (2%)	11	55
66	AZ	119/121 (98%)	110 (92%)	7 (6%)	2 (2%)	11	55
67	A3	117/119 (98%)	107 (92%)	9 (8%)	1 (1%)	21	67
68	A5	221/223 (99%)	195 (88%)	21 (10%)	5 (2%)	8	48
69	AD	245/247 (99%)	223 (91%)	20 (8%)	2 (1%)	24	69
70	AE	378/380 (100%)	353 (93%)	21 (6%)	4 (1%)	17	63
71	AF	388/390 (100%)	356 (92%)	26 (7%)	6 (2%)	13	57
72	AG	116/159 (73%)	104 (90%)	11 (10%)	1 (1%)	21	67
73	AU	178/180 (99%)	169 (95%)	6 (3%)	3 (2%)	11	55
74	AH	183/185 (99%)	166 (91%)	14 (8%)	3 (2%)	12	56
75	AV	153/155 (99%)	141 (92%)	9 (6%)	3 (2%)	9	51
76	Ag	35/37 (95%)	30 (86%)	3 (9%)	2 (6%)	2	27
77	AX	95/97 (98%)	88 (93%)	5 (5%)	2 (2%)	9	50
78	A0	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
All	All	10111/10698 (94%)	9269 (92%)	652 (6%)	190 (2%)	14	52

5 of 190 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	I	42	HIS
6	I	70	HIS
8	M	41	GLU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
9	W	4	VAL
10	R	42	ILE

### 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	
3	D	132/177 (75%)	128 (97%)	4 (3%)	48	77
4	E	161/164 (98%)	156 (97%)	5 (3%)	47	77
5	G	191/191 (100%)	185 (97%)	6 (3%)	47	77
6	I	154/160 (96%)	151 (98%)	3 (2%)	65	86
7	K	115/115 (100%)	113 (98%)	2 (2%)	68	87
8	M	116/116 (100%)	115 (99%)	1 (1%)	84	93
9	W	86/99 (87%)	83 (96%)	3 (4%)	43	74
10	R	83/97 (86%)	81 (98%)	2 (2%)	57	82
11	O	76/76 (100%)	71 (93%)	5 (7%)	21	57
12	Y	137/137 (100%)	132 (96%)	5 (4%)	42	74
13	Z	60/60 (100%)	59 (98%)	1 (2%)	68	87
14	1	104/104 (100%)	100 (96%)	4 (4%)	40	73
15	2	35/61 (57%)	34 (97%)	1 (3%)	50	78
16	3	87/87 (100%)	83 (95%)	4 (5%)	33	68
17	4	70/70 (100%)	69 (99%)	1 (1%)	74	89
18	5	47/52 (90%)	46 (98%)	1 (2%)	61	84
19	6	36/36 (100%)	35 (97%)	1 (3%)	51	78
20	B	195/195 (100%)	191 (98%)	4 (2%)	61	84
21	F	233/233 (100%)	223 (96%)	10 (4%)	35	70
22	H	182/190 (96%)	173 (95%)	9 (5%)	31	66
23	J	177/177 (100%)	171 (97%)	6 (3%)	44	75
24	L	151/190 (80%)	144 (95%)	7 (5%)	33	68

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	N	91/91 (100%)	89 (98%)	2 (2%)	60	83
26	P	99/99 (100%)	97 (98%)	2 (2%)	63	85
27	Q	120/120 (100%)	119 (99%)	1 (1%)	86	94
28	S	114/114 (100%)	109 (96%)	5 (4%)	35	69
29	T	43/43 (100%)	40 (93%)	3 (7%)	19	56
30	U	132/132 (100%)	129 (98%)	3 (2%)	58	82
31	V	131/140 (94%)	128 (98%)	3 (2%)	58	82
32	X	88/94 (94%)	88 (100%)	0	100	100
33	C	167/167 (100%)	161 (96%)	6 (4%)	42	74
37	AL	190/190 (100%)	188 (99%)	2 (1%)	80	91
38	A1	127/131 (97%)	124 (98%)	3 (2%)	57	82
39	A2	97/109 (89%)	96 (99%)	1 (1%)	82	92
40	A4	60/60 (100%)	57 (95%)	3 (5%)	30	66
41	A6	83/83 (100%)	76 (92%)	7 (8%)	14	48
42	A7	90/96 (94%)	87 (97%)	3 (3%)	45	76
43	AN	135/135 (100%)	130 (96%)	5 (4%)	41	73
44	A8	114/114 (100%)	108 (95%)	6 (5%)	28	64
45	A9	90/90 (100%)	86 (96%)	4 (4%)	35	69
46	Aa	89/89 (100%)	85 (96%)	4 (4%)	34	69
47	Ab	82/92 (89%)	81 (99%)	1 (1%)	78	90
48	Ad	69/73 (94%)	68 (99%)	1 (1%)	74	89
49	Ae	40/47 (85%)	38 (95%)	2 (5%)	30	66
50	Af	45/45 (100%)	45 (100%)	0	100	100
51	AP	179/179 (100%)	175 (98%)	4 (2%)	60	83
52	Ah	70/70 (100%)	70 (100%)	0	100	100
53	Ai	87/87 (100%)	87 (100%)	0	100	100
54	AI	189/195 (97%)	183 (97%)	6 (3%)	46	76
55	AJ	204/224 (91%)	200 (98%)	4 (2%)	63	85
56	Ac	74/74 (100%)	68 (92%)	6 (8%)	15	49
57	AK	181/181 (100%)	178 (98%)	3 (2%)	68	87
58	AM	106/106 (100%)	104 (98%)	2 (2%)	65	86

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	AS	158/158 (100%)	151 (96%)	7 (4%)	35	69
60	AO	121/121 (100%)	119 (98%)	2 (2%)	68	87
61	AQ	165/176 (94%)	160 (97%)	5 (3%)	48	77
62	AR	215/250 (86%)	208 (97%)	7 (3%)	45	76
63	AW	128/128 (100%)	126 (98%)	2 (2%)	70	88
64	AY	90/90 (100%)	88 (98%)	2 (2%)	60	83
65	AT	162/162 (100%)	161 (99%)	1 (1%)	90	95
66	AZ	111/111 (100%)	111 (100%)	0	100	100
67	A3	110/110 (100%)	108 (98%)	2 (2%)	66	87
68	A5	201/201 (100%)	196 (98%)	5 (2%)	55	81
69	AD	191/191 (100%)	185 (97%)	6 (3%)	47	77
70	AE	335/335 (100%)	329 (98%)	6 (2%)	66	87
71	AF	336/336 (100%)	327 (97%)	9 (3%)	52	79
72	AG	110/142 (78%)	106 (96%)	4 (4%)	42	74
73	AU	162/162 (100%)	158 (98%)	4 (2%)	55	81
74	AH	168/168 (100%)	164 (98%)	4 (2%)	57	82
75	AV	140/140 (100%)	137 (98%)	3 (2%)	61	84
76	Ag	34/34 (100%)	33 (97%)	1 (3%)	50	78
77	AX	92/92 (100%)	91 (99%)	1 (1%)	80	91
78	A0	53/53 (100%)	52 (98%)	1 (2%)	65	86
All	All	9096/9417 (97%)	8847 (97%)	249 (3%)	56	79

5 of 249 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	A1	86	GLN
44	A8	77	LYS
71	AF	366	LYS
39	A2	94	GLN
42	A7	52	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
42	A7	29	HIS
52	Ah	34	HIS
73	AU	97	HIS
43	AN	130	GLN
44	A8	98	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1588/1608 (98%)	476 (29%)	86 (5%)
2	7	73/74 (98%)	23 (31%)	3 (4%)
34	AA	3167/3193 (99%)	966 (30%)	190 (5%)
35	AC	148/151 (98%)	51 (34%)	6 (4%)
36	AB	117/118 (99%)	28 (23%)	4 (3%)
All	All	5093/5144 (99%)	1544 (30%)	289 (5%)

5 of 1544 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	17	C
1	A	25	C
1	A	26	A
1	A	27	U
1	A	34	G

5 of 289 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	AA	620	U
34	AA	1078	C
34	AA	3627	C
34	AA	652	A
34	AA	721	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 [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](#)

There are no chain breaks in this entry.