



wwPDB EM Map/Model Validation Report ⓘ

May 31, 2016 – 11:49 PM EDT

PDB ID : 3JBO
EMDB ID: : EMD-6452
Title : Cryo-electron microscopy reconstruction of the Plasmodium falciparum 80S ribosome bound to P/E-tRNA
Authors : Sun, M.; Li, W.; Blomqvist, K.; Das, S.; Hashem, Y.; Dvorin, J.D.; Frank, J.
Deposited on : 2015-09-16
Resolution : 5.80 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
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) : rb-20027674

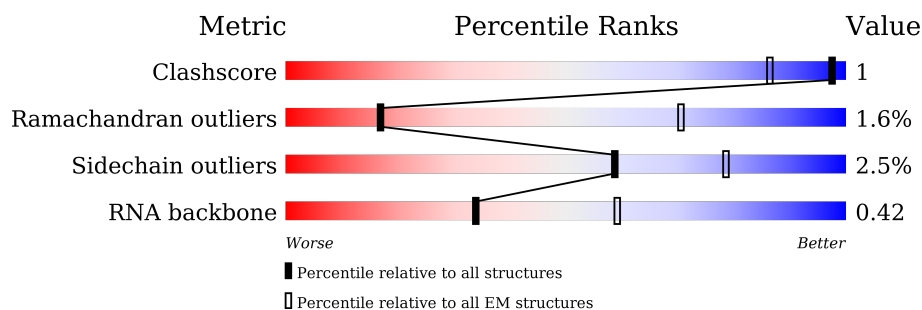
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





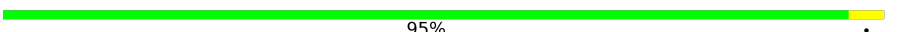









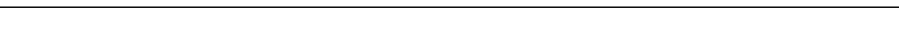

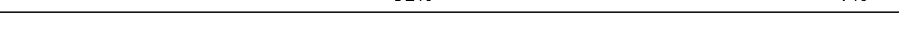

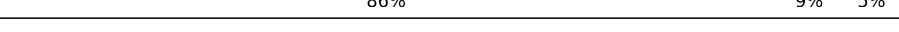
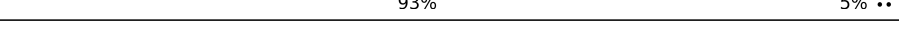





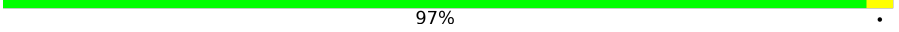

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	1608	32% 45% 20% .
2	7	75	17% 49% 32% .
3	Q	144	86% 12% .
4	S	128	85% 12% .
5	T	48	90% 8% .
6	M	138	90% 9% .
7	U	149	92% 7% ..
8	V	156	83% 9% . 6%

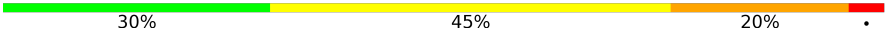
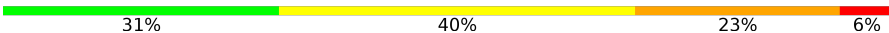
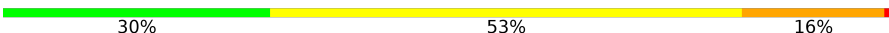













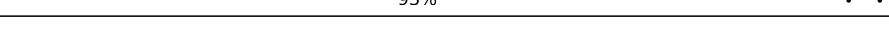



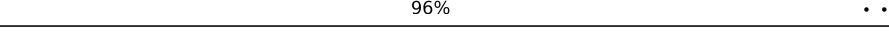

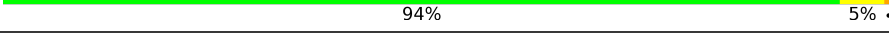


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Mol	Chain	Length	Quality of chain
9	E	185	 91% 8% .
10	X	103	 83% 9% . 7%
11	G	224	 95% .
12	W	108	 81% 7% 12%
13	R	114	 82% . 14%
14	I	189	 87% 7% . 5%
15	O	79	 87% 13%
16	Y	154	 86% 14%
17	Z	72	 97% .
18	1	120	 88% 12% .
19	2	68	 54% 6% 40%
20	C	195	 95% 5% .
21	3	95	 87% 12% .
22	4	76	 92% 7% .
23	5	65	 77% 12% 11%
24	6	43	 86% 9% 5%
25	B	210	 93% 5% ..
26	D	209	 70% . 25%
27	F	257	 92% 6% .
28	H	214	 88% 7% 5%
29	K	129	 90% 9% .
30	J	188	 91% 9%
31	N	98	 97% .
32	P	127	 89% 9% .
33	L	214	 71% 8% 20%

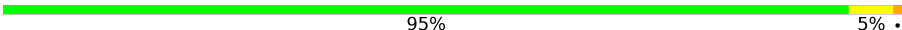









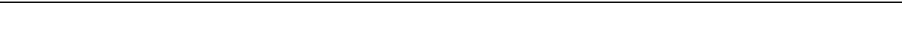

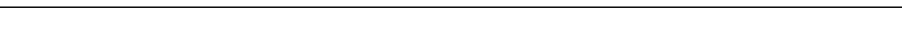
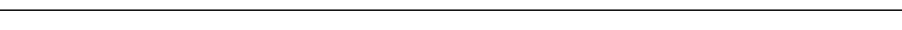
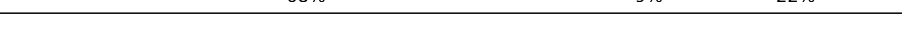

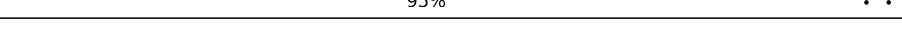



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Mol	Chain	Length	Quality of chain
34	AA	3192	
35	AC	151	
36	AB	118	
37	AL	211	
38	A0	62	
39	AO	147	
40	Ai	95	
41	A2	118	
42	A4	66	
43	A6	98	
44	A7	102	
45	A1	145	
46	AN	146	
47	A8	125	
48	A9	103	
49	Aa	106	
50	Ab	105	
51	Ad	76	
52	Ae	50	
53	Af	51	
54	AP	204	
55	Ah	85	
56	AI	213	
57	Ac	89	
58	AK	201	

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Mol	Chain	Length	Quality of chain
59	AM	132	 95% 5% .
60	AS	186	 87% 8% 5%
61	AQ	205	 79% 10% . 8%
62	AR	289	 79% 6% . 13%
63	AW	170	 91% 8% ..
64	AY	101	 96% . .
65	AT	181	 89% 9% .
66	AZ	121	 88% 11% .
67	A3	119	 88% 9% . .
68	A5	223	 89% 9% .
69	AD	247	 89% 9% .
70	AE	380	 92% 7% .
71	AF	390	 89% 10% .
72	AG	159	 68% 9% . 22%
73	AU	180	 88% 10% .
74	AH	185	 95% . .
75	AV	155	 90% 9% .
76	Ag	37	 76% 19% 5%
77	AX	97	 92% 7% .
78	AJ	244	 86% . . 9%

2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 193017 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/E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	75	Total	C	N	O	P	0	0
			1598	713	290	521	74		

- Molecule 3 is a protein called 40S ribosomal protein uS12.

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

- Molecule 4 is a protein called 40S ribosomal protein uS13.

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

- Molecule 5 is a protein called 40S ribosomal protein uS14.

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

- Molecule 6 is a protein called 40S ribosomal protein uS9.

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

- Molecule 7 is a protein called 40S ribosomal protein uS15.

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

- Molecule 8 is a protein called 40S ribosomal protein uS17.

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

- Molecule 9 is a protein called 40S ribosomal protein uS4.

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

- Molecule 10 is a protein called 40S ribosomal protein uS19.

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

- Molecule 11 is a protein called 40S ribosomal protein uS5.

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

- Molecule 12 is a protein called 40S ribosomal protein eS17.

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

- Molecule 13 is a protein called 40S ribosomal protein eS12.

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

- Molecule 14 is a protein called 40S ribosomal protein uS7.

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

- Molecule 15 is a protein called 40S ribosomal protein eS10.

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

- Molecule 16 is a protein called 40S ribosomal protein eS19.

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

- Molecule 17 is a protein called 40S ribosomal protein eS21.

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

- Molecule 18 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	1	120	Total	C	N	O	S	0	0
			986	632	189	163	2		

- Molecule 19 is a protein called 40S ribosomal protein eS25.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	2	41	Total	C	N	O	0	0
			321	208	56	57		

- Molecule 20 is a protein called 40S ribosomal protein uS2.

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

- Molecule 21 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	3	95	Total	C	N	O	S	0	0
			782	478	169	129	6		

- Molecule 22 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	4	76	Total	C	N	O	S	0	0
			586	368	102	107	9		

- Molecule 23 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	5	58	Total	C	N	O	0	0
			458	285	93	80		

- Molecule 24 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	6	43	Total	C	N	O	0	0
			346	213	75	58		

- Molecule 25 is a protein called 40S ribosomal protein eS1.

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

- Molecule 26 is a protein called 40S ribosomal protein uS3.

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

- Molecule 27 is a protein called 40S ribosomal protein eS4.

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

- Molecule 28 is a protein called 40S ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	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 29 is a protein called 40S ribosomal protein uS8.

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

- Molecule 30 is a protein called 40S ribosomal protein eS7.

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

- Molecule 31 is a protein called 40S ribosomal protein uS10.

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

- Molecule 32 is a protein called 40S ribosomal protein uS11.

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

- Molecule 33 is a protein called 40S ribosomal protein eS8.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AA	3192	Total	C	N	O	P	0	0
			67862	30436	12049	22217	3160		

- 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 eL24.

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

- Molecule 39 is a protein called 60S ribosomal protein uL15.

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

- Molecule 40 is a protein called 60S ribosomal protein eL44.

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

- Molecule 41 is a protein called 60S ribosomal protein eL28.

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

- Molecule 42 is a protein called 60S ribosomal protein eL29.

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

- Molecule 43 is a protein called 60S ribosomal protein eL30.

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

- Molecule 44 is a protein called 60S ribosomal protein eL31.

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

- Molecule 45 is a protein called 60S ribosomal protein eL27.

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

- Molecule 46 is a protein called 60S ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	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 47 is a protein called 60S ribosomal protein eL32.

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

- Molecule 48 is a protein called 60S ribosomal protein eL33.

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

- Molecule 49 is a protein called 60S ribosomal protein eL34.

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

- Molecule 50 is a protein called 60S ribosomal protein eL36.

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

- Molecule 51 is a protein called 60S ribosomal protein eL38.

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

- Molecule 52 is a protein called 60S ribosomal protein eL39.

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

- Molecule 53 is a protein called 60S ribosomal protein eL40.

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

- Molecule 54 is a protein called 60S ribosomal protein eL15.

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

- Molecule 55 is a protein called 60S ribosomal protein eL43.

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

- Molecule 56 is a protein called 60S ribosomal protein eL6.

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

- Molecule 57 is a protein called 60S ribosomal protein eL37.

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

- Molecule 58 is a protein called 60S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	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 59 is a protein called 60S ribosomal protein uL14.

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

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

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

- 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		

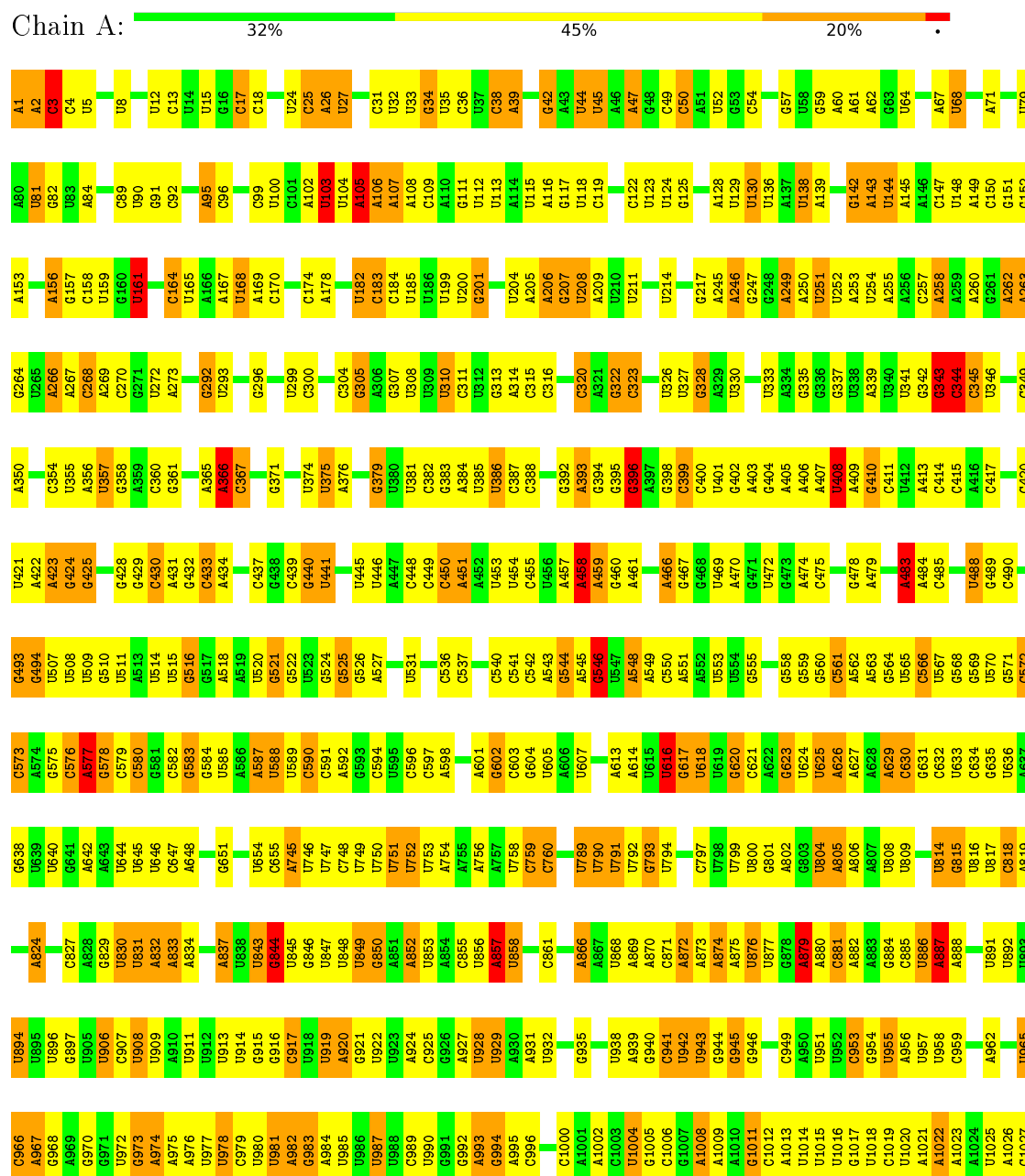
- Molecule 78 is a protein called 60S ribosomal protein eL8.

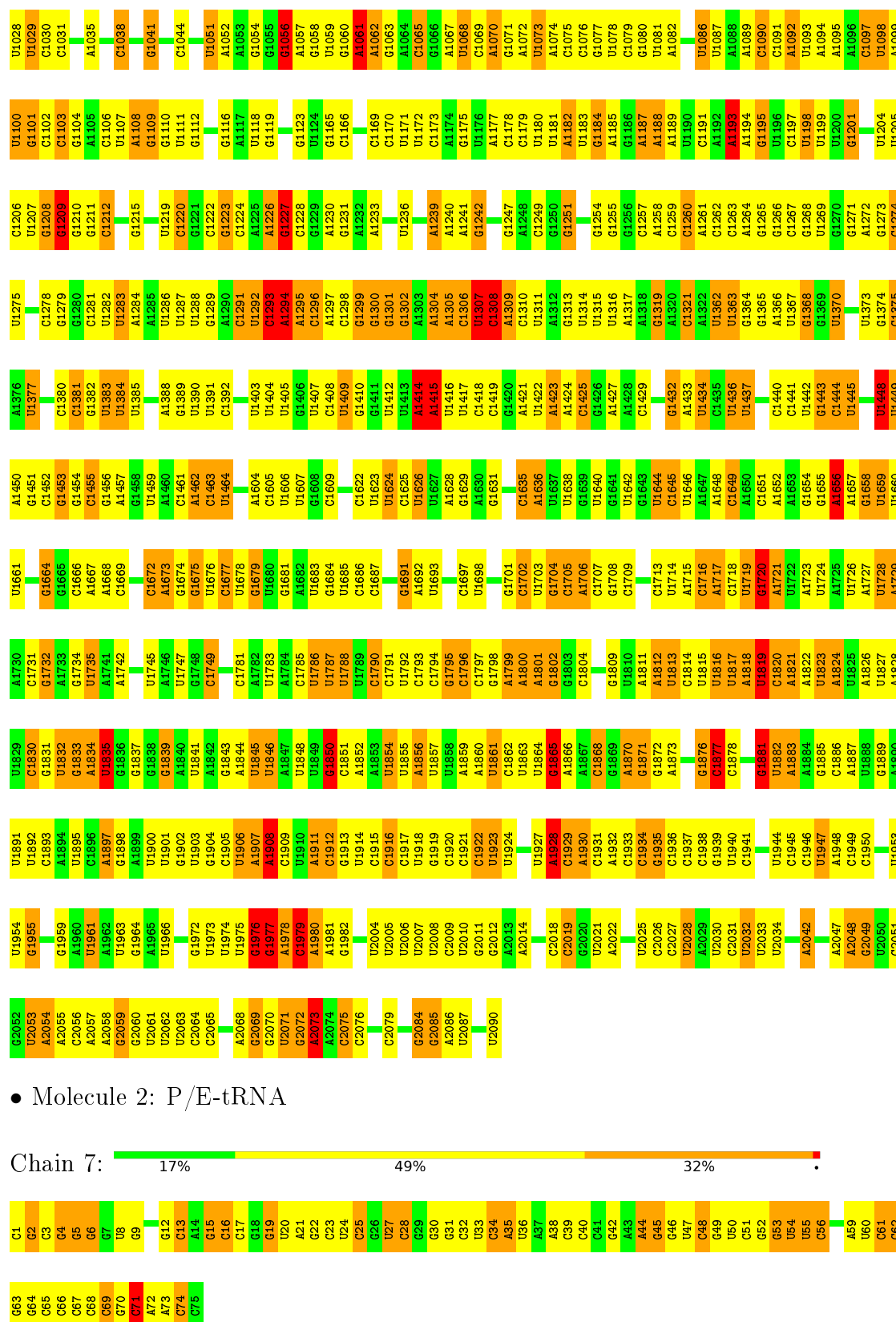
Mol	Chain	Residues	Atoms					AltConf	Trace
78	AJ	222	Total	C	N	O	S	0	0
			1813	1174	323	309	7		

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 3: 40S ribosomal protein uS12

Chain Q:  86% 12% .




- Molecule 4: 40S ribosomal protein uS13

Chain S:  85% 12% .



- Molecule 5: 40S ribosomal protein uS14

Chain T:  90% 8% .




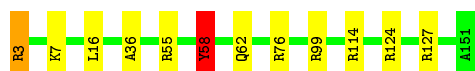
- Molecule 6: 40S ribosomal protein uS9

Chain M:  90% 9% .




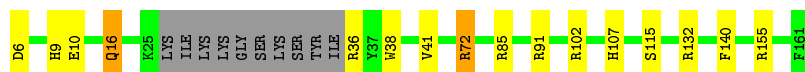
- Molecule 7: 40S ribosomal protein uS15

Chain U:  92% 7% ..




- Molecule 8: 40S ribosomal protein uS17

Chain V:  83% 9% • 6%




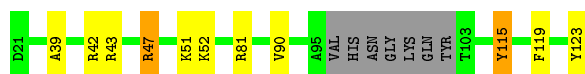
- Molecule 9: 40S ribosomal protein uS4

Chain E:  91% 8% .



- Molecule 10: 40S ribosomal protein uS19

Chain X:  83% 9% • 7%



- Molecule 11: 40S ribosomal protein uS5

Chain G: 95%



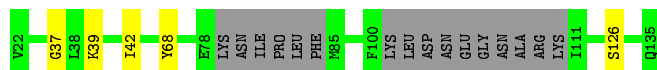
- Molecule 12: 40S ribosomal protein eS17

Chain W: 81% 7% 12%



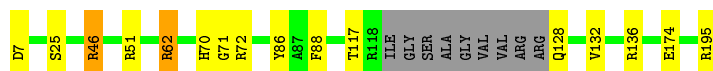
- Molecule 13: 40S ribosomal protein eS12

Chain R: 82% 14%



- Molecule 14: 40S ribosomal protein uS7

Chain I: 87% 7% 5%



- Molecule 15: 40S ribosomal protein eS10

Chain O: 87% 13%



- Molecule 16: 40S ribosomal protein eS19

Chain Y: 86% 14%




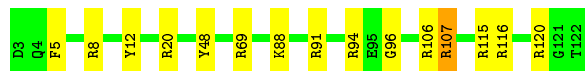
- Molecule 17: 40S ribosomal protein eS21

Chain Z: 97%



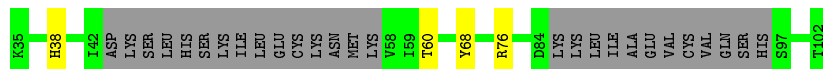
- Molecule 18: 40S ribosomal protein eS24

Chain 1:  88% 12%



- Molecule 19: 40S ribosomal protein eS25

Chain 2:  54% 6% 40%



- Molecule 20: 40S ribosomal protein uS2

Chain C:  95% 5%



- Molecule 21: 40S ribosomal protein eS26

Chain 3:  87% 12%




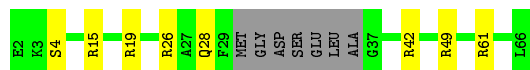
- Molecule 22: 40S ribosomal protein eS27

Chain 4:  92% 7%




- Molecule 23: 40S ribosomal protein eS28

Chain 5:  77% 12% 11%



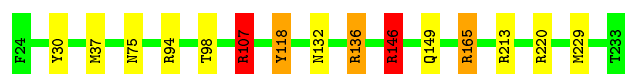
- Molecule 24: 40S ribosomal protein eS30

Chain 6:  86% 9% 5%



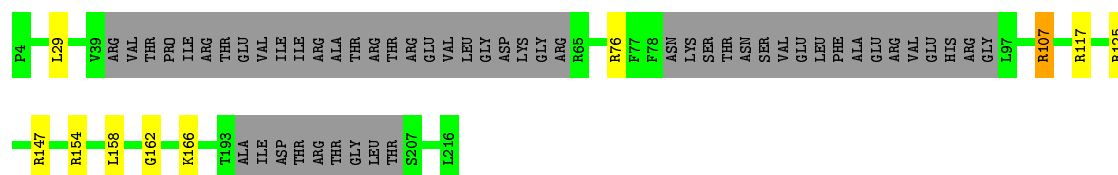
- Molecule 25: 40S ribosomal protein eS1

Chain B:  93% 5% ..




- Molecule 26: 40S ribosomal protein uS3

Chain D:  70% 25%




- Molecule 27: 40S ribosomal protein eS4

Chain F:  92% 6% .




- Molecule 28: 40S ribosomal protein eS6

Chain H:  88% 7% 5%




- Molecule 29: 40S ribosomal protein uS8

Chain K:  90% 9% .



- Molecule 30: 40S ribosomal protein eS7

Chain J:  91% 9%



- Molecule 31: 40S ribosomal protein uS10

Chain N:  97%



- Molecule 32: 40S ribosomal protein uS11

- Molecule 33: 40S ribosomal protein eS8

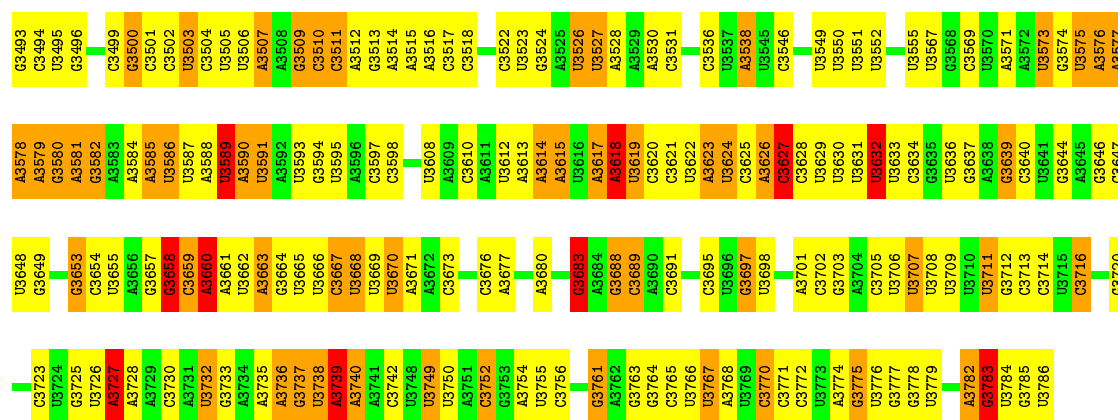
- Molecule 34: 28S ribosomal RNA

WORLDWIDE
PDB
PROTEIN DATA BANK

 **EMDataBank**
Unified Data Resource for 3DEM

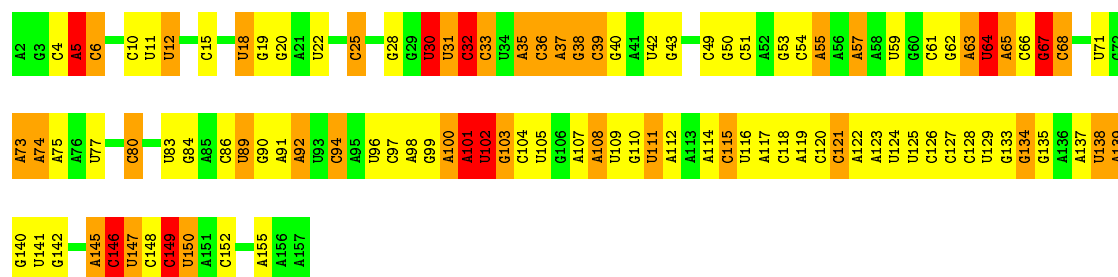
U1963	C1852	A1787	C1720	A1636	G1562	G1475	U1343	C1281	A1215	G1141	U1075	C941	C875	A774
G1964	C1853	C1788	C1721	G1637	U1563	A1476	C1344	U1282	C1216	C1154	C1076	C942	C876	C775
U1965	A1789	A1789	C1722	G1641	G1564	A1479	A1345	C1283	U1217	C1155	U1077	G943	U879	U779
A1966	U1855	A1790	C1723	G1642	G1565	G1480	U1346	C1284	C1218	C1156	C1078	G944	A880	U792
G1967	A1856	A1791	G1725	U1643	A1566	A1481	A1415	U1285	U1220	U1157	U1079	G945	A881	A793
A1968	A1857	A1792	U1725	U1644	A1567	A1486	G1417	A1287	U1223	G1158	G1082	G946	G882	C794
U1970	C1861	A1793	C1726	U1645	C1568	U1487	A1418	C1288	U1224	A1159	U1017	G948	C883	C795
A1971	U1865	U1794	U1727	U1646	U1570	U1493	A1419	G1289	A1224	C1160	C1018	A949	A884	C796
U1974	C1866	A1797	A1729	U1647	C1571	U1496	C1420	C1290	A1225	C1161	C1086	G950	A885	A797
A1975	A1866	A1798	U1730	U1648	U1572	U1497	U1421	U1291	A1226	U1162	C1087	A951	A888	U798
A1976	U1867	A1799	A1731	G1649	C1573	U1498	G1422	U1292	U1227	A1163	U1089	U952	U889	A799
U1977	A1868	U1800	A1732	U1650	C1574	U1499	G1423	G1293	A1228	U1164	U1092	U953	G890	A800
G1978	G1869	G1801	U1733	C1651	C1575	U1576	C1424	G1294	A1229	U1165	U1024	G954	C891	U801
U1978	U1870	U1802	G1735	C1654	U1577	G1502	C1425	A1295	A1230	A1092	U1092	A955	U892	U802
A1979	A1871	A1736	A1736	U1655	G1583	A1503	C1426	U1298	A1231	C1166	G1093	A956	U893	A803
G1980	A1872	U1737	U1737	G1656	U1584	A1504	U1427	G1299	U1232	U1167	G1026	U957	U894	A804
U1981	G1873	A1806	A1738	G1657	C1585	U1505	G1428	G1300	A1233	C1168	U1095	C959	A895	U805
A1983	C1874	C1807	C1739	U1657	U1586	U1506	A1429	U1301	C1234	A1170	G1028	A960	U896	G806
U1990	U1808	U1808	A1740	G1658	U1587	U1507	A1430	U1302	C1235	A1171	U1098	C963	A899	U807
U1991	U1809	U1809	G1741	G1659	U1588	U1508	A1431	C1303	C1236	C1172	U1099	G964	G900	A808
U1994	A1810	A1811	U1742	U1660	G1589	U1510	A1432	C1304	C1237	U1173	A1100	G965	U901	U810
C1995	C1881	C1812	U1743	U1661	U1590	U1511	A1433	C1305	C1238	U1174	A1101	A966	U902	A811
G1996	U1882	U1813	U1744	C1665	G1592	A1512	G1434	U1306	A1239	C1175	U1102	A967	G804	U812
C1997	G1883	A1814	G1745	A1666	A1593	U1513	G1435	A1307	A1240	C1176	U1103	G968	A905	G813
A1998	U1885	U1815	A1748	A1667	A1594	U1514	U1437	A1308	G1243	U1179	U1105	U969	G906	U817
A1999	G1886	A1816	U1749	G1668	G1595	A1515	A1440	U1309	G1244	A1188	A1106	C970	G907	C818
G2000	U1887	G1817	U1750	U1670	U1596	G1516	C1441	A1310	G1245	U1183	U1107	G971	A908	C821
U2001	A1888	C1818	C1751	U1672	A1598	U1517	G1442	U1311	C1246	A1184	U1108	U909	U916	A822
G2002	U1889	U1826	U1752	A1673	G1599	A1518	C1443	U1312	C1247	U1185	U1109	G972	A910	U823
G2003	U1890	C1827	U1753	G1674	C1600	G1519	U1444	C1313	U1251	A1186	U1110	C976	U911	U824
U2004	G1893	U1821	U1754	C1675	A1601	U1524	A1445	C1314	U1252	A1187	A1111	U912	U912	G825
G2008	A1894	A1822	C1756	G1676	A1602	U1525	A1446	U1315	U1253	A1188	C1112	G979	U913	G828
A2009	U1895	C1823	C1757	C1677	C1603	G1526	U1447	U1316	G1254	A1189	C1113	A980	G914	A829
C2010	G1897	A1824	A1759	C1678	A1604	U1527	G1448	C1317	G1255	A1190	A1114	U981	G915	G830
U2013	U1898	U1825	U1760	C1680	U1605	U1527	U1449	U1318	U1256	G1191	G1115	C982	U916	U831
C2014	U1899	U1826	A1763	C1681	U1606	U1533	G1450	U1319	A1257	C1192	G1116	G983	A917	U832
C2015	A1900	C1827	U1761	U1682	U1607	U1534	A1451	G1320	U1257	G1193	U1117	A984	G918	U833
U2016	U1901	A1823	G1762	A1683	C1608	G1535	A1452	A1321	G1258	A1194	A1052	G985	G919	G833
U2017	C1903	G1834	A1765	G1685	G1613	U1536	U1453	U1324	C1259	A1195	A1120	U986	A920	U834
G2018	U1904	C1835	U1766	U1688	G1614	U1537	A1454	C1325	A1261	U1197	G1121	C921	C922	C835
A2019	C1905	U1836	U1767	U1689	A1617	U1538	C1455	C1326	G1262	A1198	U1058	G988	C923	C857
A2020	U1906	U1837	A1768	A1690	C1618	U1539	C1456	C1327	A1263	A1199	G1059	A989	G924	C858
A2021	U1907	U1838	G1770	G1691	C1619	G1540	G1457	U1328	A1264	C1200	G1060	A991	A925	C859
A2022	U1908	U1839	U1771	C1692	U1619	C1544	A1458	U1329	C1265	U1201	U1061	C992	G926	A860
G2030	C1910	C1840	A1772	U1693	A1624	U1549	U1459	A1330	U1266	C1202	U1126	U993	A927	C861
C2033	A1913	U1841	U1773	U1694	G1625	U1550	A1460	A1331	G1269	A1203	A1063	C996	C930	U862
G2034	A1914	A1842	U1774	A1695	A1626	A1550	C1461	A1332	G1270	A1204	U1064	G997	U931	U863
G2035	G1844	U1843	A1779	C1627	C1551	U1551	C1462	A1333	A1271	U1205	U1066	U998	U932	U864
C2036	G1845	G1780	U1779	U1628	U1552	U1552	C1466	G1334	U1272	U1207	U1067	G999	U933	G865
U2037	A1846	A1781	U1704	C1630	U1553	U1553	C1467	G1335	G1273	U1208	G1132	C1000	G934	A867
U2038	C1847	U1782	A1705	A1631	U1554	A1554	A1468	U1336	A1274	U1209	A1133	G1069	A935	U868
U2039	U1848	U1783	A1706	G1632	A1555	G1556	U1469	U1337	G1275	A1210	G1134	A936	A869	U869
U2040	U1849	U1784	U1785	U1633	U1560	U1560	A1470	U1338	A1276	U1211	G1135	C1005	C937	C870
U2041	A1850	A1851	G1712	G1634	U1561	U1561	A1473	G1340	A1278	U1212	A1136	U1007	U938	U873
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														A874



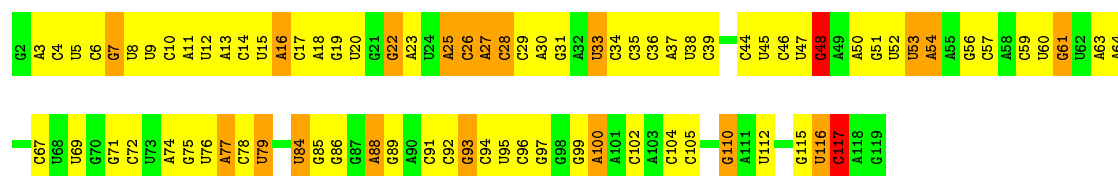
• Molecule 35: 5.8S ribosomal RNA

Chain AC: 31% 40% 23% 6%



• Molecule 36: 5S ribosomal RNA

Chain AB: 30% 53% 16% .



• Molecule 37: 60S ribosomal protein eL13

Chain AL: 87% 13%



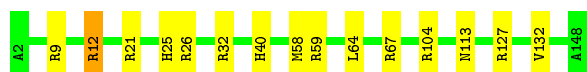
• Molecule 38: 60S ribosomal protein eL24

Chain A0: 94% 6%



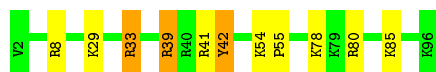
• Molecule 39: 60S ribosomal protein uL15

Chain AO:  90% 10%




- Molecule 40: 60S ribosomal protein eL44

Chain Ai:  88% 8%



- Molecule 41: 60S ribosomal protein eL28

Chain A2:  81% 8% 12%



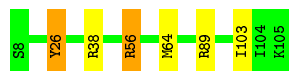
- Molecule 42: 60S ribosomal protein eL29

Chain A4:  94%




- Molecule 43: 60S ribosomal protein eL30

Chain A6:  94%



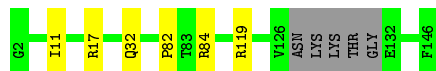
- Molecule 44: 60S ribosomal protein eL31

Chain A7:  87% 6% 6%



- Molecule 45: 60S ribosomal protein eL27

Chain A1:  92%

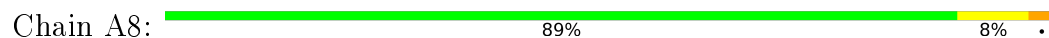


- Molecule 46: 60S ribosomal protein eL14

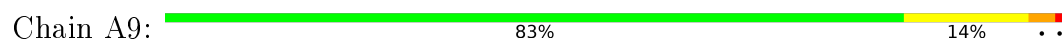
Chain AN:  91% 8%



- Molecule 47: 60S ribosomal protein eL32



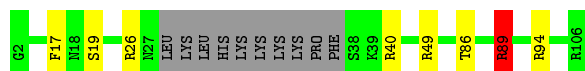
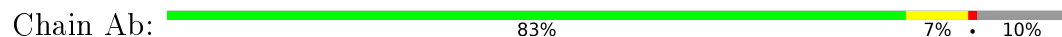
- Molecule 48: 60S ribosomal protein eL33



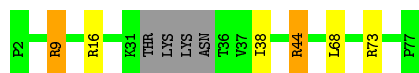
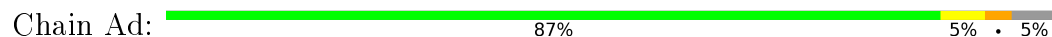
- Molecule 49: 60S ribosomal protein eL34



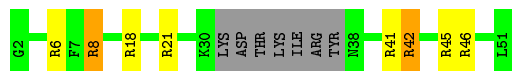
- Molecule 50: 60S ribosomal protein eL36



- Molecule 51: 60S ribosomal protein eL38



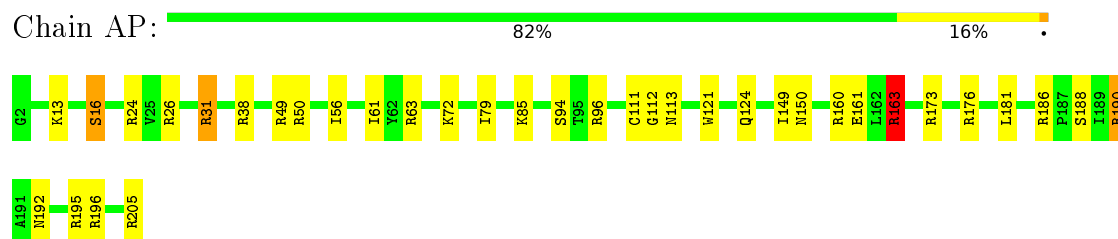
- Molecule 52: 60S ribosomal protein eL39



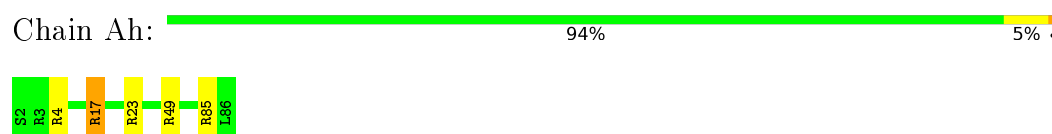
- Molecule 53: 60S ribosomal protein eL40



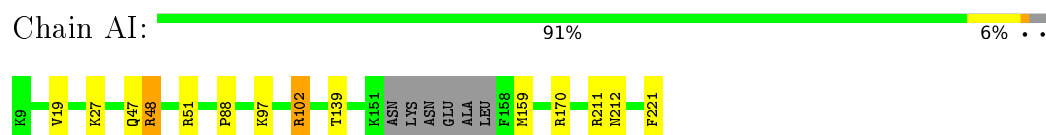
- Molecule 54: 60S ribosomal protein eL15



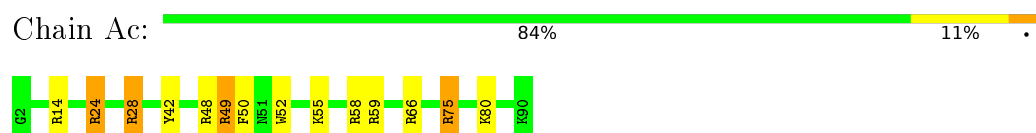
- Molecule 55: 60S ribosomal protein eL43



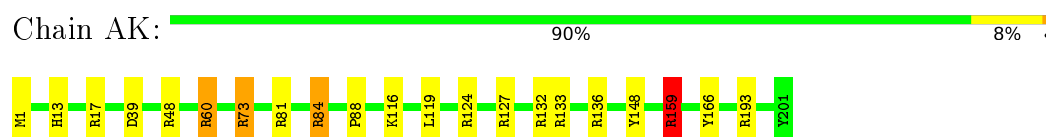
- Molecule 56: 60S ribosomal protein eL6



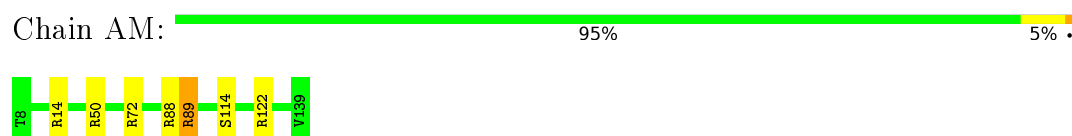
- Molecule 57: 60S ribosomal protein eL37



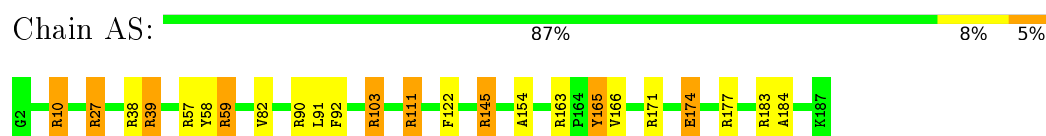
- Molecule 58: 60S ribosomal protein uL13



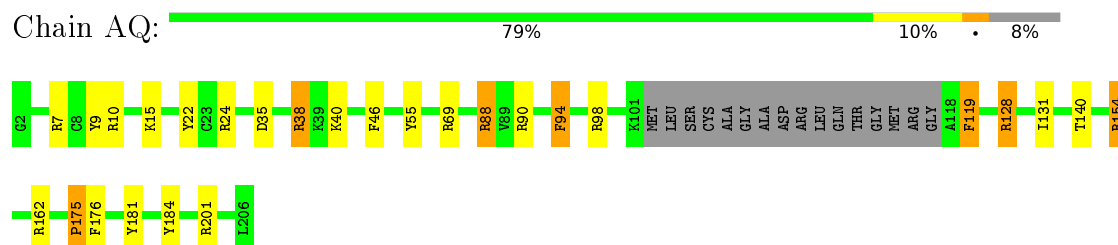
- Molecule 59: 60S ribosomal protein uL14



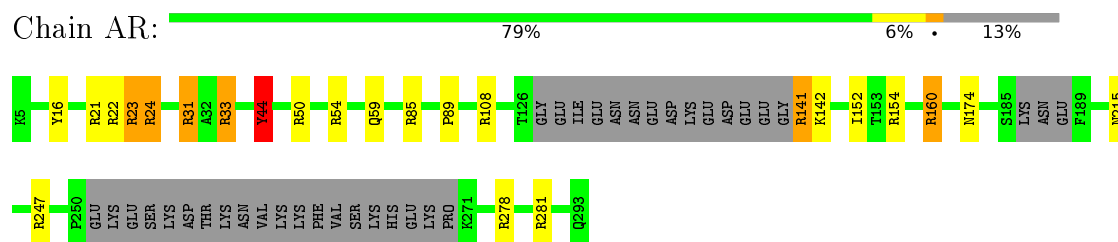
- Molecule 60: 60S ribosomal protein eL18



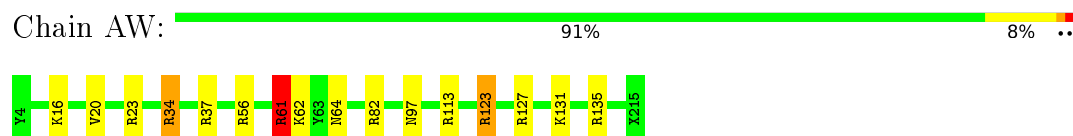
- Molecule 61: 60S ribosomal protein uL16



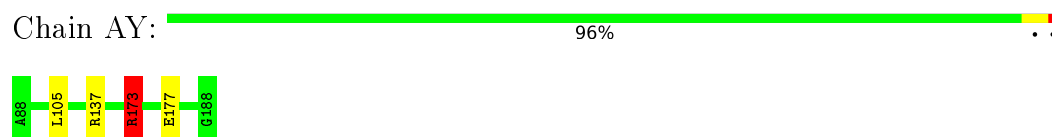
- Molecule 62: 60S ribosomal protein uL18



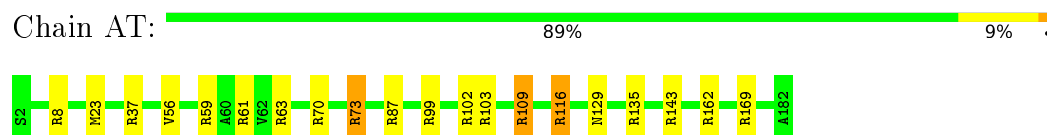
- Molecule 63: 60S ribosomal protein uL22



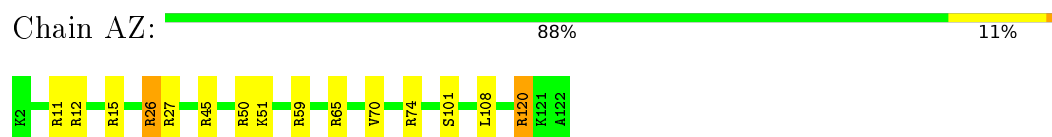
- Molecule 64: 60S ribosomal protein uL23



- 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: 89% 9% .



- Molecule 69: 60S ribosomal protein uL2

Chain AD: 89% 9% .



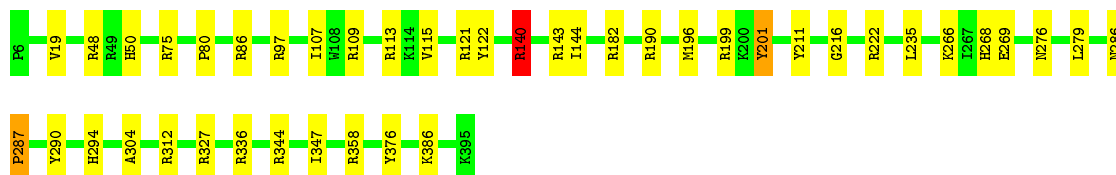
- Molecule 70: 60S ribosomal protein uL3

Chain AE: 92% 7% .



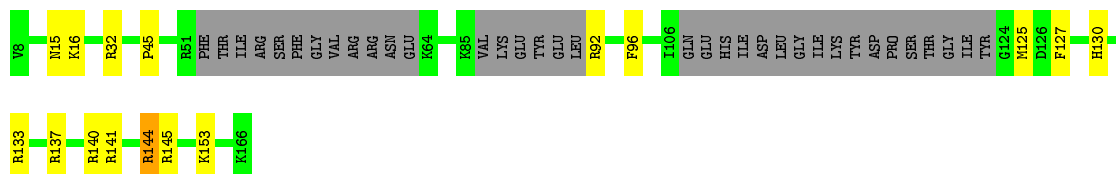
- Molecule 71: 60S ribosomal protein uL4

Chain AF: 89% 10% .



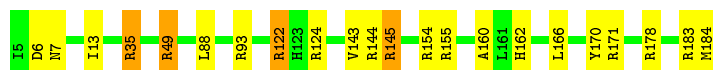
- Molecule 72: 60S ribosomal protein uL5

Chain AG: 68% 9% 22%



- Molecule 73: 60S ribosomal protein eL20

Chain AU: 88% 10% .



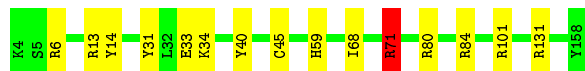
- Molecule 74: 60S ribosomal protein uL6

Chain AH:  95% . .




- Molecule 75: 60S ribosomal protein eL21

Chain AV:  90% 9% .



- Molecule 76: 60S ribosomal protein eL41

Chain Ag:  76% 19% 5%




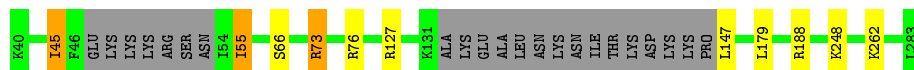
- Molecule 77: 60S ribosomal protein eL22

Chain AX:  92% 7% .



- Molecule 78: 60S ribosomal protein eL8

Chain AJ:  86% . . 9%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	22793	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	7/38275 (0.0%)	1.52	877/59596 (1.5%)
10	X	0.70	0/788	1.18	7/1050 (0.7%)
11	G	0.69	0/1800	1.00	5/2429 (0.2%)
12	W	0.71	0/793	1.13	4/1053 (0.4%)
13	R	0.73	0/755	1.02	2/1013 (0.2%)
14	I	0.71	0/1443	1.06	7/1936 (0.4%)
15	O	0.74	0/706	1.08	8/950 (0.8%)
16	Y	0.70	0/1295	1.17	15/1742 (0.9%)
17	Z	0.70	0/565	0.97	1/758 (0.1%)
18	1	0.73	0/999	1.26	13/1321 (1.0%)
19	2	0.78	0/324	0.92	0/435
2	7	1.15	0/1785	1.70	63/2782 (2.3%)
20	C	0.68	0/1570	1.06	7/2129 (0.3%)
21	3	0.73	0/794	1.26	13/1055 (1.2%)
22	4	0.67	0/597	0.98	0/801
23	5	0.76	0/459	1.20	6/606 (1.0%)
24	6	0.75	0/349	1.23	4/458 (0.9%)
25	B	0.67	0/1738	1.05	8/2321 (0.3%)
26	D	0.76	0/1241	1.09	6/1652 (0.4%)
27	F	0.68	0/2098	1.11	12/2819 (0.4%)
28	H	0.69	0/1665	1.08	9/2210 (0.4%)
29	K	0.71	0/1054	1.12	8/1411 (0.6%)
3	Q	0.72	0/1149	1.13	11/1532 (0.7%)
30	J	0.69	0/1545	1.03	5/2064 (0.2%)
31	N	0.69	0/780	1.10	2/1053 (0.2%)
32	P	0.69	0/966	1.21	12/1295 (0.9%)
33	L	0.72	0/1407	1.12	15/1879 (0.8%)
34	AA	1.23	16/75922 (0.0%)	1.52	1781/118216 (1.5%)
35	AC	1.12	0/3599	1.55	91/5603 (1.6%)
36	AB	1.13	2/2823 (0.1%)	1.48	71/4400 (1.6%)
37	AL	0.69	0/1789	1.15	13/2381 (0.5%)
38	A0	0.76	0/534	1.16	3/711 (0.4%)
39	AO	0.68	0/1199	1.17	10/1597 (0.6%)
4	S	0.65	0/1063	1.17	10/1425 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	Ai	0.69	0/789	1.17	9/1032 (0.9%)
41	A2	0.74	0/840	0.98	4/1114 (0.4%)
42	A4	0.68	0/564	1.00	2/737 (0.3%)
43	A6	0.70	0/749	1.06	4/1001 (0.4%)
44	A7	0.71	0/806	1.20	8/1073 (0.7%)
45	A1	0.69	0/1151	1.00	5/1531 (0.3%)
46	AN	0.71	0/1218	1.11	7/1621 (0.4%)
47	A8	0.72	0/1054	1.28	15/1399 (1.1%)
48	A9	0.71	0/865	1.22	12/1160 (1.0%)
49	Aa	0.68	0/872	1.20	7/1161 (0.6%)
5	T	0.79	0/412	1.14	5/544 (0.9%)
50	Ab	0.72	0/763	1.06	3/1008 (0.3%)
51	Ad	0.72	0/612	1.15	5/812 (0.6%)
52	Ae	0.77	0/396	1.45	8/521 (1.5%)
53	Af	0.68	0/419	1.19	4/556 (0.7%)
54	AP	0.72	0/1735	1.22	16/2320 (0.7%)
55	Ah	0.68	0/668	1.16	6/887 (0.7%)
56	AI	0.67	0/1708	1.03	7/2274 (0.3%)
57	Ac	0.74	0/723	1.24	10/951 (1.1%)
58	AK	0.70	0/1690	1.08	9/2260 (0.4%)
59	AM	0.68	0/1012	1.10	9/1363 (0.7%)
6	M	0.71	0/1114	1.14	9/1487 (0.6%)
60	AS	0.71	0/1531	1.22	18/2040 (0.9%)
61	AQ	0.74	0/1580	1.21	21/2113 (1.0%)
62	AR	0.71	0/2079	1.17	18/2777 (0.6%)
63	AW	0.71	0/1244	1.15	10/1663 (0.6%)
64	AY	0.67	0/806	0.97	2/1074 (0.2%)
65	AT	0.69	0/1525	1.18	20/2016 (1.0%)
66	AZ	0.70	0/1013	1.24	14/1339 (1.0%)
67	A3	0.69	0/1005	1.18	11/1329 (0.8%)
68	A5	0.71	0/1917	1.18	22/2562 (0.9%)
69	AD	0.68	0/1902	1.16	17/2544 (0.7%)
7	U	0.68	0/1223	1.10	10/1634 (0.6%)
70	AE	0.68	0/3130	1.12	21/4195 (0.5%)
71	AF	0.70	0/3145	1.10	19/4205 (0.5%)
72	AG	0.75	0/1021	1.16	7/1349 (0.5%)
73	AU	0.71	0/1527	1.18	15/2043 (0.7%)
74	AH	0.67	0/1501	1.08	6/2025 (0.3%)
75	AV	0.69	0/1301	1.10	9/1732 (0.5%)
76	Ag	0.82	0/348	1.50	10/448 (2.2%)
77	AX	0.72	0/842	1.14	8/1125 (0.7%)
78	AJ	0.84	1/1840 (0.1%)	0.99	5/2456 (0.2%)
8	V	0.73	0/1233	1.12	10/1645 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
9	E	0.71	0/1539	1.12	14/2055 (0.7%)
All	All	1.01	26/207281 (0.0%)	1.39	3550/303864 (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	141
10	X	0	2
12	W	0	3
14	I	0	3
16	Y	0	2
18	1	0	3
19	2	0	1
2	7	1	5
21	3	0	2
23	5	0	1
24	6	0	4
25	B	1	4
27	F	0	4
28	H	0	4
29	K	0	1
3	Q	0	4
32	P	0	5
33	L	0	2
34	AA	1	328
35	AC	0	13
36	AB	0	8
37	AL	0	7
38	A0	0	1
39	AO	0	1
40	Ai	0	3
41	A2	2	0
42	A4	0	5
43	A6	0	1
44	A7	0	1
46	AN	0	3
47	A8	0	3
48	A9	0	3
49	Aa	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
5	T	0	1
50	Ab	0	3
51	Ad	0	2
52	Ae	0	2
53	Af	0	2
54	AP	0	7
55	Ah	0	1
56	AI	0	2
57	Ac	0	3
58	AK	0	8
6	M	0	2
60	AS	0	9
61	AQ	0	6
62	AR	0	7
63	AW	0	4
64	AY	0	1
65	AT	0	3
66	AZ	0	4
67	A3	0	1
68	A5	0	5
69	AD	0	4
7	U	0	1
70	AE	0	6
71	AF	0	10
72	AG	0	3
73	AU	0	5
74	AH	0	2
75	AV	0	6
76	Ag	0	3
77	AX	0	1
78	AJ	0	2
8	V	0	3
9	E	0	3
All	All	5	692

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	AA	2915	U	C2-N3	70.80	1.87	1.37
34	AA	2915	U	C4-C5	67.04	2.03	1.43
34	AA	2915	U	N1-C2	60.98	1.93	1.38
34	AA	2915	U	N1-C6	57.12	1.89	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	AA	2915	U	N3-C4	56.47	1.89	1.38

The worst 5 of 3550 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	181	C	P-O3'-C3'	14.44	137.03	119.70
1	A	981	U	P-O3'-C3'	14.26	136.81	119.70
1	A	844	G	P-O3'-C3'	13.99	136.49	119.70
1	A	1912	C	P-O3'-C3'	13.97	136.47	119.70
34	AA	1202	C	P-O3'-C3'	13.95	136.44	119.70

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	7	31	G	C3'
25	B	225	ILE	CB
34	AA	3018	A	C3'
41	A2	55	THR	CA
41	A2	116	SER	CA

5 of 692 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3	C	Sidechain
1	A	38	C	Sidechain
1	A	39	A	Sidechain
1	A	47	A	Sidechain
1	A	62	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	45	0
2	7	1598	0	816	1	0
3	Q	1129	0	1196	3	0
4	S	1047	0	1101	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	T	405	0	419	0	0
6	M	1099	0	1183	1	0
7	U	1202	0	1299	1	0
8	V	1206	0	1239	1	0
9	E	1515	0	1605	0	0
10	X	777	0	832	2	0
11	G	1758	0	1811	1	0
12	W	786	0	858	0	0
13	R	747	0	754	0	0
14	I	1424	0	1471	1	0
15	O	687	0	695	0	0
16	Y	1267	0	1316	0	0
17	Z	557	0	558	0	0
18	1	986	0	1076	0	0
19	2	321	0	338	0	0
20	C	1539	0	1600	0	0
21	3	782	0	820	1	0
22	4	586	0	604	1	0
23	5	458	0	496	0	0
24	6	346	0	381	0	0
25	B	1714	0	1838	2	0
26	D	1229	0	1311	0	0
27	F	2062	0	2200	1	0
28	H	1648	0	1803	0	0
29	K	1037	0	1099	3	0
30	J	1529	0	1680	1	0
31	N	772	0	813	0	0
32	P	954	0	997	1	0
33	L	1383	0	1434	1	0
34	AA	67862	0	34233	156	0
35	AC	3215	0	1633	6	0
36	AB	2522	0	1275	2	0
37	AL	1757	0	1888	1	0
38	A0	522	0	539	0	0
39	AO	1172	0	1230	1	0
40	Ai	779	0	861	0	0
41	A2	831	0	887	1	0
42	A4	555	0	599	3	0
43	A6	741	0	763	1	0
44	A7	794	0	869	0	0
45	A1	1134	0	1245	1	0
46	AN	1202	0	1316	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	A8	1037	0	1139	1	0
48	A9	845	0	886	1	0
49	Aa	859	0	912	0	0
50	Ab	757	0	842	0	0
51	Ad	604	0	686	0	0
52	Ae	388	0	421	0	0
53	Af	414	0	452	0	0
54	AP	1697	0	1802	2	0
55	Ah	659	0	727	0	0
56	AI	1685	0	1849	0	0
57	Ac	710	0	761	0	0
58	AK	1660	0	1785	1	0
59	AM	996	0	1044	0	0
60	AS	1503	0	1636	0	0
61	AQ	1545	0	1582	0	0
62	AR	2050	0	2140	1	0
63	AW	1319	0	1303	0	0
64	AY	797	0	850	0	0
65	AT	1509	0	1682	0	0
66	AZ	1001	0	1099	1	0
67	A3	995	0	1121	1	0
68	A5	1879	0	2005	0	0
69	AD	1867	0	1964	1	0
70	AE	3062	0	3205	4	0
71	AF	3095	0	3333	3	0
72	AG	1011	0	1073	1	0
73	AU	1497	0	1556	2	0
74	AH	1476	0	1574	0	0
75	AV	1276	0	1355	1	0
76	Ag	343	0	388	0	0
77	AX	825	0	882	1	0
78	AJ	1813	0	1985	25	0
All	All	193017	0	144286	249	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 249 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:2915:U:C5	34:AA:2915:U:C4	2.03	1.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:2915:U:C2	34:AA:2915:U:N3	1.87	1.42
34:AA:2915:U:N1	34:AA:2915:U:C6	1.89	1.39
34:AA:2915:U:N3	34:AA:2915:U:C4	1.89	1.37
34:AA:2915:U:N1	34:AA:2915:U:C2	1.93	1.35

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	Q	142/144 (99%)	134 (94%)	6 (4%)	2 (1%)	14	58
4	S	126/128 (98%)	107 (85%)	11 (9%)	8 (6%)	2	25
5	T	46/48 (96%)	44 (96%)	2 (4%)	0	100	100
6	M	136/138 (99%)	128 (94%)	6 (4%)	2 (2%)	13	57
7	U	147/149 (99%)	144 (98%)	2 (1%)	1 (1%)	26	71
8	V	142/156 (91%)	134 (94%)	4 (3%)	4 (3%)	6	44
9	E	183/185 (99%)	176 (96%)	7 (4%)	0	100	100
10	X	92/103 (89%)	82 (89%)	6 (6%)	4 (4%)	3	34
11	G	222/224 (99%)	209 (94%)	10 (4%)	3 (1%)	14	58
12	W	91/108 (84%)	87 (96%)	3 (3%)	1 (1%)	17	63
13	R	92/114 (81%)	78 (85%)	10 (11%)	4 (4%)	3	34
14	I	176/189 (93%)	166 (94%)	7 (4%)	3 (2%)	11	55
15	O	77/79 (98%)	70 (91%)	3 (4%)	4 (5%)	2	29
16	Y	152/154 (99%)	141 (93%)	7 (5%)	4 (3%)	7	45
17	Z	70/72 (97%)	65 (93%)	4 (6%)	1 (1%)	14	58
18	1	118/120 (98%)	109 (92%)	7 (6%)	2 (2%)	11	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	2	35/68 (52%)	32 (91%)	1 (3%)	2 (6%)	2	27
20	C	193/195 (99%)	180 (93%)	11 (6%)	2 (1%)	19	65
21	3	93/95 (98%)	81 (87%)	12 (13%)	0	100	100
22	4	74/76 (97%)	67 (90%)	4 (5%)	3 (4%)	3	35
23	5	54/65 (83%)	52 (96%)	1 (2%)	1 (2%)	10	52
24	6	41/43 (95%)	38 (93%)	3 (7%)	0	100	100
25	B	208/210 (99%)	188 (90%)	16 (8%)	4 (2%)	10	52
26	D	149/209 (71%)	143 (96%)	4 (3%)	2 (1%)	15	60
27	F	255/257 (99%)	244 (96%)	10 (4%)	1 (0%)	39	80
28	H	200/214 (94%)	186 (93%)	13 (6%)	1 (0%)	34	77
29	K	127/129 (98%)	119 (94%)	6 (5%)	2 (2%)	12	56
30	J	186/188 (99%)	175 (94%)	7 (4%)	4 (2%)	8	49
31	N	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
32	P	125/127 (98%)	110 (88%)	15 (12%)	0	100	100
33	L	165/214 (77%)	149 (90%)	15 (9%)	1 (1%)	30	74
37	AL	209/211 (99%)	190 (91%)	13 (6%)	6 (3%)	6	43
38	A0	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
39	AO	145/147 (99%)	134 (92%)	8 (6%)	3 (2%)	9	50
40	Ai	93/95 (98%)	84 (90%)	6 (6%)	3 (3%)	5	41
41	A2	96/118 (81%)	92 (96%)	3 (3%)	1 (1%)	19	65
42	A4	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
43	A6	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
44	A7	92/102 (90%)	90 (98%)	2 (2%)	0	100	100
45	A1	136/145 (94%)	131 (96%)	5 (4%)	0	100	100
46	AN	144/146 (99%)	138 (96%)	4 (3%)	2 (1%)	14	58
47	A8	123/125 (98%)	111 (90%)	10 (8%)	2 (2%)	12	56
48	A9	101/103 (98%)	93 (92%)	5 (5%)	3 (3%)	5	42
49	Aa	104/106 (98%)	97 (93%)	7 (7%)	0	100	100
50	Ab	91/105 (87%)	86 (94%)	3 (3%)	2 (2%)	8	49
51	Ad	68/76 (90%)	65 (96%)	2 (3%)	1 (2%)	13	57
52	Ae	39/50 (78%)	38 (97%)	1 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	Af	49/51 (96%)	44 (90%)	5 (10%)	0	100	100
54	AP	202/204 (99%)	182 (90%)	11 (5%)	9 (4%)	3	33
55	Ah	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
56	AI	203/213 (95%)	188 (93%)	10 (5%)	5 (2%)	7	46
57	Ac	87/89 (98%)	78 (90%)	6 (7%)	3 (3%)	5	40
58	AK	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	34	77
59	AM	130/132 (98%)	122 (94%)	7 (5%)	1 (1%)	24	69
60	AS	184/186 (99%)	166 (90%)	13 (7%)	5 (3%)	6	44
61	AQ	185/205 (90%)	169 (91%)	11 (6%)	5 (3%)	6	44
62	AR	244/289 (84%)	219 (90%)	19 (8%)	6 (2%)	7	46
63	AW	149/170 (88%)	137 (92%)	10 (7%)	2 (1%)	15	60
64	AY	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	19	65
65	AT	179/181 (99%)	174 (97%)	3 (2%)	2 (1%)	17	63
66	AZ	119/121 (98%)	113 (95%)	5 (4%)	1 (1%)	24	69
67	A3	117/119 (98%)	110 (94%)	5 (4%)	2 (2%)	11	55
68	A5	221/223 (99%)	197 (89%)	19 (9%)	5 (2%)	8	48
69	AD	245/247 (99%)	232 (95%)	9 (4%)	4 (2%)	12	56
70	AE	378/380 (100%)	350 (93%)	27 (7%)	1 (0%)	46	83
71	AF	388/390 (100%)	355 (92%)	24 (6%)	9 (2%)	8	48
72	AG	116/159 (73%)	106 (91%)	7 (6%)	3 (3%)	7	45
73	AU	178/180 (99%)	162 (91%)	12 (7%)	4 (2%)	8	49
74	AH	183/185 (99%)	163 (89%)	17 (9%)	3 (2%)	12	56
75	AV	153/155 (99%)	142 (93%)	10 (6%)	1 (1%)	26	71
76	Ag	35/37 (95%)	29 (83%)	5 (14%)	1 (3%)	6	43
77	AX	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
78	AJ	216/244 (88%)	201 (93%)	12 (6%)	3 (1%)	14	58
All	All	10111/10698 (94%)	9380 (93%)	565 (6%)	166 (2%)	17	56

5 of 166 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	M	41	GLU
8	V	41	VAL

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Mol	Chain	Res	Type
10	X	52	LYS
13	R	42	ILE
14	I	70	HIS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Q	120/120 (100%)	116 (97%)	4 (3%)	45	76
4	S	114/114 (100%)	111 (97%)	3 (3%)	54	80
5	T	43/43 (100%)	41 (95%)	2 (5%)	32	68
6	M	116/116 (100%)	112 (97%)	4 (3%)	44	75
7	U	132/132 (100%)	129 (98%)	3 (2%)	58	83
8	V	131/140 (94%)	128 (98%)	3 (2%)	58	83
9	E	161/164 (98%)	159 (99%)	2 (1%)	78	90
10	X	88/94 (94%)	87 (99%)	1 (1%)	80	91
11	G	191/191 (100%)	186 (97%)	5 (3%)	54	80
12	W	86/99 (87%)	86 (100%)	0	100	100
13	R	83/97 (86%)	83 (100%)	0	100	100
14	I	154/160 (96%)	150 (97%)	4 (3%)	54	80
15	O	76/76 (100%)	74 (97%)	2 (3%)	54	80
16	Y	137/137 (100%)	132 (96%)	5 (4%)	42	74
17	Z	60/60 (100%)	60 (100%)	0	100	100
18	1	104/104 (100%)	102 (98%)	2 (2%)	65	86
19	2	35/61 (57%)	34 (97%)	1 (3%)	50	78
20	C	167/167 (100%)	164 (98%)	3 (2%)	66	87
21	3	87/87 (100%)	87 (100%)	0	100	100
22	4	70/70 (100%)	68 (97%)	2 (3%)	50	78
23	5	47/52 (90%)	46 (98%)	1 (2%)	61	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	6	36/36 (100%)	36 (100%)	0	100	100
25	B	195/195 (100%)	191 (98%)	4 (2%)	61	84
26	D	132/177 (75%)	127 (96%)	5 (4%)	40	73
27	F	233/233 (100%)	223 (96%)	10 (4%)	35	70
28	H	182/190 (96%)	175 (96%)	7 (4%)	40	73
29	K	115/115 (100%)	114 (99%)	1 (1%)	84	93
30	J	177/177 (100%)	170 (96%)	7 (4%)	38	71
31	N	91/91 (100%)	90 (99%)	1 (1%)	80	91
32	P	99/99 (100%)	97 (98%)	2 (2%)	63	85
33	L	151/190 (80%)	147 (97%)	4 (3%)	54	80
37	AL	190/190 (100%)	185 (97%)	5 (3%)	54	80
38	A0	53/53 (100%)	52 (98%)	1 (2%)	65	86
39	AO	121/121 (100%)	117 (97%)	4 (3%)	45	76
40	Ai	87/87 (100%)	85 (98%)	2 (2%)	58	83
41	A2	97/109 (89%)	94 (97%)	3 (3%)	47	77
42	A4	60/60 (100%)	59 (98%)	1 (2%)	68	87
43	A6	83/83 (100%)	80 (96%)	3 (4%)	42	74
44	A7	90/96 (94%)	89 (99%)	1 (1%)	80	91
45	A1	127/131 (97%)	126 (99%)	1 (1%)	86	94
46	AN	135/135 (100%)	132 (98%)	3 (2%)	60	83
47	A8	114/114 (100%)	113 (99%)	1 (1%)	84	93
48	A9	90/90 (100%)	84 (93%)	6 (7%)	20	57
49	Aa	89/89 (100%)	86 (97%)	3 (3%)	44	75
50	Ab	82/92 (89%)	80 (98%)	2 (2%)	57	82
51	Ad	69/73 (94%)	67 (97%)	2 (3%)	50	78
52	Ae	40/47 (85%)	38 (95%)	2 (5%)	30	66
53	Af	45/45 (100%)	44 (98%)	1 (2%)	60	83
54	AP	179/179 (100%)	170 (95%)	9 (5%)	30	66
55	Ah	70/70 (100%)	70 (100%)	0	100	100
56	AI	189/195 (97%)	186 (98%)	3 (2%)	70	88
57	Ac	74/74 (100%)	71 (96%)	3 (4%)	37	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	AK	181/181 (100%)	175 (97%)	6 (3%)	45	76
59	AM	106/106 (100%)	105 (99%)	1 (1%)	84	93
60	AS	158/158 (100%)	154 (98%)	4 (2%)	55	81
61	AQ	165/176 (94%)	159 (96%)	6 (4%)	42	74
62	AR	215/250 (86%)	210 (98%)	5 (2%)	58	83
63	AW	128/128 (100%)	121 (94%)	7 (6%)	27	64
64	AY	90/90 (100%)	88 (98%)	2 (2%)	60	83
65	AT	162/162 (100%)	160 (99%)	2 (1%)	78	90
66	AZ	111/111 (100%)	109 (98%)	2 (2%)	66	87
67	A3	110/110 (100%)	106 (96%)	4 (4%)	42	74
68	A5	201/201 (100%)	197 (98%)	4 (2%)	63	85
69	AD	191/191 (100%)	181 (95%)	10 (5%)	29	65
70	AE	335/335 (100%)	332 (99%)	3 (1%)	84	93
71	AF	336/336 (100%)	327 (97%)	9 (3%)	52	79
72	AG	110/142 (78%)	107 (97%)	3 (3%)	52	79
73	AU	162/162 (100%)	160 (99%)	2 (1%)	78	90
74	AH	168/168 (100%)	166 (99%)	2 (1%)	78	90
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	AJ	204/224 (91%)	200 (98%)	4 (2%)	63	85
All	All	9096/9417 (97%)	8871 (98%)	225 (2%)	59	81

5 of 225 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	A2	59	LEU
51	Ad	38	ILE
71	AF	376	TYR
43	A6	26	TYR
48	A9	53	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
46	AN	130	GLN
55	Ah	34	HIS
70	AE	253	HIS
49	Aa	10	HIS
29	K	113	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1588/1608 (98%)	480 (30%)	100 (6%)
2	7	74/75 (98%)	33 (44%)	5 (6%)
34	AA	3165/3192 (99%)	971 (30%)	189 (5%)
35	AC	148/151 (98%)	49 (33%)	10 (6%)
36	AB	117/118 (99%)	27 (23%)	2 (1%)
All	All	5092/5144 (98%)	1560 (30%)	306 (6%)

5 of 1560 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	3	C
1	A	5	U
1	A	17	C
1	A	26	A

5 of 306 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	AA	594	C
34	AA	998	U
34	AA	3627	C
34	AA	607	A
34	AA	703	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.