



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:38 PM BST

PDB ID : 3JBN  
EMDB ID: : EMD-6456  
Title : Cryo-electron microscopy reconstruction of the Plasmodium falciparum 80S ribosome bound to P-tRNA  
Authors : Sun, M.; Li, W.; Blomqvist, K.; Das, S.; Hashem, Y.; Dvorin, J.D.; Frank, J.  
Deposited on : 2015-09-16  
Resolution : 4.70 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>

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

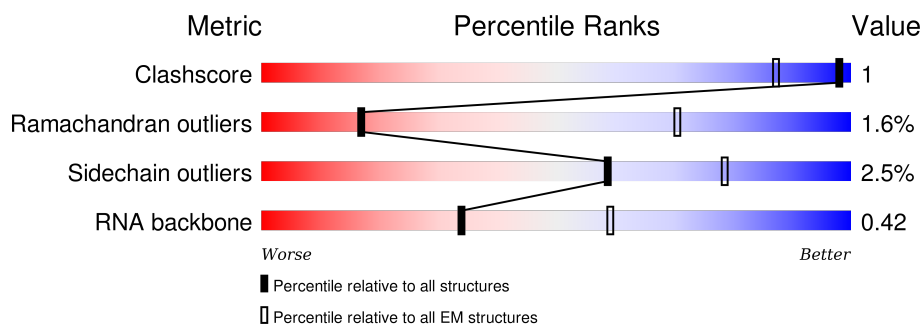
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.70 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.







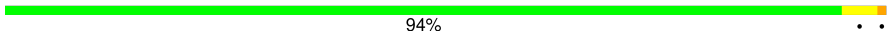
















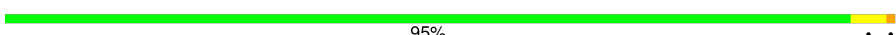



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	34% 45% 19% .
2	7	76	28% 49% 20% .
3	D	209	72% . 25%
4	E	185	88% 12% .
5	G	224	93% 5% .
6	I	189	88% 5% . 5%
7	K	129	89% 10% .
8	M	138	90% 9% .


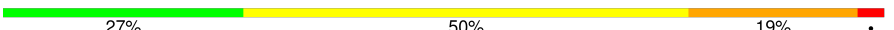








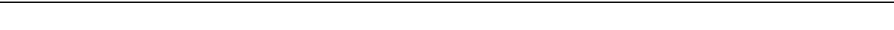

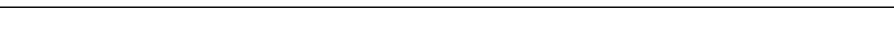
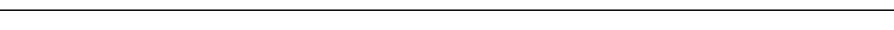



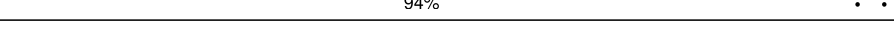

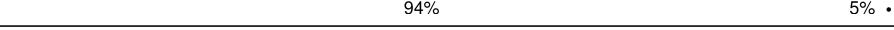





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Mol	Chain	Length	Quality of chain
9	W	108	
10	R	114	
11	O	79	
12	Y	154	
13	Z	72	
14	1	120	
15	2	68	
16	3	95	
17	4	76	
18	5	65	
19	6	43	
20	B	210	
21	F	257	
22	H	214	
23	J	188	
24	L	214	
25	N	98	
26	P	127	
27	Q	144	
28	S	128	
29	T	48	
30	U	149	
31	V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











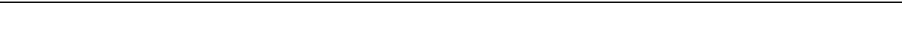

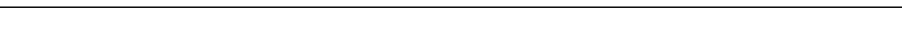
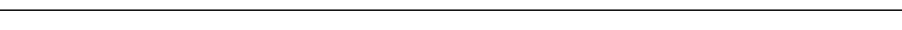
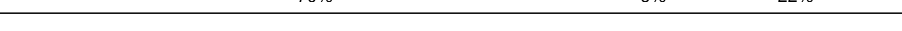




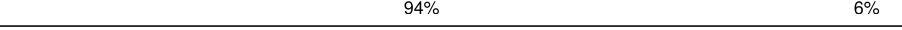
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Mol	Chain	Length	Quality of chain
34	AA	3193	
35	AC	151	
36	AB	118	
37	AL	211	
38	A1	145	
39	A2	118	
40	A4	66	
41	A6	98	
42	A7	102	
43	AN	146	
44	A8	125	
45	A9	103	
46	Aa	106	
47	Ab	105	
48	Ad	76	
49	Ae	50	
50	Af	51	
51	AP	204	
52	Ah	85	
53	Ai	95	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

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Mol	Chain	Length	Quality of chain
59	AS	186	 88% 10% .
60	AO	147	 85% 12% ..
61	AQ	205	 80% 11% . 8%
62	AR	289	 77% 9% . 13%
63	AW	170	 89% 8% .
64	AY	101	 95% 5%
65	AT	181	 92% 8% .
66	AZ	121	 88% 9% .
67	A3	119	 92% 8% .
68	A5	223	 88% 10% ..
69	AD	247	 92% 6% .
70	AE	380	 88% 11% .
71	AF	390	 90% 8% ..
72	AG	159	 70% 6% .. 22%
73	AU	180	 89% 8% .
74	AH	185	 91% 8% .
75	AV	155	 88% 11% .
76	Ag	37	 70% 24% 5%
77	AX	97	 94% 6%
78	A0	62	 90% 5% 5%

## 2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 193061 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 P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	76	Total	C	N	O	P	0	0
			1620	723	295	527	75		

- 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		

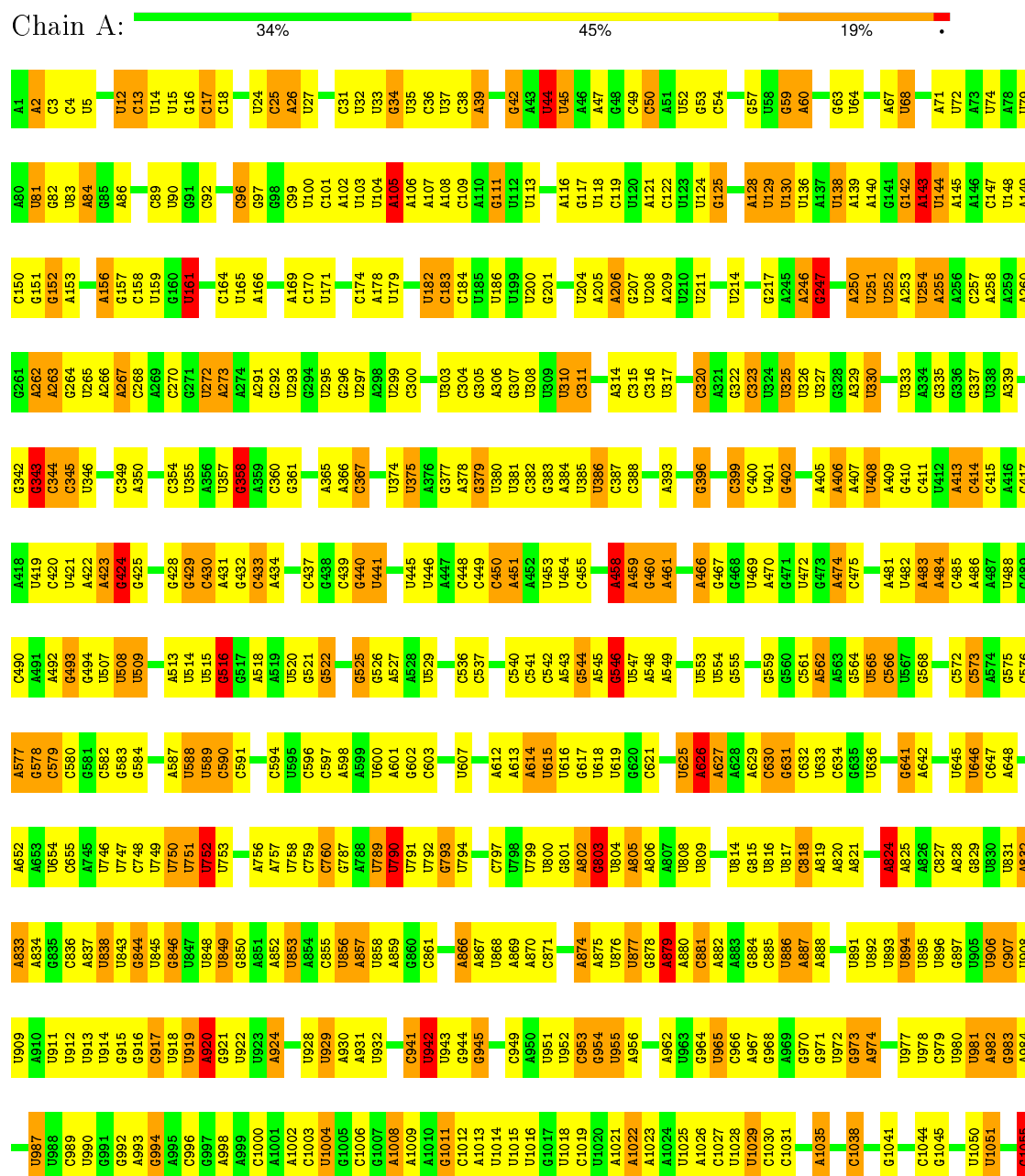
- Molecule 78 is a protein called 60S ribosomal protein eL24.

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

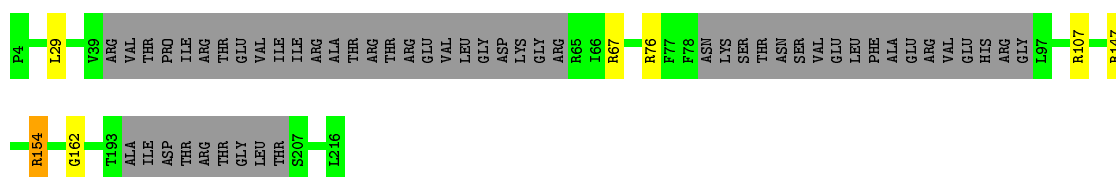
### 3 Residue-property plots

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% 12% •



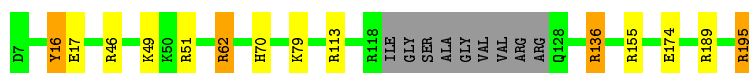
- Molecule 5: 40S ribosomal protein uS5

Chain G: 93% 5% •



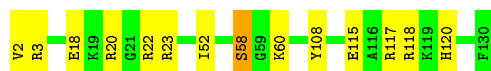
- Molecule 6: 40S ribosomal protein uS7

Chain I: 88% 5% • 5%



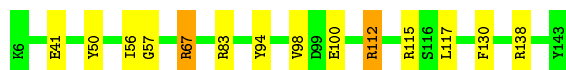
- Molecule 7: 40S ribosomal protein uS8

Chain K: 89% 10% •



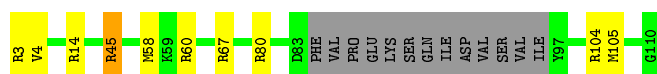
- Molecule 8: 40S ribosomal protein uS9

Chain M: 90% 9% •



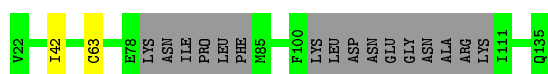
- Molecule 9: 40S ribosomal protein eS17

Chain W: 79% 8% • 12%

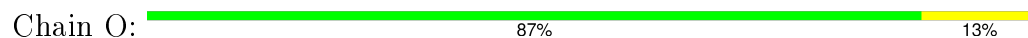


- Molecule 10: 40S ribosomal protein eS12

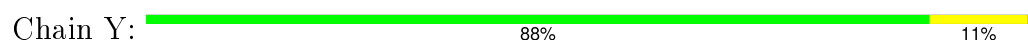
Chain R: 84% • 14%



- Molecule 11: 40S ribosomal protein eS10



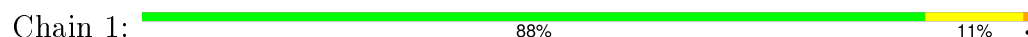
- Molecule 12: 40S ribosomal protein eS19



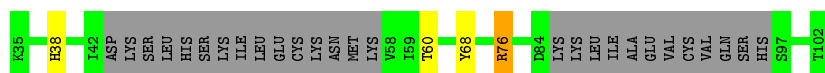
- Molecule 13: 40S ribosomal protein eS21



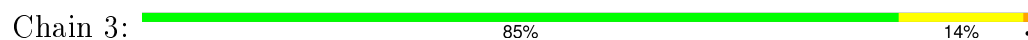
- Molecule 14: 40S ribosomal protein eS24



- Molecule 15: 40S ribosomal protein eS25



- Molecule 16: 40S ribosomal protein eS26



- Molecule 17: 40S ribosomal protein eS27



- 
- | Amino Acid | Information Content (bits) |
|------------|----------------------------|
| THR        | ~0.02                      |
| TYR        | ~0.02                      |
| GLY        | ~0.02                      |
| VAL        | ~0.02                      |
| ILE        | ~0.02                      |
| LYS        | ~0.02                      |
| LYS        | ~0.02                      |
| I162       | ~0.35                      |
| Y198       | ~0.05                      |
| G202       | ~0.02                      |
| R210       | ~0.02                      |
| D213       | ~0.02                      |
| LYS        | ~0.02                      |
| LYS        | ~0.02                      |
| K216       | ~0.02                      |
| R217       | ~0.02                      |
| N218       | ~0.02                      |

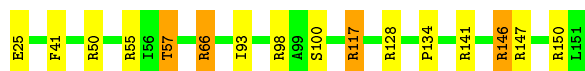
- Molecule 25: 40S ribosomal protein uS10

Chain N:  91% 8%




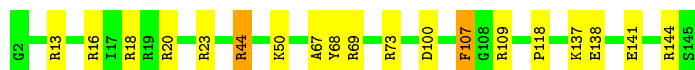
- Molecule 26: 40S ribosomal protein uS11

Chain P:  87% 9%




- Molecule 27: 40S ribosomal protein uS12

Chain Q:  87% 12%




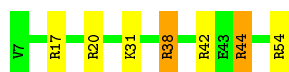
- Molecule 28: 40S ribosomal protein uS13

Chain S:  86% 13%



- Molecule 29: 40S ribosomal protein uS14

Chain T:  85% 10%




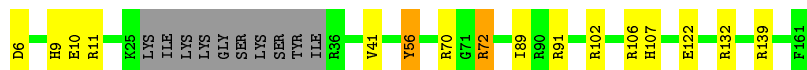
- Molecule 30: 40S ribosomal protein uS15

Chain U:  95%




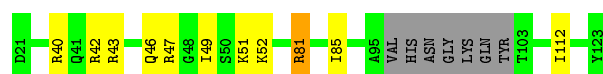
- Molecule 31: 40S ribosomal protein uS17

Chain V:  83% 9% 6%



- Molecule 32: 40S ribosomal protein uS19

Chain X:  83% 10% 7%



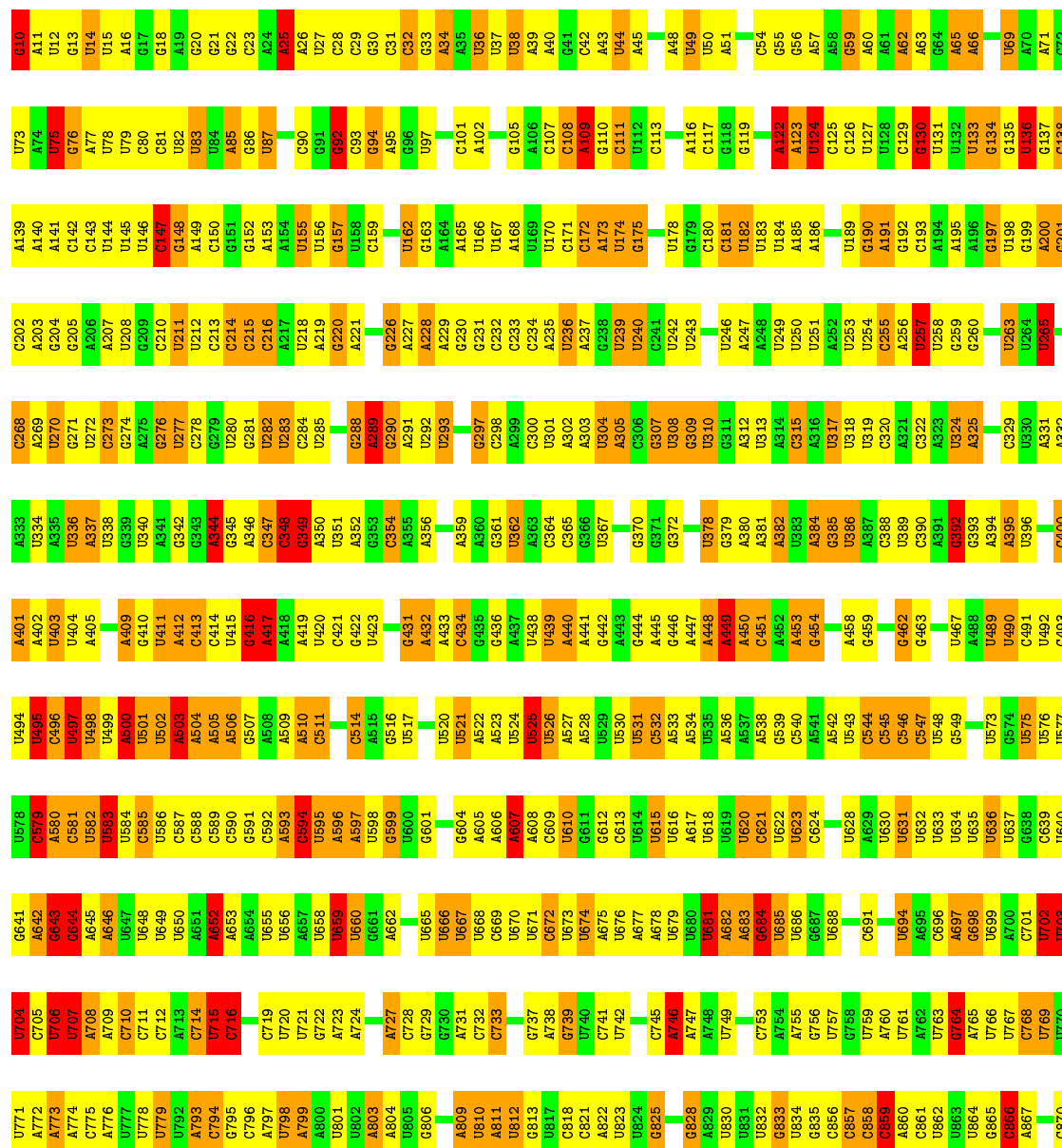
- Molecule 33: 40S ribosomal protein uS2

Chain C:  93% 7%



- Molecule 34: 28S ribosomal RNA

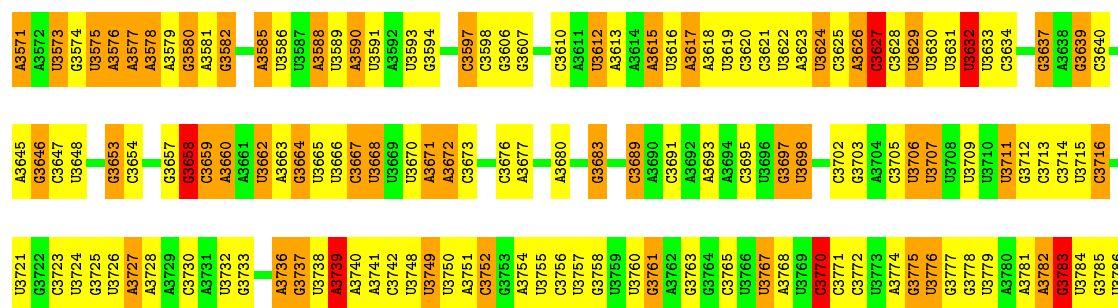
Chain AA:  31% 45% 20%



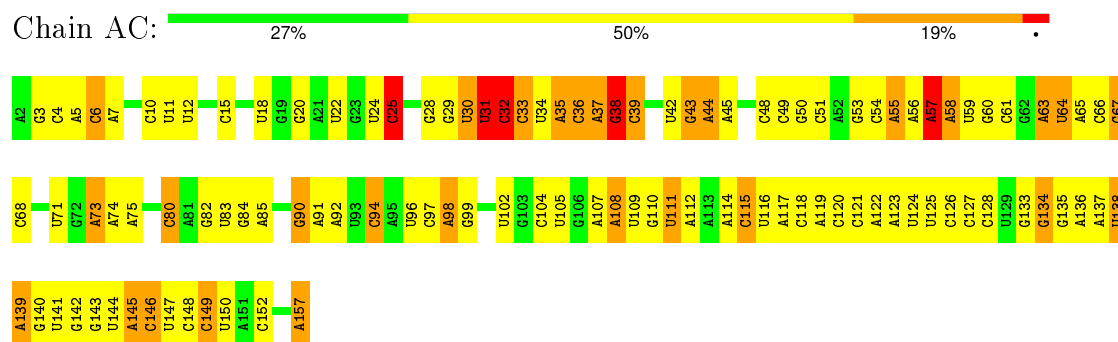


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C2036	A1915	G1844	A1771	A1631	G1564	G1481	U1346	C1283	A1215	C1139	A1070	A1001	U938	A874
U2037	U1957	C1845	G1772	C1632	G1565	A1486	A1415	C1284	U1217	G1143	A1071	C1005	A939	C875
U2041	U1957	A1846	U1773	U1633	A1566	A1486	A1416	U1285	U1218	G1143	G1073	G1006	A940	C876
G2068	U1958	C1847	U1774	G1634	A1567	U1487	A1417	A1286	C1218	C1154	A1074	U1007	G941	
C2069	G1959	U1848	U1775	G1635	C1568	U1493	A1418	A1287	A1219	C1155	G1075	U1008	C942	U879
U2070	U1960	U1849	A1705	A1636	A1569	U1496	U1420	C1288	U1220	U1157	C1076	U1009	G943	A880
U2071	U1961	U1850	A1706	G1637	U1570	U1497	U1421	G1289	A1221	G1158	U1077	G1012	U944	
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U2072	G1852	G1783	G1710	G1642	U1572	U1498	A1422	A1291	A1223	A1159	C1079	U1013	A946	A884
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C2074	U1965	U1785	G1712	U1643	C1574	U1499	C1424	G1293	A1225	C1161	A1081	C1014	G948	A886
U2075	A1966	A1786	G1713	U1644	C1575	G1502	C1425	G1294	A1226	U1162	G1082	A1015	A949	A888
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U2081	A1969	A1857	C1720	C1646	U1580	U1505	G1428	A1298	A1230	U1165	C1086	C1018	U952	C891
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U1994	A1876	C1876	U1738	U1666	G1599	G1526	A1445	C1313	G1245	U1183	U1102	A1033	A967	G906
C1996	A1880	A1880	A1738	U1667	G1600	U1529	A1446	G1314	C1246	U1184	A1103	A1034	G968	C907
G1997	C1881	C1881	C1739	U1668	A1601	G1530	G1447	U1315	C1247	A1184	U1104	G1035	U969	A908
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A2105	G2000	G1885	U1744	U1672	C1603	U1533	G1449	G1320	U1251	A1186	U1107	U1038	U971	A910
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		U1842	A1695	U1628	U1628	A1476	A1476	U1343	G1280	U1212	G1132	C1068	U998	A935
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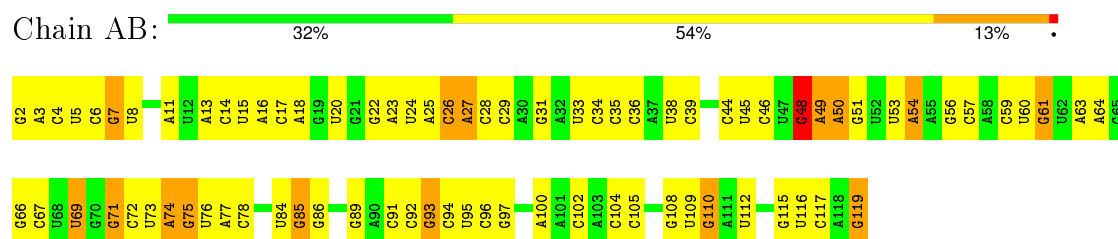
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	A3435	U3361	U3294	G3230	A3161	U3096	G3026	C2955	A2811	A2690	C2624	U2557	U2486	A2412	U2171
U3508	U3436	A3362	A3295	A3231	A3162	A3097	U3027	U2956	G2812	G2693	C2625	C2558	G2487	A2413	C2172
C3510		U3363	G3296	U3232	U3166	U3098	A3028	G2957	U2813	G2694	A2626	U2559	C2488	G2414	G2173
C3511	C3442	A3364	G3297	G3233	A3167	C3099	G3029	C2958	U2814	A2695	U2627	C2560	C2489	G2415	G2174
G3513	A3443	U3365	U3298	U3234	C3168	G3100	A3030	C2959	A2815	G2696	U2628	U2561	C2490	G2416	C2175
A3514	G3444	A3373	C3235	G3235	A3169	A3101	C3031	G2960	U2816	G2697	U2629	A2563			A2176
A3515	C3445	U3374			C3169	C3102	U3032	C2961	U2817	C2698	U2630	A2564	U2498	A2419	A2177
A3516		A3375	G3302	C3238	A3170	C3103	A3033	G2962	U2818	C2699	C2631	A2565	U2499	U2420	
C3517	U3449	U3376	U3303	U3239	C3171	C3104	A3034		U2819	C2708	U2640	C2566	G2499	C2421	U2180
C3518		A3377	G3304	C3240	A3172	U3105	A3035	A2967	A2820	U2709	A2641	C2567	A2500	C2422	
U3452	U3452	C3378	A3305	G3241	G3173	A3106	A3036	C2968	C2821	U2710	U2642	U2575	G2423	C2185	C2185
U3453	U3453	U3379	G3306	U3242	G3174	U3107	G3037	U2969	U2822	G2702	U2643	U2576	U2503	G2195	C2186
C3456	C3456	A3381	C3307	G3243	G3175	A3108	U3038	C2969	U2823	U2703	C2635	C2570	C2425	G2187	G2187
A3457	A3457	U3382	U3308	C3244	A3176	U3109	A3043	U2970		U2704	U2644	C2571	U2504	U2426	
A3458	A3458	A3383	U3309	U3245	U3177	A3110		G2971	C2826	G2705	C2639	A2572	U2505	G2427	C2191
A3459	U3459	U3384	U3312	A3246	A3178	U3111	C3046	U2972	C2827	C2708	U2645	A2573	A2506	U2428	U2192
C3460	C3247	A3179	U3112	U3247	A3179	U3113	U3047			U2709	U2646	A2574	A2507	U2429	U2193
C3461	A3248	C3180	U3114	G3249	C3180	G3114	U3048	A2978	U2833	U2710	U2647	U2575	C2508	U2430	C2194
A3462	A3249	U3181	G3114	A3249	U3181	G3115	G3049	U2979	U2834	U2711	U2648	U2576	U2509		G2195
U3250	U3250	C3184	C3115	U3251	A3185	A3116	U3050	U2980	G2835	A2712	C2643	C2577	U2510	U2434	
G3252	G3252	U3186	A3116	G3253	U3186	A3117	U3051	A2981		C2713	U2644	C2578	G2511	A2435	G2203
G3253	G3253						G3052	A2982	G2836	U2714	C2647	C2579		A2436	A2204
C3256	G3256	C3191	G3121	C3256	C3191	G3122	U3055		U2833	U2715	G2648	C2580	A2515	A2437	U2205
G3257	G3257	U3192	A3122	C3258	G3192	A3123	U3056	A2987	U2834	C2716	A2649	U2582	A2516	A2438	U2206
C3258	A3259	C3194	G3124	A3259	C3194	U3125	U3057	U2988	U2835	U2717	A2650	C2583	A2517	G2439	G2207
G3260	C3260	C3195	A3126	G3260	C3195	A3127	C3063	U2991	U2836	G2718	A2651	A2584	U2519		G2208
A3261	A3261	A3196	A3128	A3261	A3196	A3128	U3062	U2992	U2837	U2719	C2652	C2585	U2519	C2444	C2209
G3262	G3262	A3197	A3128	G3263	A3197	A3128	U3063	C2993	U2838	C2720	A2653	U2586	A2519		U2210
G3263	G3263	A3198	A3128	G3263	A3198	A3128	U3064	C2994	U2839	U2721	A2654	U2587	A2522	U2448	C2211
A3330	A3330	C3199	U3129	A3330	C3199	U3129	C3065	C2995	U2915	G2722	A2655	U2588	U2523	U2449	G2212
G3331	G3331	G3200	U3130	C3265	G3200	U3130	A3066	C2996	C2917	C2724	A2656	A2589	A2524	G2450	G2215
G3332	G3332	U3201	A3131	U3266	U3201	A3131	G3067	A2995	C2918		G2657	U2590	A2525	A2451	G2216
U3334	C3267	U3202	C3132	C3267	U3202	C3132	A3068	A2996	A2919	U2727	C2658	U2591	A2526	A2452	A2217
										G2728	C2659	A2592	G2527	A2453	A2218
												G2593	C2528	A2454	A2219



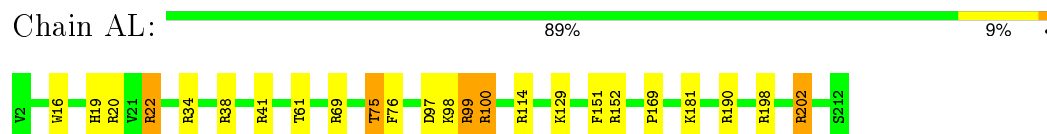
- Molecule 35: 5.8S ribosomal RNA



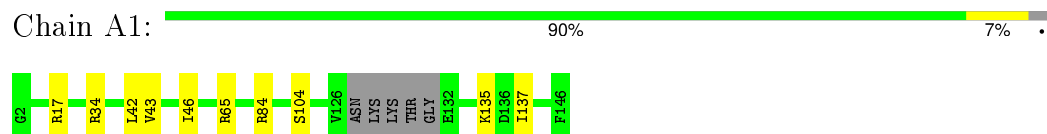
- Molecule 36: 5S ribosomal RNA



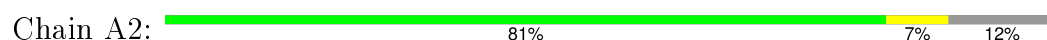
- Molecule 37: 60S ribosomal protein eL13



- Molecule 38: 60S ribosomal protein eL27



- Molecule 39: 60S ribosomal protein eL28





- Molecule 40: 60S ribosomal protein eL29

Chain A4: 94% 6%



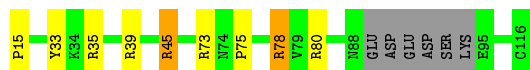
- Molecule 41: 60S ribosomal protein eL30

Chain A6: 96% .



- Molecule 42: 60S ribosomal protein eL31

Chain A7: 85% 7% 6%



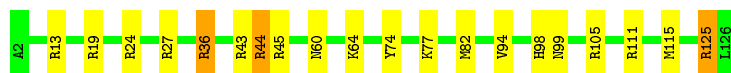
- Molecule 43: 60S ribosomal protein eL14

Chain AN: 90% 10%



- Molecule 44: 60S ribosomal protein eL32

Chain A8: 84% 14% .



- Molecule 45: 60S ribosomal protein eL33

Chain A9: 89% 10% .



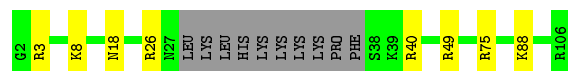
- Molecule 46: 60S ribosomal protein eL34

Chain Aa: 88% 8% .



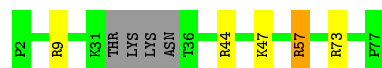
- Molecule 47: 60S ribosomal protein eL36

Chain Ab:  83% 8% 10%



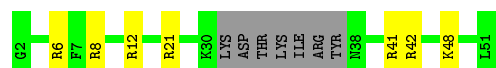
- Molecule 48: 60S ribosomal protein eL38

Chain Ad:  88% 5% • 5%



- Molecule 49: 60S ribosomal protein eL39

Chain Ae: 



- Molecule 50: 60S ribosomal protein eL40

Chain Af:  94%



- Molecule 51: 60S ribosomal protein eL15

Chain AP:  83% 13%



- Molecule 52: 60S ribosomal protein eL43

Chain Ah:  94% 5%



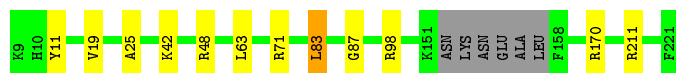
- Molecule 53: 60S ribosomal protein eL44

Chain Ai:  91% 8%




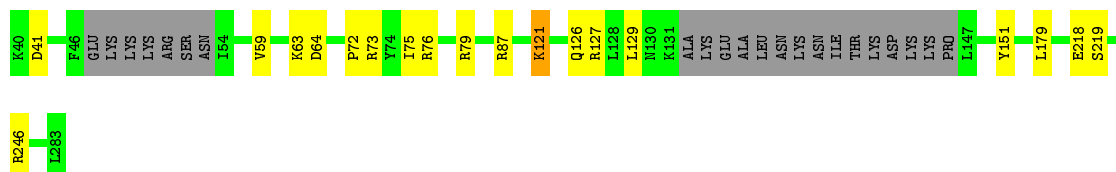
- Molecule 54: 60S ribosomal protein eL6

Chain AI:  92% 5%




- Molecule 55: 60S ribosomal protein eL8

Chain AJ:  83% 7% 9%



- Molecule 56: 60S ribosomal protein eL37

Chain Ac:  87% 10%



- Molecule 57: 60S ribosomal protein uL13

Chain AK:  92%



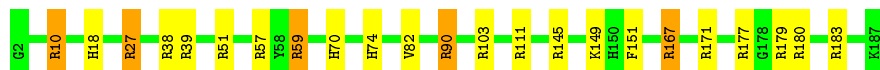
- Molecule 58: 60S ribosomal protein uL14

Chain AM:  95%



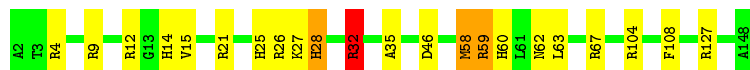
- Molecule 59: 60S ribosomal protein eL18

Chain AS:  88% 10%

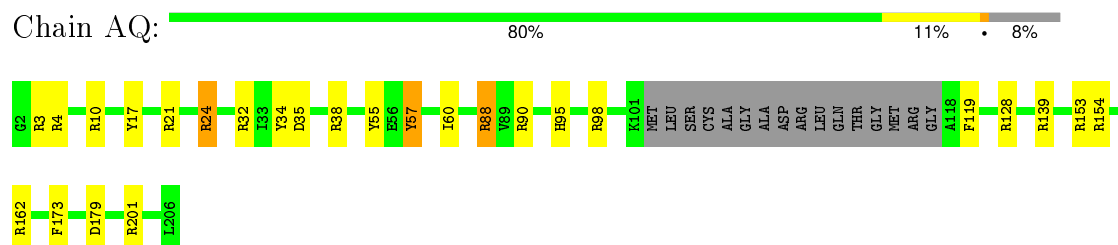


- Molecule 60: 60S ribosomal protein uL15

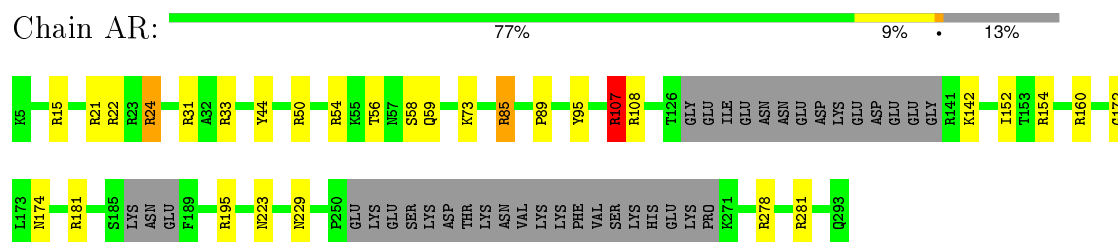
Chain AO:  85% 12%



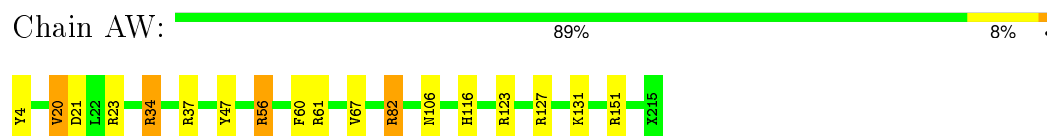
- Molecule 61: 60S ribosomal protein uL16



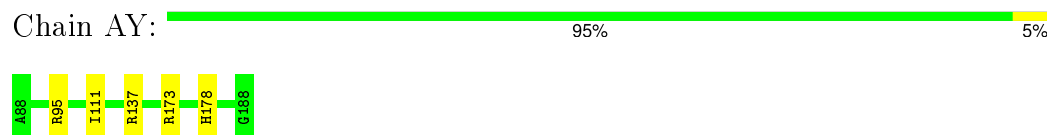
- Molecule 62: 60S ribosomal protein uL18



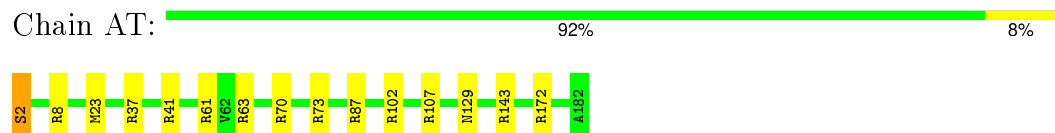
- Molecule 63: 60S ribosomal protein uL22



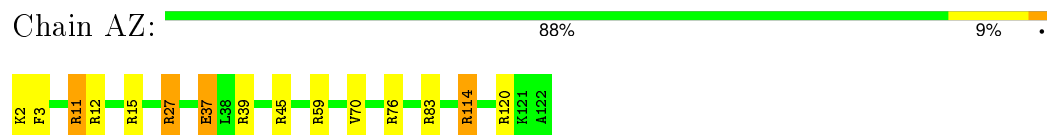
- Molecule 64: 60S ribosomal protein uL23



- Molecule 65: 60S ribosomal protein eL19



- Molecule 66: 60S ribosomal protein uL24



- Molecule 67: 60S ribosomal protein uL29





- Molecule 68: 60S ribosomal protein uL30

Chain A5: 88% 10% ..



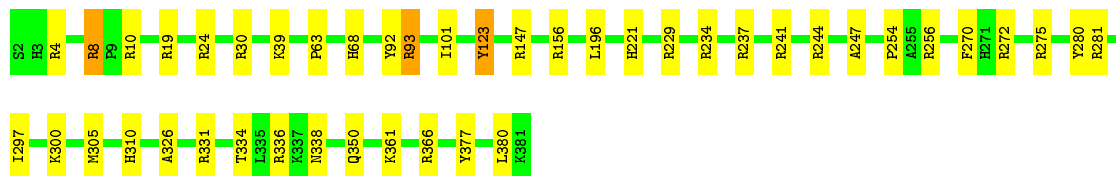
- Molecule 69: 60S ribosomal protein uL2

Chain AD: 92% 6% •



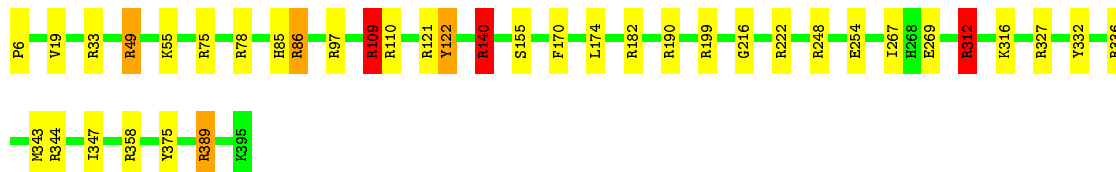
- Molecule 70: 60S ribosomal protein uL3

Chain AE: 88% 11% •



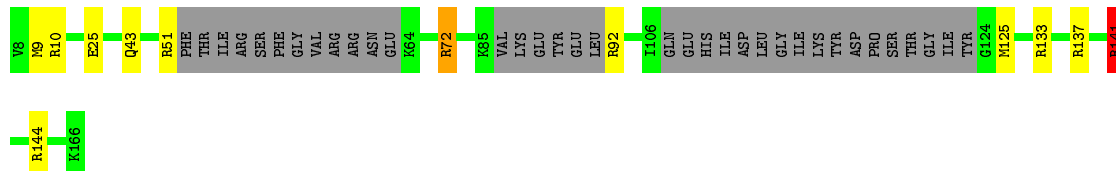
- Molecule 71: 60S ribosomal protein uL4

Chain AF: 90% 8% ..



- Molecule 72: 60S ribosomal protein uL5

Chain AG: 70% 6% 22% ..



- Molecule 73: 60S ribosomal protein eL20

Chain AU: 89% 8% •





- Molecule 74: 60S ribosomal protein uL6

Chain AH: 91% 8%



- Molecule 75: 60S ribosomal protein eL21

Chain AV: 88% 11%



- Molecule 76: 60S ribosomal protein eL41

Chain Ag: 70% 24% 5%



- Molecule 77: 60S ribosomal protein eL22

Chain AX: 94% 6%



- Molecule 78: 60S ribosomal protein eL24

Chain A0: 90% 5% 5%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	14696	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	1.10	4/38275 (0.0%)	1.54	870/59596 (1.5%)
10	R	0.75	0/755	0.94	0/1013
11	O	0.74	0/706	1.02	4/950 (0.4%)
12	Y	0.71	0/1295	1.15	10/1742 (0.6%)
13	Z	0.70	0/565	0.99	2/758 (0.3%)
14	1	0.72	0/999	1.17	9/1321 (0.7%)
15	2	0.76	0/324	1.01	3/435 (0.7%)
16	3	0.75	0/794	1.32	14/1055 (1.3%)
17	4	0.66	0/597	1.01	2/801 (0.2%)
18	5	0.78	0/459	1.24	5/606 (0.8%)
19	6	0.75	0/349	1.21	5/458 (1.1%)
2	7	1.12	0/1810	1.64	62/2821 (2.2%)
20	B	0.67	0/1738	1.11	8/2321 (0.3%)
21	F	0.68	0/2098	1.11	18/2819 (0.6%)
22	H	0.69	0/1665	1.09	11/2210 (0.5%)
23	J	0.69	0/1545	1.07	8/2064 (0.4%)
24	L	0.73	0/1407	1.18	12/1879 (0.6%)
25	N	0.68	0/780	1.17	5/1053 (0.5%)
26	P	0.70	0/966	1.26	14/1295 (1.1%)
27	Q	0.72	0/1149	1.19	13/1532 (0.8%)
28	S	0.65	0/1063	1.17	10/1425 (0.7%)
29	T	0.76	0/412	1.13	3/544 (0.6%)
3	D	0.76	0/1241	1.05	5/1652 (0.3%)
30	U	0.70	0/1223	1.03	6/1634 (0.4%)
31	V	0.74	0/1233	1.06	8/1645 (0.5%)
32	X	0.71	0/788	1.17	7/1050 (0.7%)
33	C	0.68	0/1570	1.04	4/2129 (0.2%)
34	AA	1.11	8/75947 (0.0%)	1.54	1829/118255 (1.5%)
35	AC	1.13	0/3599	1.55	91/5603 (1.6%)
36	AB	1.11	2/2823 (0.1%)	1.50	67/4400 (1.5%)
37	AL	0.70	0/1789	1.16	13/2381 (0.5%)
38	A1	0.71	0/1151	1.02	5/1531 (0.3%)
39	A2	0.73	0/840	0.97	1/1114 (0.1%)
4	E	0.72	0/1539	1.14	14/2055 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
40	A4	0.67	0/564	0.99	0/737
41	A6	0.71	0/749	0.98	1/1001 (0.1%)
42	A7	0.72	0/806	1.20	9/1073 (0.8%)
43	AN	0.70	0/1218	1.04	3/1621 (0.2%)
44	A8	0.71	0/1054	1.25	11/1399 (0.8%)
45	A9	0.72	0/865	1.24	12/1160 (1.0%)
46	Aa	0.70	0/872	1.24	12/1161 (1.0%)
47	Ab	0.72	0/763	1.11	4/1008 (0.4%)
48	Ad	0.72	0/612	1.14	5/812 (0.6%)
49	Ae	0.81	0/396	1.27	4/521 (0.8%)
5	G	0.70	0/1800	1.03	10/2429 (0.4%)
50	Af	0.71	0/419	1.06	2/556 (0.4%)
51	AP	0.72	0/1735	1.24	26/2320 (1.1%)
52	Ah	0.69	0/668	1.10	2/887 (0.2%)
53	Ai	0.69	0/789	1.14	8/1032 (0.8%)
54	AI	0.68	0/1708	1.01	5/2274 (0.2%)
55	AJ	0.68	0/1840	1.02	6/2456 (0.2%)
56	Ac	0.74	0/723	1.24	9/951 (0.9%)
57	AK	0.70	0/1690	1.11	12/2260 (0.5%)
58	AM	0.69	0/1012	1.12	9/1363 (0.7%)
59	AS	0.71	0/1531	1.24	25/2040 (1.2%)
6	I	0.71	0/1443	1.10	12/1936 (0.6%)
60	AO	0.70	0/1199	1.13	11/1597 (0.7%)
61	AQ	0.75	0/1580	1.21	20/2113 (0.9%)
62	AR	0.72	0/2079	1.15	19/2777 (0.7%)
63	AW	0.71	0/1244	1.18	14/1663 (0.8%)
64	AY	0.66	0/806	1.03	4/1074 (0.4%)
65	AT	0.70	0/1525	1.09	12/2016 (0.6%)
66	AZ	0.71	0/1013	1.20	12/1339 (0.9%)
67	A3	0.70	0/1005	1.09	9/1329 (0.7%)
68	A5	0.72	0/1917	1.15	21/2562 (0.8%)
69	AD	0.68	0/1902	1.17	18/2544 (0.7%)
7	K	0.72	0/1054	1.09	4/1411 (0.3%)
70	AE	0.70	0/3130	1.14	23/4195 (0.5%)
71	AF	0.70	0/3145	1.10	23/4205 (0.5%)
72	AG	0.76	0/1021	1.14	9/1349 (0.7%)
73	AU	0.73	0/1527	1.18	13/2043 (0.6%)
74	AH	0.67	0/1501	1.14	11/2025 (0.5%)
75	AV	0.69	0/1301	1.18	12/1732 (0.7%)
76	Ag	0.80	0/348	1.54	10/448 (2.2%)
77	AX	0.72	0/842	1.10	8/1125 (0.7%)
78	A0	0.79	0/534	1.19	5/711 (0.7%)
8	M	0.72	0/1114	1.12	8/1487 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
9	W	0.72	0/793	1.14	5/1053 (0.5%)
All	All	0.96	14/207331 (0.0%)	1.40	3596/303942 (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	127
12	Y	0	3
14	1	0	3
15	2	0	1
16	3	0	3
18	5	0	2
19	6	0	3
2	7	0	8
20	B	1	5
21	F	0	3
22	H	0	2
23	J	0	4
24	L	0	4
25	N	0	1
26	P	0	3
27	Q	0	3
28	S	0	1
29	T	0	5
30	U	0	1
31	V	0	4
32	X	0	3
33	C	0	2
34	AA	1	304
35	AC	0	10
36	AB	0	9
37	AL	0	6
38	A1	0	1
4	E	0	7
40	A4	0	1
41	A6	0	1
42	A7	0	3
43	AN	0	5
44	A8	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
45	A9	0	2
46	Aa	0	3
47	Ab	0	1
48	Ad	0	1
49	Ae	0	2
5	G	0	1
50	Af	0	2
51	AP	0	7
52	Ah	0	1
53	Ai	0	1
54	AI	0	4
55	AJ	0	2
56	Ac	0	4
57	AK	0	7
58	AM	0	3
59	AS	0	7
6	I	0	2
60	AO	0	3
61	AQ	0	6
62	AR	0	4
63	AW	0	4
64	AY	0	1
65	AT	0	4
66	AZ	0	5
67	A3	0	1
68	A5	0	5
69	AD	0	1
7	K	0	3
70	AE	0	7
71	AF	0	10
72	AG	0	3
73	AU	0	5
75	AV	0	3
76	Ag	0	2
78	A0	0	4
8	M	0	3
9	W	0	2
All	All	2	668

The worst 5 of 14 bond length outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	AB	28	C	P-O5'	-6.19	1.53	1.59
1	A	1819	U	C5'-C4'	5.69	1.58	1.51
36	AB	5	U	O3'-P	-5.30	1.54	1.61
1	A	1853	A	P-O5'	-5.29	1.54	1.59
34	AA	211	U	N1-C2	-5.23	1.33	1.38

The worst 5 of 3596 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1659	U	P-O3'-C3'	16.14	139.06	119.70
1	A	981	U	P-O3'-C3'	15.61	138.43	119.70
34	AA	811	A	P-O3'-C3'	15.26	138.02	119.70
1	A	1865	G	P-O3'-C3'	13.78	136.24	119.70
1	A	1912	C	P-O3'-C3'	13.59	136.01	119.70

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
20	B	225	ILE	CB
34	AA	3018	A	C3'

5 of 668 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	129	U	Sidechain
1	A	143	A	Sidechain
1	A	39	A	Sidechain
1	A	44	U	Sidechain
1	A	84	A	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	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	7	1620	0	827	1	0
3	D	1229	0	1311	0	0
4	E	1515	0	1605	0	0
5	G	1758	0	1811	1	0
6	I	1424	0	1471	0	0
7	K	1037	0	1099	3	0
8	M	1099	0	1183	1	0
9	W	786	0	858	0	0
10	R	747	0	754	0	0
11	O	687	0	695	0	0
12	Y	1267	0	1316	0	0
13	Z	557	0	558	2	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	0	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	1	0
22	H	1648	0	1803	1	0
23	J	1529	0	1680	0	0
24	L	1383	0	1434	1	0
25	N	772	0	813	0	0
26	P	954	0	997	0	0
27	Q	1129	0	1196	1	0
28	S	1047	0	1101	1	0
29	T	405	0	419	0	0
30	U	1202	0	1299	0	0
31	V	1206	0	1239	1	0
32	X	777	0	832	0	0
33	C	1539	0	1600	1	0
34	AA	67884	0	34242	118	0
35	AC	3215	0	1633	4	0
36	AB	2522	0	1275	2	0
37	AL	1757	0	1888	3	0
38	A1	1134	0	1245	1	0
39	A2	831	0	887	1	0
40	A4	555	0	599	1	0
41	A6	741	0	763	0	0
42	A7	794	0	869	0	0
43	AN	1202	0	1316	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	A8	1037	0	1139	3	0
45	A9	845	0	886	0	0
46	Aa	859	0	912	0	0
47	Ab	757	0	842	0	0
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	1	0
55	AJ	1813	0	1985	1	0
56	Ac	710	0	761	0	0
57	AK	1660	0	1785	0	0
58	AM	996	0	1044	0	0
59	AS	1503	0	1636	1	0
60	AO	1172	0	1230	5	0
61	AQ	1545	0	1582	1	0
62	AR	2050	0	2140	1	0
63	AW	1319	0	1303	3	0
64	AY	797	0	850	0	0
65	AT	1509	0	1682	1	0
66	AZ	1001	0	1099	2	0
67	A3	995	0	1121	0	0
68	A5	1879	0	2005	1	0
69	AD	1867	0	1964	1	0
70	AE	3062	0	3205	4	0
71	AF	3095	0	3333	2	0
72	AG	1011	0	1073	0	0
73	AU	1497	0	1556	2	0
74	AH	1476	0	1574	2	0
75	AV	1276	0	1355	1	0
76	Ag	343	0	388	0	0
77	AX	825	0	882	0	0
78	A0	522	0	539	0	0
All	All	193061	0	144306	200	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 1.

The worst 5 of 200 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)
34:AA:3770:C:H4'	70:AE:310:HIS:CE1	2.36	0.61
1:A:458:A:H3'	1:A:459:A:C5'	2.32	0.60
34:AA:445:A:C2	34:AA:702:U:C4	2.91	0.59
34:AA:236:U:HO2'	66:AZ:2:LYS:N	2.01	0.59
44:A8:36:ARG:HE	60:AO:14:HIS:CE1	2.22	0.57

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	
3	D	149/209 (71%)	144 (97%)	3 (2%)	2 (1%)	15	60
4	E	183/185 (99%)	175 (96%)	6 (3%)	2 (1%)	17	64
5	G	222/224 (99%)	206 (93%)	14 (6%)	2 (1%)	21	67
6	I	176/189 (93%)	161 (92%)	12 (7%)	3 (2%)	11	56
7	K	127/129 (98%)	118 (93%)	7 (6%)	2 (2%)	12	57
8	M	136/138 (99%)	127 (93%)	5 (4%)	4 (3%)	6	44
9	W	91/108 (84%)	84 (92%)	6 (7%)	1 (1%)	17	64
10	R	92/114 (81%)	80 (87%)	10 (11%)	2 (2%)	8	50
11	O	77/79 (98%)	67 (87%)	4 (5%)	6 (8%)	1	19
12	Y	152/154 (99%)	137 (90%)	11 (7%)	4 (3%)	7	47
13	Z	70/72 (97%)	65 (93%)	4 (6%)	1 (1%)	14	58
14	1	118/120 (98%)	111 (94%)	4 (3%)	3 (2%)	7	47
15	2	35/68 (52%)	31 (89%)	3 (9%)	1 (3%)	6	44
16	3	93/95 (98%)	81 (87%)	11 (12%)	1 (1%)	17	64
17	4	74/76 (97%)	65 (88%)	7 (10%)	2 (3%)	6	46
18	5	54/65 (83%)	53 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	6	41/43 (95%)	35 (85%)	5 (12%)	1 (2%)	7	48
20	B	208/210 (99%)	186 (89%)	19 (9%)	3 (1%)	14	58
21	F	255/257 (99%)	238 (93%)	13 (5%)	4 (2%)	12	57
22	H	200/214 (94%)	191 (96%)	8 (4%)	1 (0%)	34	77
23	J	186/188 (99%)	176 (95%)	5 (3%)	5 (3%)	6	46
24	L	165/214 (77%)	147 (89%)	14 (8%)	4 (2%)	7	48
25	N	96/98 (98%)	91 (95%)	3 (3%)	2 (2%)	9	52
26	P	125/127 (98%)	114 (91%)	8 (6%)	3 (2%)	7	48
27	Q	142/144 (99%)	130 (92%)	7 (5%)	5 (4%)	4	41
28	S	126/128 (98%)	108 (86%)	14 (11%)	4 (3%)	5	42
29	T	46/48 (96%)	44 (96%)	2 (4%)	0	100	100
30	U	147/149 (99%)	142 (97%)	4 (3%)	1 (1%)	26	71
31	V	142/156 (91%)	129 (91%)	10 (7%)	3 (2%)	9	52
32	X	92/103 (89%)	78 (85%)	10 (11%)	4 (4%)	3	34
33	C	193/195 (99%)	181 (94%)	9 (5%)	3 (2%)	12	57
37	AL	209/211 (99%)	190 (91%)	16 (8%)	3 (1%)	14	58
38	A1	136/145 (94%)	127 (93%)	7 (5%)	2 (2%)	13	58
39	A2	96/118 (81%)	89 (93%)	5 (5%)	2 (2%)	9	52
40	A4	64/66 (97%)	58 (91%)	4 (6%)	2 (3%)	5	43
41	A6	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
42	A7	92/102 (90%)	89 (97%)	3 (3%)	0	100	100
43	AN	144/146 (99%)	140 (97%)	2 (1%)	2 (1%)	14	58
44	A8	123/125 (98%)	114 (93%)	8 (6%)	1 (1%)	24	69
45	A9	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
46	Aa	104/106 (98%)	99 (95%)	5 (5%)	0	100	100
47	Ab	91/105 (87%)	85 (93%)	5 (6%)	1 (1%)	17	64
48	Ad	68/76 (90%)	68 (100%)	0	0	100	100
49	Ae	39/50 (78%)	39 (100%)	0	0	100	100
50	Af	49/51 (96%)	46 (94%)	3 (6%)	0	100	100
51	AP	202/204 (99%)	183 (91%)	14 (7%)	5 (2%)	7	47
52	Ah	83/85 (98%)	76 (92%)	5 (6%)	2 (2%)	7	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	Ai	93/95 (98%)	87 (94%)	5 (5%)	1 (1%)	17	64
54	AI	203/213 (95%)	187 (92%)	14 (7%)	2 (1%)	19	65
55	AJ	216/244 (88%)	196 (91%)	13 (6%)	7 (3%)	5	42
56	Ac	87/89 (98%)	74 (85%)	12 (14%)	1 (1%)	17	64
57	AK	199/201 (99%)	191 (96%)	6 (3%)	2 (1%)	19	65
58	AM	130/132 (98%)	121 (93%)	9 (7%)	0	100	100
59	AS	184/186 (99%)	171 (93%)	12 (6%)	1 (0%)	34	77
60	AO	145/147 (99%)	132 (91%)	10 (7%)	3 (2%)	9	52
61	AQ	185/205 (90%)	170 (92%)	12 (6%)	3 (2%)	12	57
62	AR	244/289 (84%)	224 (92%)	13 (5%)	7 (3%)	6	44
63	AW	149/170 (88%)	135 (91%)	12 (8%)	2 (1%)	15	60
64	AY	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
65	AT	179/181 (99%)	173 (97%)	5 (3%)	1 (1%)	30	74
66	AZ	119/121 (98%)	113 (95%)	5 (4%)	1 (1%)	24	69
67	A3	117/119 (98%)	108 (92%)	9 (8%)	0	100	100
68	A5	221/223 (99%)	201 (91%)	15 (7%)	5 (2%)	8	50
69	AD	245/247 (99%)	230 (94%)	14 (6%)	1 (0%)	39	80
70	AE	378/380 (100%)	346 (92%)	26 (7%)	6 (2%)	12	57
71	AF	388/390 (100%)	363 (94%)	21 (5%)	4 (1%)	19	65
72	AG	116/159 (73%)	107 (92%)	6 (5%)	3 (3%)	7	47
73	AU	178/180 (99%)	167 (94%)	9 (5%)	2 (1%)	17	64
74	AH	183/185 (99%)	168 (92%)	12 (7%)	3 (2%)	12	57
75	AV	153/155 (99%)	141 (92%)	9 (6%)	3 (2%)	9	53
76	Ag	35/37 (95%)	29 (83%)	5 (14%)	1 (3%)	6	44
77	AX	95/97 (98%)	90 (95%)	4 (4%)	1 (1%)	17	64
78	A0	60/62 (97%)	57 (95%)	2 (3%)	1 (2%)	11	56
All	All	10111/10698 (94%)	9361 (93%)	590 (6%)	160 (2%)	17	57

5 of 160 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	K	120	HIS
8	M	41	GLU

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Mol	Chain	Res	Type
9	W	4	VAL
10	R	42	ILE
12	Y	55	LYS

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	132/177 (75%)	129 (98%)	3 (2%)	58	83
4	E	161/164 (98%)	159 (99%)	2 (1%)	78	90
5	G	191/191 (100%)	185 (97%)	6 (3%)	47	78
6	I	154/160 (96%)	150 (97%)	4 (3%)	54	81
7	K	115/115 (100%)	112 (97%)	3 (3%)	54	81
8	M	116/116 (100%)	114 (98%)	2 (2%)	68	88
9	W	86/99 (87%)	83 (96%)	3 (4%)	43	76
10	R	83/97 (86%)	83 (100%)	0	100	100
11	O	76/76 (100%)	74 (97%)	2 (3%)	54	81
12	Y	137/137 (100%)	131 (96%)	6 (4%)	35	71
13	Z	60/60 (100%)	60 (100%)	0	100	100
14	1	104/104 (100%)	102 (98%)	2 (2%)	65	86
15	2	35/61 (57%)	34 (97%)	1 (3%)	50	79
16	3	87/87 (100%)	87 (100%)	0	100	100
17	4	70/70 (100%)	67 (96%)	3 (4%)	35	71
18	5	47/52 (90%)	45 (96%)	2 (4%)	35	71
19	6	36/36 (100%)	35 (97%)	1 (3%)	51	79
20	B	195/195 (100%)	192 (98%)	3 (2%)	72	89
21	F	233/233 (100%)	230 (99%)	3 (1%)	76	89
22	H	182/190 (96%)	178 (98%)	4 (2%)	60	84
23	J	177/177 (100%)	176 (99%)	1 (1%)	90	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	L	151/190 (80%)	148 (98%)	3 (2%)	63	86
25	N	91/91 (100%)	88 (97%)	3 (3%)	45	77
26	P	99/99 (100%)	95 (96%)	4 (4%)	38	72
27	Q	120/120 (100%)	117 (98%)	3 (2%)	55	82
28	S	114/114 (100%)	108 (95%)	6 (5%)	28	66
29	T	43/43 (100%)	41 (95%)	2 (5%)	32	69
30	U	132/132 (100%)	129 (98%)	3 (2%)	58	83
31	V	131/140 (94%)	127 (97%)	4 (3%)	47	78
32	X	88/94 (94%)	87 (99%)	1 (1%)	80	91
33	C	167/167 (100%)	164 (98%)	3 (2%)	66	87
37	AL	190/190 (100%)	187 (98%)	3 (2%)	70	88
38	A1	127/131 (97%)	124 (98%)	3 (2%)	57	83
39	A2	97/109 (89%)	93 (96%)	4 (4%)	37	72
40	A4	60/60 (100%)	60 (100%)	0	100	100
41	A6	83/83 (100%)	81 (98%)	2 (2%)	57	83
42	A7	90/96 (94%)	89 (99%)	1 (1%)	80	91
43	AN	135/135 (100%)	131 (97%)	4 (3%)	48	78
44	A8	114/114 (100%)	109 (96%)	5 (4%)	35	71
45	A9	90/90 (100%)	89 (99%)	1 (1%)	80	91
46	Aa	89/89 (100%)	84 (94%)	5 (6%)	26	65
47	Ab	82/92 (89%)	80 (98%)	2 (2%)	57	83
48	Ad	69/73 (94%)	68 (99%)	1 (1%)	74	89
49	Ae	40/47 (85%)	38 (95%)	2 (5%)	30	68
50	Af	45/45 (100%)	44 (98%)	1 (2%)	60	84
51	AP	179/179 (100%)	173 (97%)	6 (3%)	44	77
52	Ah	70/70 (100%)	69 (99%)	1 (1%)	74	89
53	Ai	87/87 (100%)	83 (95%)	4 (5%)	33	69
54	AI	189/195 (97%)	186 (98%)	3 (2%)	70	88
55	AJ	204/224 (91%)	199 (98%)	5 (2%)	55	82
56	Ac	74/74 (100%)	71 (96%)	3 (4%)	37	72
57	AK	181/181 (100%)	178 (98%)	3 (2%)	68	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	AM	106/106 (100%)	105 (99%)	1 (1%)	84	92
59	AS	158/158 (100%)	156 (99%)	2 (1%)	76	89
60	AO	121/121 (100%)	113 (93%)	8 (7%)	21	59
61	AQ	165/176 (94%)	161 (98%)	4 (2%)	57	83
62	AR	215/250 (86%)	208 (97%)	7 (3%)	45	77
63	AW	128/128 (100%)	127 (99%)	1 (1%)	86	93
64	AY	90/90 (100%)	88 (98%)	2 (2%)	60	84
65	AT	162/162 (100%)	162 (100%)	0	100	100
66	AZ	111/111 (100%)	110 (99%)	1 (1%)	84	92
67	A3	110/110 (100%)	107 (97%)	3 (3%)	52	80
68	A5	201/201 (100%)	195 (97%)	6 (3%)	48	78
69	AD	191/191 (100%)	184 (96%)	7 (4%)	41	75
70	AE	335/335 (100%)	325 (97%)	10 (3%)	48	78
71	AF	336/336 (100%)	323 (96%)	13 (4%)	39	73
72	AG	110/142 (78%)	108 (98%)	2 (2%)	66	87
73	AU	162/162 (100%)	156 (96%)	6 (4%)	41	75
74	AH	168/168 (100%)	163 (97%)	5 (3%)	48	78
75	AV	140/140 (100%)	136 (97%)	4 (3%)	50	79
76	Ag	34/34 (100%)	33 (97%)	1 (3%)	50	79
77	AX	92/92 (100%)	92 (100%)	0	100	100
78	A0	53/53 (100%)	52 (98%)	1 (2%)	65	86
All	All	9096/9417 (97%)	8870 (98%)	226 (2%)	59	82

5 of 226 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	A8	82	MET
53	Ai	79	LYS
72	AG	43	GLN
45	A9	135	MET
49	Ae	42	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
46	Aa	12	HIS
57	AK	71	HIS
72	AG	20	ASN
51	AP	20	HIS
59	AS	14	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1586/1608 (98%)	481 (30%)	89 (5%)
2	7	75/76 (98%)	13 (17%)	2 (2%)
34	AA	3168/3193 (99%)	979 (30%)	187 (5%)
35	AC	148/151 (98%)	50 (33%)	9 (6%)
36	AB	117/118 (99%)	27 (23%)	1 (0%)
All	All	5094/5146 (98%)	1550 (30%)	288 (5%)

5 of 1550 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	C
1	A	5	U
1	A	17	C
1	A	25	C
1	A	26	A

5 of 288 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	AA	645	A
34	AA	1206	U
34	AA	3624	U
34	AA	681	U
34	AA	859	C

## 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.