



wwPDB EM Validation Summary Report ⓘ

Feb 12, 2024 – 04:59 PM EST

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

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

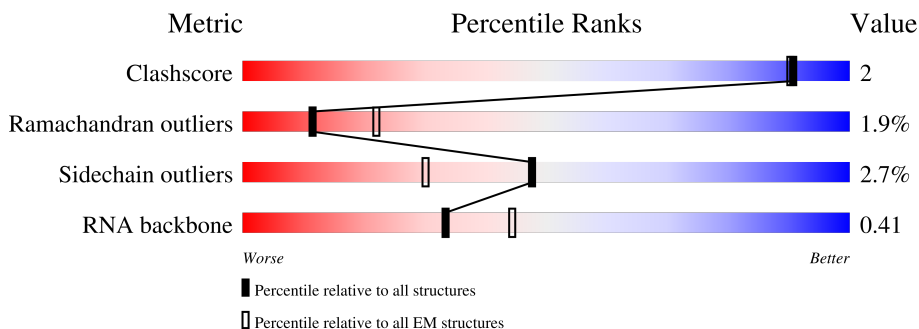
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	29% (green), 44% (yellow), 22% (orange), 5% (red)
2	7	74	9% (green), 41% (yellow), 38% (orange), 12% (red)
3	D	209	70% (green), 25% (grey)
4	E	185	88% (green), 11% (yellow), 1% (red)
5	G	224	93% (green), 7% (yellow)
6	I	189	87% (green), 5% (yellow), 5% (grey)
7	K	129	90% (green), 5% (yellow), 5% (orange), 1% (red)


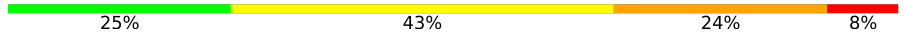
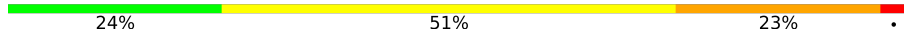
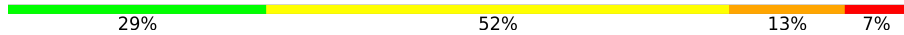













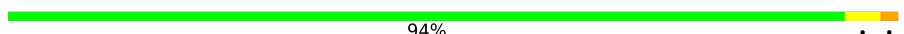

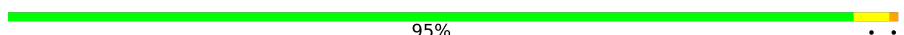





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Mol	Chain	Length	Quality of chain
8	M	138	94% 6%
9	W	108	75% 13% 12%
10	R	114	80% 6% 14%
11	O	79	86% 14%
12	Y	154	86% 13%
13	Z	72	94% 6%
14	1	120	90% 8%
15	2	68	57% 40%
16	3	95	85% 13%
17	4	76	88% 11%
18	5	65	80% 9% 11%
19	6	43	86% 14%
20	B	210	92% 5%
21	F	257	89% 10%
22	H	214	86% 8% 5%
23	J	188	88% 12%
24	L	214	69% 9% 20%
25	N	98	90% 8%
26	P	127	90% 9%
27	Q	144	92% 7%
28	S	128	84% 14%
29	T	48	85% 12%
30	U	149	91% 7%
31	V	156	86% 6% 6%
32	X	103	83% 10% 7%

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Mol	Chain	Length	Quality of chain
33	C	195	 89% 10%
34	AA	3193	 25% 43% 24% 8%
35	AC	151	 24% 51% 23%
36	AB	118	 29% 52% 13% 7%
37	AL	211	 92% 7%
38	A1	145	 89% 8%
39	A2	118	 82% 6% 12%
40	A4	66	 86% 8% 5%
41	A6	98	 90% 8%
42	A7	102	 86% 8% 6%
43	AN	146	 90% 8%
44	A8	125	 88% 10%
45	A9	103	 88% 9%
46	Aa	106	 83% 16%
47	Ab	105	 87% 10%
48	Ad	76	 91% 5%
49	Ae	50	 68% 14% 14%
50	Af	51	 94%
51	AP	204	 84% 15%
52	Ah	85	 95%
53	Ai	95	 91% 8%
54	AI	213	 91% 6%
55	AJ	244	 87% 9%
56	Ac	89	 82% 16%
57	AK	201	 90% 9%

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Mol	Chain	Length	Quality of chain
58	AM	132	93% 5% .
59	AS	186	86% 12% .
60	AO	147	89% 10% .
61	AQ	205	80% 11% . 8%
62	AR	289	77% 9% . 13%
63	AW	170	88% 9% .
64	AY	101	94% 5% .
65	AT	181	91% 8% ..
66	AZ	121	93% 5% .
67	A3	119	92% 8% .
68	A5	223	86% 11% .
69	AD	247	89% 9% ..
70	AE	380	89% 10% .
71	AF	390	92% 7% .
72	AG	159	70% 6% . 22%
73	AU	180	88% 7% . .
74	AH	185	91% 8% .
75	AV	155	89% 10% .
76	Ag	37	76% 16% 8%
77	AX	97	94% 6%
78	A0	62	92% 6% .

2 Entry composition

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
27	Q	144	1129	712	222	193	2	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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
			Total	C	N	O	S		
38	A1	140	1134	736	204	191	3	0	0

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

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

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

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

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

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

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

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

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

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

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
			Total	C	N	O	S		
44	A8	125	1037	660	206	164	7	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
59	AS	186	1503	958	299	241	5	0	0

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

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

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

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

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

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

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
			Total	C	N	O	S		
63	AW	170	1319	824	266	222	7	0	0

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

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

- 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		

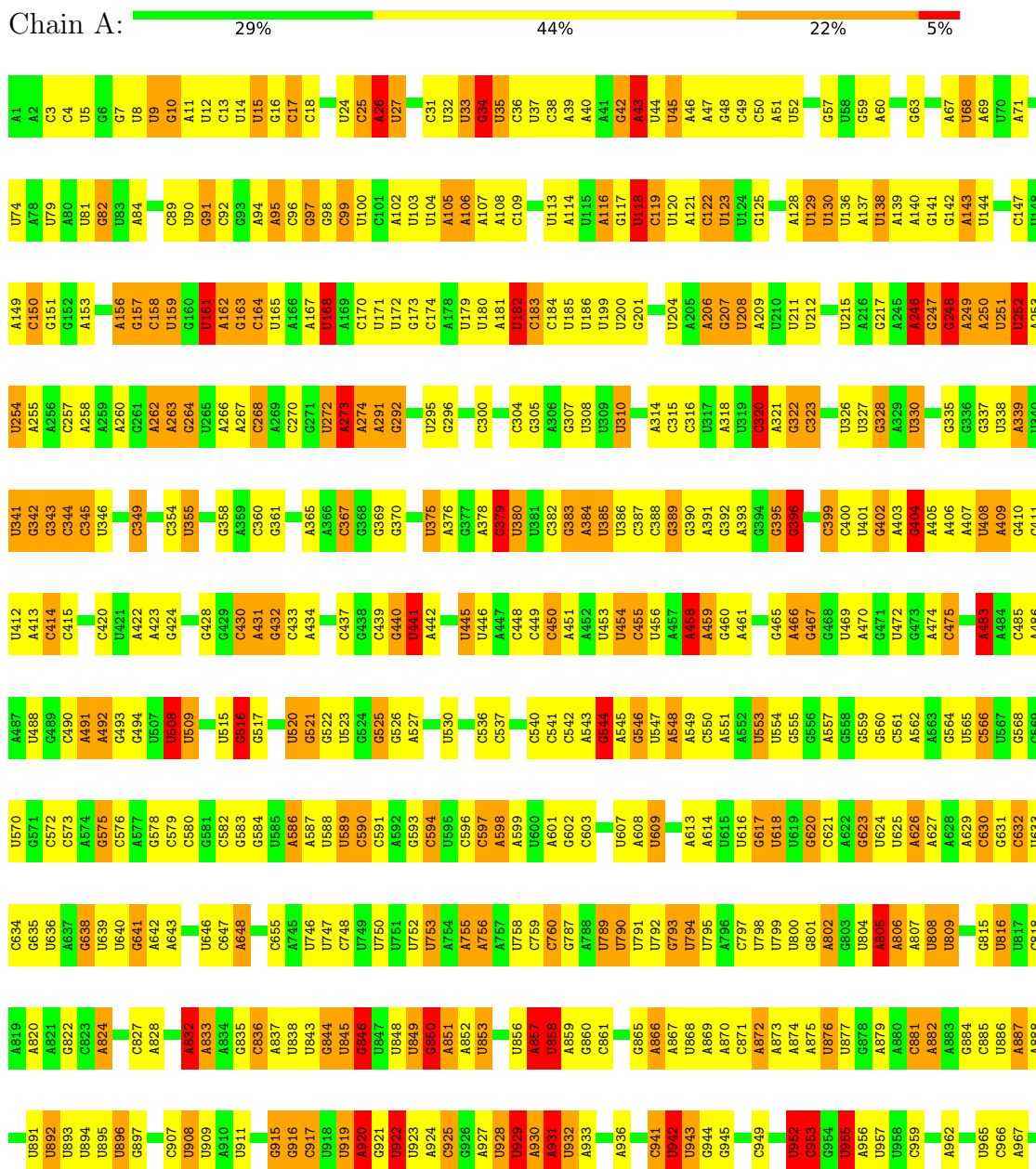
- Molecule 78 is a protein called 60S ribosomal protein eL24.

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

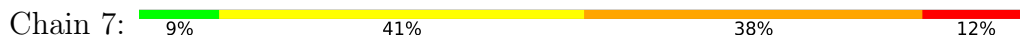
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

- Molecule 1: 18S ribosomal RNA



U2068	G970	C1031	C1087	U1207	U1275	G1378	U1661	U1728	A1822	A1884	C1945	U2068
A2029	G971	A1032	U1086	G1208	U1276	G1379	U1662	A1729	U1823	G1885	C1946	A2029
C2031	U972	A1035	A1099	C1209	G1277	C1380	G1664	A1730	A1824	C1886	U1947	C2031
U2032	G973	G1038	U1100	G1210	C1278	C1381	U1665	C1731	A1825	A1887	A1948	U2032
U2034	A974	G1039	C1102	C1211	G1279	C1382	C1666	G1732	A1826	G1888	C1949	U2034
U2035	U975	A1039	G1101	G1212	C1280	U1383	A1667	A1733	U1827	U1889	C1950	U2035
A2042	U976	A1040	C1103	G1213	C1281	U1384	A1668	G1734	G1880	A1890	G1951	U2042
G2043	U977	G1041	G1104	A1214	U1282	U1385	C1669	A1735	C1881	U1891	A1952	G2043
G2044	C979	A1042	A1105	G1215	U1283	U1386	A1455	A1736	G1882	U1892	U1953	G2044
A2048	U980	A1043	C1106	U1216	A1284	U1387	G1456	A1742	U1832	C1893	A1954	A2048
U2049	U981	A1044	U1107	U1219	A1285	A1388	G1672	A1743	G1833	A1894	G1955	U2049
C2051	U982	C1044	A1108	U1220	U1286	U1389	A1673	A1744	A1834	A1895	A1956	C2051
G2052	G983	G1045	A1109	G1221	U1287	U1390	G1674	U1745	U1835	C1896	A1957	G2052
A2054	G984	A1046	G1109	G1222	U1288	U1391	G1675	A1746	G1836	A1897	A1958	A2054
C2055	U984	A1047	G1112	G1223	G1289	U1392	U1676	U1747	G1837	G1898	G1959	C2055
A2056	U985	U1050	U1116	G1224	A1290	U1400	C1677	G1748	G1838	A1899	A1960	A2056
C2057	U986	U1051	G1116	A1225	A1291	G1401	U1678	C1749	G1839	A1900	U1961	C2057
A2058	U987	U1055	U1118	A1226	C1293	A1402	U1679	U1750	A1840	U1901	A1962	A2058
G2059	U988	G1056	U1119	G1227	A1294	A1403	A1682	C1781	U1841	G1902	U1963	G2059
C2060	C989	G1055	G1166	U1228	C1295	U1404	U1683	A1782	A1842	U1903	G1964	C2060
U2061	U990	G1056	C1167	C1229	C1296	U1407	U1684	U1783	A1843	G1904	A1968	U2061
U2062	A993	A1057	U1168	A1230	A1297	U1408	U1685	U1784	U1844	C1905	A1969	U2062
U2063	G994	G1058	U1169	G1231	C1298	U1409	U1686	C1785	U1845	U1906	A1970	U2063
C2064	A995	U1059	U1169	U1232	C1299	U1410	U1687	U1786	A1846	A1907	U1971	C2064
G2065	G996	G1060	C1170	U1236	G1300	G1410	U1688	U1787	U1847	U1908	U1971	G2065
A2066	U997	A1061	U1171	U1239	G1301	G1412	G1622	U1788	U1848	U1909	G1972	A2066
C2067	U998	A1062	U1172	A1239	A1302	U1412	G1623	U1789	G1850	U1910	U1975	C2067
U2068	A999	G1063	C1173	G1239	C1296	U1413	U1624	U1790	G1851	C1912	G1976	U2068
G2069	C1000	A1064	U1174	A1241	A1297	U1414	U1625	C1791	A1852	G1913	G1977	G2069
C2070	C1001	G1065	U1175	G1242	C1298	U1414	U1626	U1792	A1853	U1914	A1978	C2070
U2071	A1002	G1065	U1176	A1243	G1299	U1415	U1627	C1793	U1854	C1915	C1979	U2071
G2072	U1003	G1066	U1177	U1244	U1307	U1416	U1628	U1794	U1855	U1916	A1980	G2072
A2073	U1004	A1067	C1178	A1247	A1308	U1418	C1697	G1795	U1856	C1917	A1981	A2073
C2074	U1005	G1071	U1179	G1248	A1309	U1419	G1697	G1796	U1857	U1918	G1982	C2074
C2075	C1006	A1072	U1181	C1249	C1310	U1420	G1700	C1797	U1858	G1919	A1983	C2075
C2076	G1007	U1073	U1182	G1250	G1313	U1422	U1703	A1799	A1859	C1921	A1984	C2076
C2079	A1008	A1074	A1182	A1252	U1314	A1423	G1704	A1800	A1860	C1922	U2004	C2079
U2080	U1009	C1075	U1183	G1255	U1314	A1424	C1705	A1801	C1862	C1923	U2005	U2080
A2081	U1010	C1076	G1185	G1256	U1315	U1425	A1706	G1802	U1863	U1924	U2006	A2081
C2082	U1011	C1076	A1185	G1257	U1320	U1426	C1707	G1803	U1864	U1924	U2007	C2082
G2083	A1013	G1079	A1187	G1258	A1321	U1427	U1708	G1804	G1865	U1927	U2008	G2083
C2084	U1014	U1081	A1188	A1259	C1322	A1428	C1709	G1805	A1866	A1928	C2009	C2084
G2085	U1015	U1082	A1189	G1260	A1322	U1429	G1710	G1806	A1867	C1929	U2009	G2085
A2086	C1018	A1083	C1191	C1261	U1362	G1430	U1711	A1807	C1868	A1930	G2012	A2086
U2087	C1019	A1084	C1192	A1262	U1363	G1431	G1712	G1808	G1869	C1931	G2012	U2087
U2088	U1020	C1085	A1193	C1263	U1364	G1432	U1713	G1809	A1870	A1932	A2013	U2088
A1021	A1021	U1086	A1194	G1264	G1365	U1433	U1714	U1810	G1871	C1933	A2014	A1021
A1022	A1022	U1087	G1195	A1264	A1366	U1434	A1715	A1811	G1872	C1934	A2015	A1022
A1023	A1023	A1088	U1196	G1265	U1367	U1435	C1716	A1812	A1873	G1935	A2016	A1023
A1024	A1024	A1089	C1197	G1266	U1368	U1436	C1717	U1813	A1874	C1936	A2017	A1024
U1025	C1091	A1090	C1198	C1267	G1369	U1437	U1718	C1814	G1875	C1937	C2018	U1025
A1026	U1091	C1091	U1199	G1268	U1370	U1440	U1719	U1815	C1877	A1938	C2019	A1026
C1027	U1092	U1092	U1199	G1268	U1370	U1440	G1720	U1816	C1878	G1939	G2020	C1027
U1029	U1093	U1093	U1200	G1271	G1374	U1441	A1721	U1817	U1879	U1940	U1942	U1029
U1030	A1094	A1094	G1201	G1272	C1374	U1442	A1722	U1818	A1880	C1941	G1942	U1030
	A1095	A1095	G1202	G1273	C1375	U1443	A1723	U1819	U1881	G1942	G1942	
			C1206	C1274	U1377	U1445	A1727	A1821	U1883	U1944	U1944	

• Molecule 2: E-tRNA

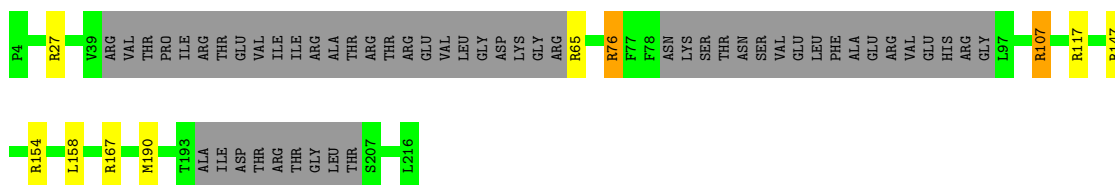


G1	G61
G2	G62
G3	
U4	
A5	
U6	
G9	
G10	
C11	
G12	
C13	
A14	
G15	
U16	
U17	
G18	
G19	
U20	
U21	
A22	
G23	
C24	
G25	
C26	
G27	
C28	
G29	
C30	
G31	
U32	
C33	
U34	
C35	
A36	
U37	
A38	
A39	
U40	
C41	
C42	
C43	
C44	
A45	
C46	
U48	
C49	
G50	
U51	
G52	
A53	
G54	
U55	
U56	
G57	
C61	
C62	



- Molecule 3: 40S ribosomal protein uS3

Chain D: 70% 25%



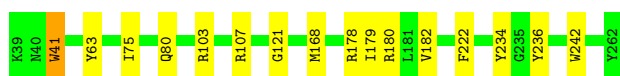
- Molecule 4: 40S ribosomal protein uS4

Chain E: 88% 11%



- Molecule 5: 40S ribosomal protein uS5

Chain G: 93% 7%



- Molecule 6: 40S ribosomal protein uS7

Chain I: 87% 5% 5%



- Molecule 7: 40S ribosomal protein uS8

Chain K: 90% 5%




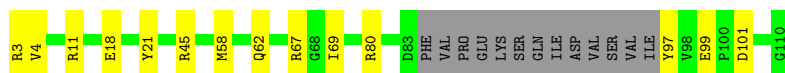
- Molecule 8: 40S ribosomal protein uS9

Chain M: 94% 6%




- Molecule 9: 40S ribosomal protein eS17

Chain W:  75% 13% 12%




- Molecule 10: 40S ribosomal protein eS12

Chain R:  80% 6% 14%




- Molecule 11: 40S ribosomal protein eS10

Chain O:  86% 14%



- Molecule 12: 40S ribosomal protein eS19

Chain Y:  86% 13%




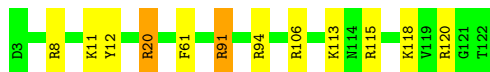
- Molecule 13: 40S ribosomal protein eS21

Chain Z:  94% 6%



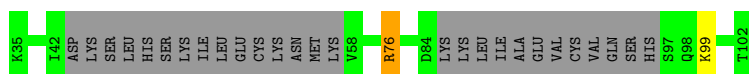
- Molecule 14: 40S ribosomal protein eS24

Chain 1:  90% 8%




- Molecule 15: 40S ribosomal protein eS25

Chain 2:  57% 40%




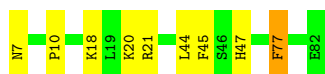
- Molecule 16: 40S ribosomal protein eS26

Chain 3:  85% 13%




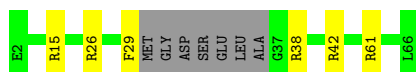
- Molecule 17: 40S ribosomal protein eS27

Chain 4:  88% 11%




- Molecule 18: 40S ribosomal protein eS28

Chain 5:  80% 9% 11%



- Molecule 19: 40S ribosomal protein eS30

Chain 6:  86% 14%




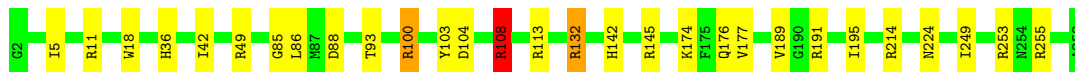
- Molecule 20: 40S ribosomal protein eS1

Chain B:  92% 5%




- Molecule 21: 40S ribosomal protein eS4

Chain F:  89% 10%



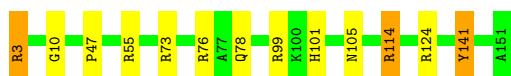
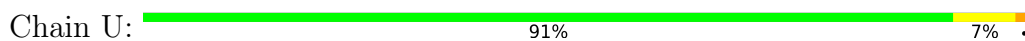
- Molecule 22: 40S ribosomal protein eS6

Chain H:  86% 8% 5%

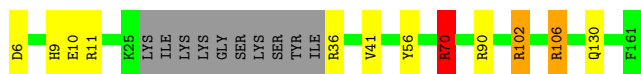
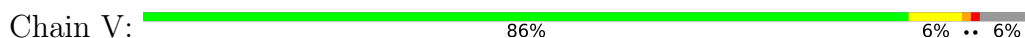


- Molecule 23: 40S ribosomal protein eS7

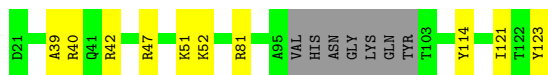
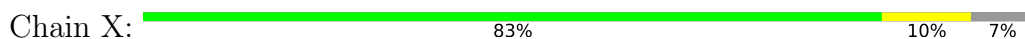
• Molecule 30: 40S ribosomal protein uS15



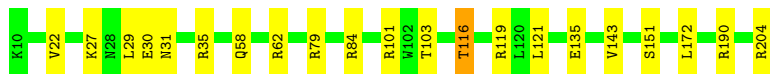
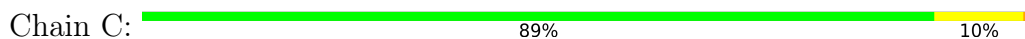
• Molecule 31: 40S ribosomal protein uS17



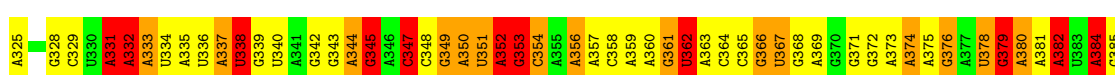
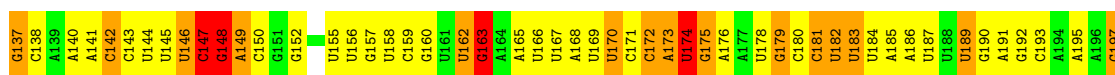
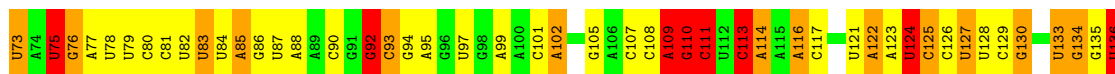
• Molecule 32: 40S ribosomal protein uS19



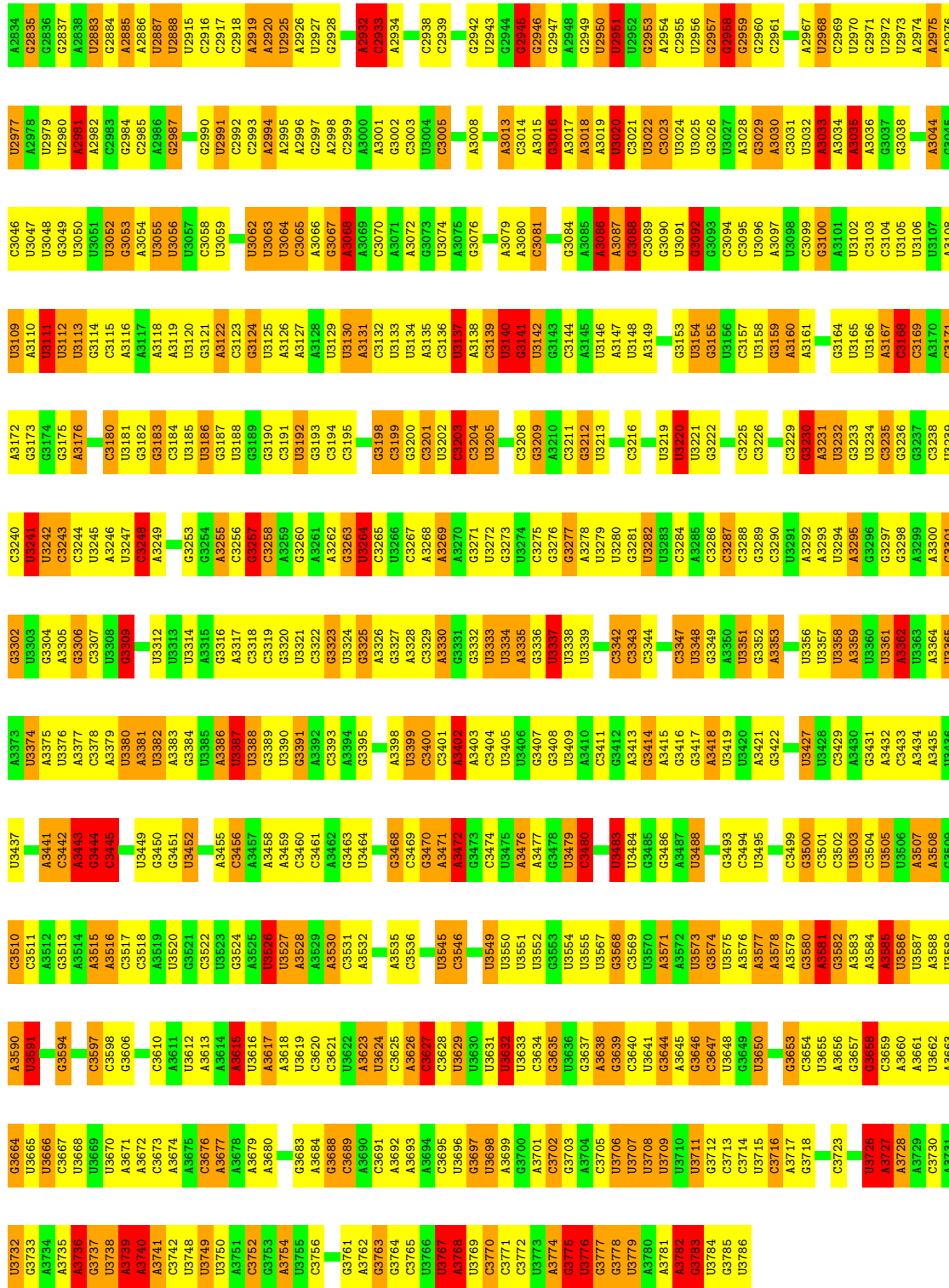
• Molecule 33: 40S ribosomal protein uS2



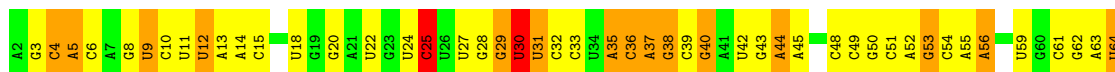
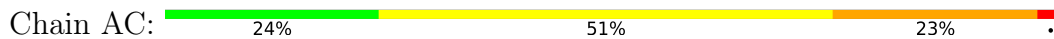
• Molecule 34: 28S ribosomal RNA

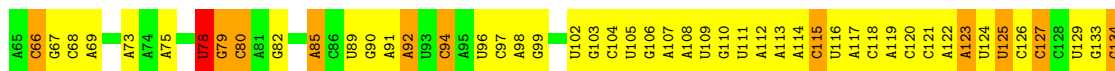


G3705	G2639	A2572	A2506	A2442	U2148	C2080	G1973	C1866	U1800	A1732	U1661	G1593	A1522
A2706	U2640	A2573	A2507	G2443	A2149	U2081	U1974	U1967	G1801	G1733	G1662	A1594	A1523
C2708	C2643	A2574	C2508	G2444	A2152	C2082	A1975	U1968	G1804	G1734	A1663	A1595	U1524
U2709	U2644	G2576	A2445	U2445	A2153	U2083	A1976	G1805	C1806	G1735	A1664	G1596	G1525
U2710	G2647	C2577	A2446	A2446	A2154	U2084	U1977	A1872	C1807	A1736	G1665	A1597	G1526
A2711	G2648	C2578	U2449	U2449	A2155	C2089	U1978	A1873	C1808	A1737	G1666	A1598	G1529
C2712	A2649	U2579	G2450	A2450	A2156	U2090	C1980	C1874	U1809	C1738	G1667	C1600	G1530
U2714	A2648	C2580	A2451	U2451	G2157	U2091	U1981	A1875	A1740	C1739	A1668	A1601	G1531
C2715	C2649	U2581	A2452	A2452	U2158	G2092	A1989	A1876	U1810	G1741	G1670	A1602	U1534
C2716	C2652	G2582	A2453	A2453	U2159	U2093	A1990	U1877	A1813	G1742	G1671	C1603	G1535
U2716	C2653	C2583	A2454	U2454	G2161	U2094	A1991	U1878	U1814	U1743	U1672	U1604	U1536
A2717	A2654	A2584	U2455	U2455	G2162	U2095	U1994	U1879	A1815	U1744	C1675	A1605	U1537
C2720	C2655	A2521	C2456	U2390	U2162	G2096	U1994	A1880	A1816	G1745	C1676	U1606	G1538
G2723	A2656	A2522	C2457	A2393	G2165	A2097	C1995	U1881	G1816	U1746	A1676	U1607	U1538
C2724	G2657	G2588	A2458	A2394	G2166	G2098	C1996	U1882	G1817	U1747	C1677	U1539	U1539
U2727	C2658	C2589	A2459	C2394	G2167	C2099	A1998	U1883	A1818	U1748	C1678	G1612	G1540
G2728	C2659	U2590	A2460	U2395	G2168	A2103	A1999	U1884	U1819	U1749	C1679	A1541	A1541
U2729	A2660	U2591	A2461	C2396	A2169	C2104	A1999	U1885	U1820	U1750	C1680	G1613	G1542
G2730	A2661	C2592	C2462	C2400	A2170	C2105	G2001	U1886	U1821	U1751	C1681	A1614	G1543
C2734	C2662	A2593	U2463	A2401	G2171	A2106	G2002	U1887	A1822	C1752	A1682	G1615	C1544
G2736	G2663	G2594	G2465	U2402	U2172	A2107	G2003	U1888	A1823	U1753	A1683	A1616	A1548
A2737	C2664	U2595	U2466	G2403	C2173	C2107	G2004	U1889	A1824	U1754	A1684	A1617	U1549
U2738	A2665	A2596	U2468	A2404	G2174	A2108	U2005	U1890	U1825	U1755	G1685	C1618	U1550
C2740	C2666	C2597	U2469	A2405	C2175	A2109	A2006	U1891	U1826	C1756	G1686	U1619	C1551
U2742	C2667	G2598	U2482	G2408	A2176	C2110	G2008	U1892	G1827	C1757	A1688	A1630	U1560
C2801	G2668	C2599	C2472	G2409	A2177	C2111	A2009	U1893	G1828	C1758	U1689	A1631	C1561
G2744	C2669	G2600	A2473	G2410	A2178	C2112	A2010	U1894	G1829	U1759	A1690	A1626	U1562
G2745	G2670	C2601	C2474	A2410	A2179	C2113	C2011	U1895	G1830	G1760	A1691	A1627	U1563
U2746	C2671	U2602	C2475	C2411	U2180	C2114	U2012	U1896	G1831	A1761	C1692	U1628	A1585
G2747	A2672	G2603	U2477	C2412	A2181	C2115	A2013	U1897	G1832	U1770	A1693	G1629	G1586
C2802	G2673	C2604	G2478	A2413	G2182	C2116	U2014	U1898	G1833	U1771	C1694	A1630	U1587
A2803	C2674	A2605	U2479	G2414	U2183	A2117	C2015	U1899	G1834	U1772	A1695	A1631	U1588
U2804	U2680	C2606	G2480	G2415	U2184	C2118	C2016	U1900	G1835	U1773	A1696	G1632	C1589
U2805	A2681	U2607	U2482	G2416	C2185	C2119	U2017	U1901	G1836	U1774	A1697	U1633	C1590
U2806	G2682	G2608	U2483	G2419	C2186	C2120	A2018	U1902	G1837	U1775	A1698	G1634	G1564
A2808	U2683	U2611	U2484	U2420	G2187	C2121	A2019	U1903	U1838	G1776	U1700	A1635	A1566
U2809	C2684	G2612	C2485	U2421	U2188	C2122	A2020	U1904	U1839	U1777	G1701	A1636	A1567
A2810	C2685	A2613	U2486	C2422	A2189	C2123	A2021	U1905	U1840	U1778	U1702	C1668	C1568
A2811	G2686	U2614	U2487	G2423	A2190	C2124	A2022	U1906	G1841	U1779	U1703	G1640	U1569
G2812	C2687	C2615	A2488	C2424	C2191	C2125	A2023	U1907	U1842	U1780	U1704	G1641	C1572
U2813	U2688	G2616	C2489	A2424	U2192	C2126	G2030	U1908	U1843	U1781	A1705	G1642	U1573
G2814	C2689	U2617	U2490	C2425	U2193	C2127	C2031	U1909	U1844	U1782	A1706	U1643	C1574
U2815	A2690	G2618	C2491	U2426	C2194	C2128	C2032	C1910	U1845	G1783	A1707	U1644	U1575
U2816	C2691	U2619	A2492	G2427	G2197	C2129	G2033	U1957	U1846	U1784	U1707	U1645	U1576
U2817	G2692	C2620	U2493	U2428	A2198	C2130	G2034	U1958	U1847	G1785	G1712	U1646	U1577
C2821	C2693	U2621	U2494	U2429	A2199	C2131	G2035	U1959	U1848	U1786	U1712	U1647	U1578
U2822	A2694	G2622	C2495	U2430	A2200	C2132	C2036	U1960	U1849	U1787	C1720	U1648	G1579
G2823	G2695	C2623	U2496	A2431	A2201	C2133	U2037	U1961	U1850	U1788	C1721	G1649	U1580
A2824	C2696	U2624	U2497	A2432	A2202	C2134	U2041	U1962	C1851	C1789	C1722	U1650	G1583
U2825	A2697	C2625	U2498	U2433	G2202	C2135	G2068	U1963	C1852	U1790	G1723	C1651	A1584
U2826	C2698	U2626	U2499	A2434	G2203	C2136	C2069	U1964	U1853	U1791	G1724	U1654	U1585
G2827	G2699	C2627	A2500	A2435	A2204	C2137	C2070	U1965	U1854	U1792	U1725	C1654	U1586
U2828	C2700	U2628	U2501	A2436	A2205	C2138	C2071	U1966	U1855	U1793	G1726	U1655	U1587
C2829	U2701	C2629	U2502	A2437	U2206	C2139	U2072	U1967	U1856	U1794	C1727	G1656	U1588
U2830	G2702	U2630	U2503	A2438	G2207	C2140	G2073	U1968	A1857	U1795	C1728	U1657	G1589
U2831	C2703	C2631	U2504	A2439	G2208	C2141	C2074	U1969	C1861	U1796	U1729	G1658	U1590
U2832	U2704	U2632	U2505	A2440	G2209	C2142	U2075	U1970	U1971	U1797	A1730	A1659	U1591
U2833	C2505	C2506	U2441	U2441	U2210	A2147	A2079	U1972	C1862	A1799	A1731	G1592	G1592

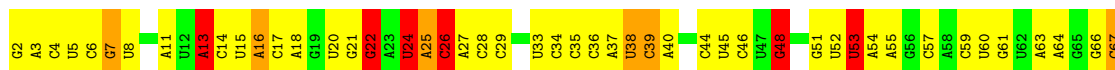


● Molecule 35: 5.8S ribosomal RNA





• Molecule 36: 5S ribosomal RNA



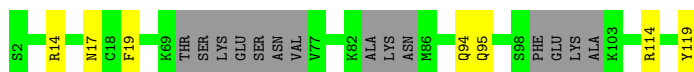
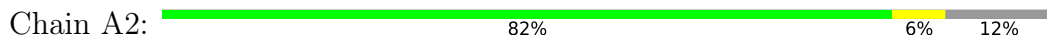
• Molecule 37: 60S ribosomal protein eL13



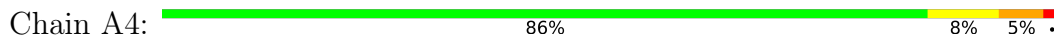
• Molecule 38: 60S ribosomal protein eL27



• Molecule 39: 60S ribosomal protein eL28



• Molecule 40: 60S ribosomal protein eL29

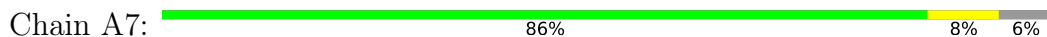


• Molecule 41: 60S ribosomal protein eL30

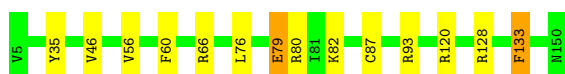




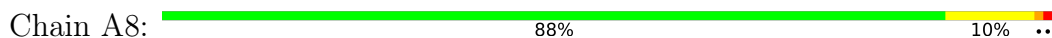
- Molecule 42: 60S ribosomal protein eL31



- Molecule 43: 60S ribosomal protein eL14



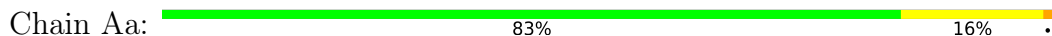
- Molecule 44: 60S ribosomal protein eL32



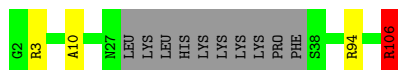
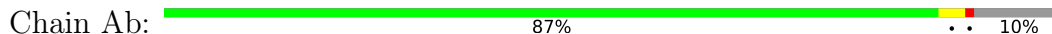
- Molecule 45: 60S ribosomal protein eL33



- Molecule 46: 60S ribosomal protein eL34

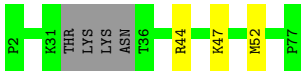


- Molecule 47: 60S ribosomal protein eL36



- Molecule 48: 60S ribosomal protein eL38





- Molecule 49: 60S ribosomal protein eL39

Chain Ae: 68% 14% 14%



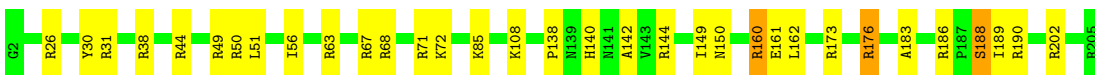
- Molecule 50: 60S ribosomal protein eL40

Chain Af: 94%



- Molecule 51: 60S ribosomal protein eL15

Chain AP: 84% 15%



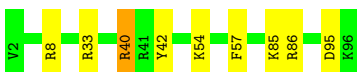
- Molecule 52: 60S ribosomal protein eL43

Chain Ah: 95%



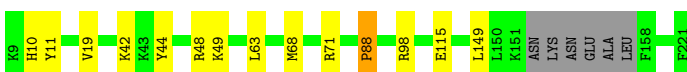
- Molecule 53: 60S ribosomal protein eL44

Chain Ai: 91% 8%



- Molecule 54: 60S ribosomal protein eL6

Chain AI: 91% 6%



- Molecule 55: 60S ribosomal protein eL8

Chain AJ: 87% 9%



- Molecule 56: 60S ribosomal protein eL37

Chain Ac: 82% 16% ..



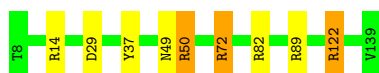
- Molecule 57: 60S ribosomal protein uL13

Chain AK: 90% 9% .



- Molecule 58: 60S ribosomal protein uL14

Chain AM: 93% 5% .



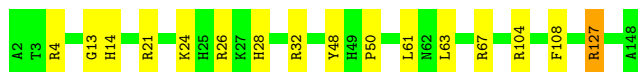
- Molecule 59: 60S ribosomal protein eL18

Chain AS: 86% 12% .



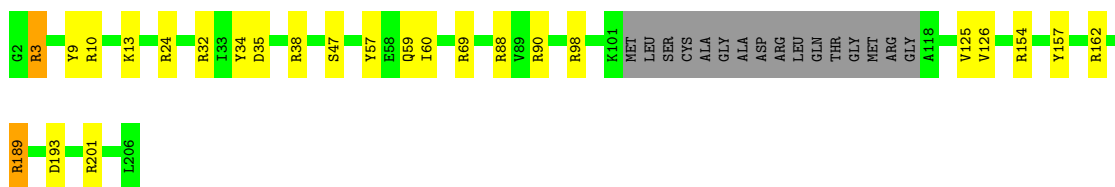
- Molecule 60: 60S ribosomal protein uL15

Chain AO: 89% 10% .




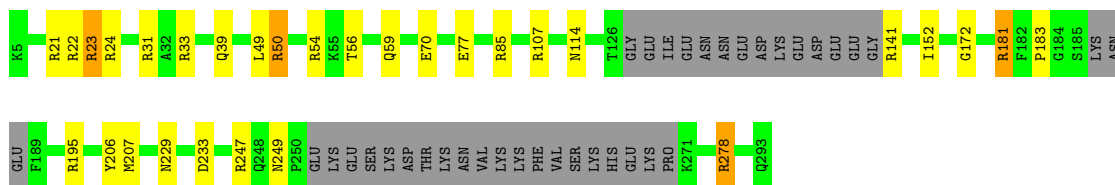
- Molecule 61: 60S ribosomal protein uL16

Chain AQ: 80% 11% 8%



- Molecule 62: 60S ribosomal protein uL18

Chain AR:  77% 9% 13%



- Molecule 63: 60S ribosomal protein uL22

Chain AW:  88% 9%



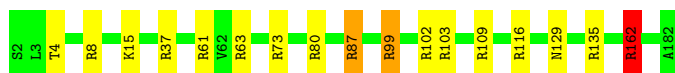
- Molecule 64: 60S ribosomal protein uL23

Chain AY:  94% 5%



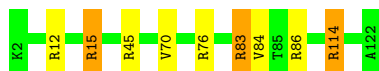
- Molecule 65: 60S ribosomal protein eL19

Chain AT:  91% 8%



- Molecule 66: 60S ribosomal protein uL24

Chain AZ:  93% 5%




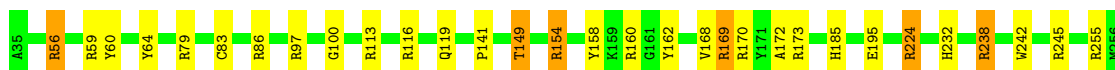
- Molecule 67: 60S ribosomal protein uL29

Chain A3:  92% 8%



- Molecule 68: 60S ribosomal protein uL30

Chain A5:  86% 11%

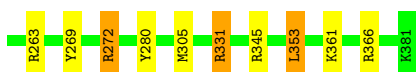
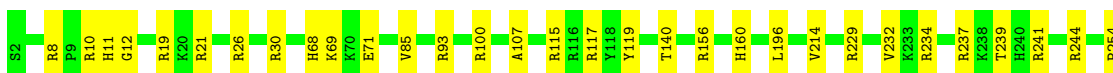


1257

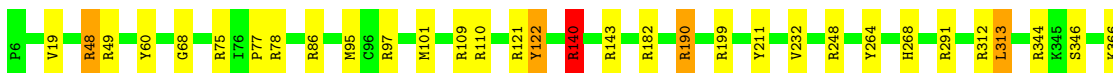
- Molecule 69: 60S ribosomal protein uL2

Chain AD:  89% 9% ..

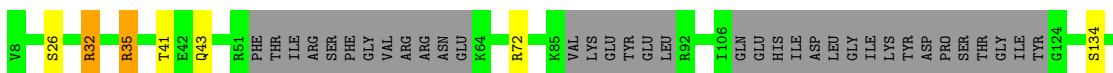
- Molecule 70: 60S ribosomal protein uL3

Chain AE:  89% 10% .


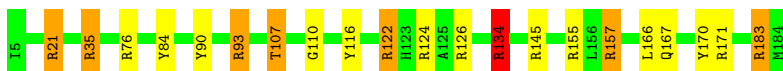
- Molecule 71: 60S ribosomal protein uL4

Chain AF:  92% 7% .

- Molecule 72: 60S ribosomal protein uL5

Chain AG:  70% 6% . 22%

- Molecule 73: 60S ribosomal protein eL20


Chain AU:  88% 7% . . .

- Molecule 74: 60S ribosomal protein uL6

Chain AH:  91% 8%




- Molecule 75: 60S ribosomal protein eL21

Chain AV:  89% 10%



- Molecule 76: 60S ribosomal protein eL41

Chain Ag:  76% 16% 8%



- Molecule 77: 60S ribosomal protein eL22

Chain AX:  94% 6%



- Molecule 78: 60S ribosomal protein eL24

Chain A0:  92% 6%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	96732	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	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	30120	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor

5 Model quality i

5.1 Standard geometry i

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 > 5$	RMSZ	# $ Z > 5$
1	A	1.23	26/38275 (0.1%)	1.58	870/59596 (1.5%)
2	7	1.23	4/1754 (0.2%)	1.79	69/2732 (2.5%)
3	D	0.75	0/1241	1.13	10/1652 (0.6%)
4	E	0.70	0/1539	1.16	13/2055 (0.6%)
5	G	0.70	0/1800	1.01	5/2429 (0.2%)
6	I	0.69	0/1443	1.22	15/1936 (0.8%)
7	K	0.70	0/1054	1.15	10/1411 (0.7%)
8	M	0.71	0/1114	1.12	4/1487 (0.3%)
9	W	0.71	0/793	1.18	4/1053 (0.4%)
10	R	0.74	0/755	1.06	0/1013
11	O	0.72	0/706	1.03	3/950 (0.3%)
12	Y	0.70	0/1295	1.18	9/1742 (0.5%)
13	Z	0.70	0/565	1.08	2/758 (0.3%)
14	1	0.70	0/999	1.17	11/1321 (0.8%)
15	2	0.75	0/324	0.98	1/435 (0.2%)
16	3	0.71	0/794	1.24	10/1055 (0.9%)
17	4	0.68	0/597	1.09	0/801
18	5	0.75	0/459	1.33	9/606 (1.5%)
19	6	0.73	0/349	1.24	3/458 (0.7%)
20	B	0.65	0/1738	1.11	9/2321 (0.4%)
21	F	0.67	0/2098	1.14	11/2819 (0.4%)
22	H	0.67	0/1665	1.10	5/2210 (0.2%)
23	J	0.68	0/1545	1.07	7/2064 (0.3%)
24	L	0.71	0/1407	1.23	16/1879 (0.9%)
25	N	0.70	0/780	1.24	7/1053 (0.7%)
26	P	0.70	0/966	1.23	8/1295 (0.6%)
27	Q	0.69	0/1149	1.25	11/1532 (0.7%)
28	S	0.65	0/1063	1.27	11/1425 (0.8%)
29	T	0.73	0/412	1.25	6/544 (1.1%)
30	U	0.67	0/1223	1.14	9/1634 (0.6%)
31	V	0.71	0/1233	1.10	4/1645 (0.2%)
32	X	0.71	0/788	1.18	7/1050 (0.7%)
33	C	0.67	0/1570	1.08	4/2129 (0.2%)
34	AA	1.30	70/75947 (0.1%)	1.59	1892/118255 (1.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AC	1.30	7/3599 (0.2%)	1.55	88/5603 (1.6%)
36	AB	1.27	2/2823 (0.1%)	1.52	57/4400 (1.3%)
37	AL	0.67	0/1789	1.14	9/2381 (0.4%)
38	A1	0.68	0/1151	1.02	1/1531 (0.1%)
39	A2	0.72	0/840	1.01	3/1114 (0.3%)
40	A4	0.66	0/564	1.01	3/737 (0.4%)
41	A6	0.69	0/749	0.99	2/1001 (0.2%)
42	A7	0.70	0/806	1.14	3/1073 (0.3%)
43	AN	0.69	0/1218	1.12	6/1621 (0.4%)
44	A8	0.70	0/1054	1.24	10/1399 (0.7%)
45	A9	0.72	0/865	1.20	7/1160 (0.6%)
46	Aa	0.68	0/872	1.26	11/1161 (0.9%)
47	Ab	0.71	0/763	1.13	5/1008 (0.5%)
48	Ad	0.72	0/612	1.09	2/812 (0.2%)
49	Ae	0.75	0/396	1.41	6/521 (1.2%)
50	Af	0.67	0/419	1.16	3/556 (0.5%)
51	AP	0.69	0/1735	1.31	21/2320 (0.9%)
52	Ah	0.68	0/668	1.13	2/887 (0.2%)
53	Ai	0.67	0/789	1.16	6/1032 (0.6%)
54	AI	0.66	0/1708	1.04	6/2274 (0.3%)
55	AJ	0.67	0/1840	1.03	3/2456 (0.1%)
56	Ac	0.72	0/723	1.29	8/951 (0.8%)
57	AK	0.67	0/1690	1.15	13/2260 (0.6%)
58	AM	0.68	0/1012	1.15	5/1363 (0.4%)
59	AS	0.69	0/1531	1.24	17/2040 (0.8%)
60	AO	0.66	0/1199	1.18	10/1597 (0.6%)
61	AQ	0.73	0/1580	1.21	16/2113 (0.8%)
62	AR	0.68	0/2079	1.16	20/2777 (0.7%)
63	AW	0.68	0/1244	1.22	12/1663 (0.7%)
64	AY	0.67	0/806	1.15	5/1074 (0.5%)
65	AT	0.66	0/1525	1.17	15/2016 (0.7%)
66	AZ	0.68	0/1013	1.17	9/1339 (0.7%)
67	A3	0.65	0/1005	1.09	8/1329 (0.6%)
68	A5	0.70	0/1917	1.25	22/2562 (0.9%)
69	AD	0.68	0/1902	1.19	17/2544 (0.7%)
70	AE	0.68	0/3130	1.16	25/4195 (0.6%)
71	AF	0.68	0/3145	1.16	23/4205 (0.5%)
72	AG	0.73	0/1021	1.19	9/1349 (0.7%)
73	AU	0.70	0/1527	1.18	15/2043 (0.7%)
74	AH	0.69	0/1501	1.17	10/2025 (0.5%)
75	AV	0.68	0/1301	1.20	11/1732 (0.6%)
76	Ag	0.74	0/348	1.57	8/448 (1.8%)
77	AX	0.72	0/842	1.06	3/1125 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	A0	0.73	0/534	1.12	4/711 (0.6%)
All	All	1.07	109/207275 (0.1%)	1.44	3594/303853 (1.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	231
2	7	0	18
3	D	0	1
4	E	0	6
5	G	0	4
6	I	0	4
7	K	0	2
8	M	0	1
9	W	0	3
11	O	0	1
12	Y	0	6
14	1	0	2
15	2	0	1
16	3	0	2
17	4	0	3
19	6	0	2
20	B	0	4
21	F	0	5
22	H	0	3
23	J	0	5
24	L	0	3
25	N	0	1
26	P	0	3
27	Q	0	2
29	T	0	1
30	U	0	2
31	V	0	6
32	X	0	1
33	C	0	6
34	AA	1	546
35	AC	0	19
36	AB	0	14
37	AL	0	5

Continued on next page...

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Mol	Chain	#Chirality outliers	#Planarity outliers
38	A1	0	1
39	A2	0	1
40	A4	0	2
41	A6	0	4
42	A7	0	1
43	AN	0	3
44	A8	0	2
45	A9	0	2
46	Aa	0	4
47	Ab	0	1
49	Ae	0	5
50	Af	0	2
51	AP	0	6
52	Ah	0	2
53	Ai	0	3
54	AI	0	2
55	AJ	0	2
56	Ac	0	3
57	AK	0	5
58	AM	0	5
59	AS	0	8
60	AO	0	3
61	AQ	0	4
62	AR	0	4
63	AW	0	6
64	AY	0	1
65	AT	0	6
66	AZ	0	4
67	A3	0	1
68	A5	0	7
69	AD	0	6
70	AE	0	4
71	AF	0	6
72	AG	0	3
73	AU	0	7
74	AH	0	3
75	AV	0	5
76	Ag	0	2
77	AX	0	1
78	A0	0	2
All	All	1	1052

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

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

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

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

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
34	AA	3018	A	C3'

5 of 1052 planarity outliers are listed below:

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

5.2 Too-close contacts

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

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

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

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

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 522 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:AE:353:LEU:H	70:AE:353:LEU:HD23	1.55	0.71
34:AA:3632:U:H3	34:AA:3653:G:H1	1.42	0.65

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

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	149/209 (71%)	142 (95%)	7 (5%)	0	100	100
4	E	183/185 (99%)	171 (93%)	11 (6%)	1 (0%)	29	69
5	G	222/224 (99%)	204 (92%)	16 (7%)	2 (1%)	17	57
6	I	176/189 (93%)	165 (94%)	9 (5%)	2 (1%)	14	52
7	K	127/129 (98%)	113 (89%)	9 (7%)	5 (4%)	3	23
8	M	136/138 (99%)	125 (92%)	9 (7%)	2 (2%)	10	46
9	W	91/108 (84%)	82 (90%)	6 (7%)	3 (3%)	4	26
10	R	92/114 (81%)	80 (87%)	7 (8%)	5 (5%)	2	19
11	O	77/79 (98%)	69 (90%)	5 (6%)	3 (4%)	3	23
12	Y	152/154 (99%)	145 (95%)	4 (3%)	3 (2%)	7	38
13	Z	70/72 (97%)	64 (91%)	5 (7%)	1 (1%)	11	46
14	1	118/120 (98%)	112 (95%)	5 (4%)	1 (1%)	19	60
15	2	35/68 (52%)	33 (94%)	2 (6%)	0	100	100
16	3	93/95 (98%)	82 (88%)	10 (11%)	1 (1%)	14	52
17	4	74/76 (97%)	62 (84%)	8 (11%)	4 (5%)	2	19
18	5	54/65 (83%)	53 (98%)	1 (2%)	0	100	100
19	6	41/43 (95%)	33 (80%)	7 (17%)	1 (2%)	6	33

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	AI	203/213 (95%)	183 (90%)	17 (8%)	3 (2%)	10	46
55	AJ	216/244 (88%)	202 (94%)	12 (6%)	2 (1%)	17	57
56	Ac	87/89 (98%)	76 (87%)	7 (8%)	4 (5%)	2	21
57	AK	199/201 (99%)	192 (96%)	5 (2%)	2 (1%)	15	54
58	AM	130/132 (98%)	123 (95%)	7 (5%)	0	100	100
59	AS	184/186 (99%)	168 (91%)	14 (8%)	2 (1%)	14	52
60	AO	145/147 (99%)	132 (91%)	12 (8%)	1 (1%)	22	63
61	AQ	185/205 (90%)	161 (87%)	19 (10%)	5 (3%)	5	31
62	AR	244/289 (84%)	224 (92%)	13 (5%)	7 (3%)	4	29
63	AW	149/170 (88%)	133 (89%)	10 (7%)	6 (4%)	3	23
64	AY	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	15	54
65	AT	179/181 (99%)	171 (96%)	5 (3%)	3 (2%)	9	42
66	AZ	119/121 (98%)	110 (92%)	7 (6%)	2 (2%)	9	42
67	A3	117/119 (98%)	107 (92%)	9 (8%)	1 (1%)	17	57
68	A5	221/223 (99%)	195 (88%)	21 (10%)	5 (2%)	6	34
69	AD	245/247 (99%)	223 (91%)	20 (8%)	2 (1%)	19	60
70	AE	378/380 (100%)	353 (93%)	21 (6%)	4 (1%)	14	52
71	AF	388/390 (100%)	356 (92%)	26 (7%)	6 (2%)	10	46
72	AG	116/159 (73%)	104 (90%)	11 (10%)	1 (1%)	17	57
73	AU	178/180 (99%)	169 (95%)	6 (3%)	3 (2%)	9	42
74	AH	183/185 (99%)	166 (91%)	14 (8%)	3 (2%)	9	44
75	AV	153/155 (99%)	141 (92%)	9 (6%)	3 (2%)	7	38
76	Ag	35/37 (95%)	30 (86%)	3 (9%)	2 (6%)	1	18
77	AX	95/97 (98%)	88 (93%)	5 (5%)	2 (2%)	7	36
78	A0	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
All	All	10111/10698 (94%)	9269 (92%)	652 (6%)	190 (2%)	11	38

5 of 190 Ramachandran outliers are listed below:

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

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

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	132/177 (75%)	128 (97%)	4 (3%)	41	63
4	E	161/164 (98%)	156 (97%)	5 (3%)	40	62
5	G	191/191 (100%)	185 (97%)	6 (3%)	40	62
6	I	154/160 (96%)	151 (98%)	3 (2%)	57	75
7	K	115/115 (100%)	113 (98%)	2 (2%)	60	78
8	M	116/116 (100%)	115 (99%)	1 (1%)	78	87
9	W	86/99 (87%)	83 (96%)	3 (4%)	36	59
10	R	83/97 (86%)	81 (98%)	2 (2%)	49	69
11	O	76/76 (100%)	71 (93%)	5 (7%)	16	41
12	Y	137/137 (100%)	132 (96%)	5 (4%)	35	59
13	Z	60/60 (100%)	59 (98%)	1 (2%)	60	78
14	1	104/104 (100%)	100 (96%)	4 (4%)	33	57
15	2	35/61 (57%)	34 (97%)	1 (3%)	42	64
16	3	87/87 (100%)	83 (95%)	4 (5%)	27	52
17	4	70/70 (100%)	69 (99%)	1 (1%)	67	80
18	5	47/52 (90%)	46 (98%)	1 (2%)	53	72
19	6	36/36 (100%)	35 (97%)	1 (3%)	43	65
20	B	195/195 (100%)	191 (98%)	4 (2%)	53	72
21	F	233/233 (100%)	223 (96%)	10 (4%)	29	54
22	H	182/190 (96%)	173 (95%)	9 (5%)	25	50
23	J	177/177 (100%)	171 (97%)	6 (3%)	37	60
24	L	151/190 (80%)	144 (95%)	7 (5%)	27	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	N	91/91 (100%)	89 (98%)	2 (2%)	52	71
26	P	99/99 (100%)	97 (98%)	2 (2%)	55	74
27	Q	120/120 (100%)	119 (99%)	1 (1%)	81	89
28	S	114/114 (100%)	109 (96%)	5 (4%)	28	53
29	T	43/43 (100%)	40 (93%)	3 (7%)	15	40
30	U	132/132 (100%)	129 (98%)	3 (2%)	50	70
31	V	131/140 (94%)	128 (98%)	3 (2%)	50	70
32	X	88/94 (94%)	88 (100%)	0	100	100
33	C	167/167 (100%)	161 (96%)	6 (4%)	35	59
37	AL	190/190 (100%)	188 (99%)	2 (1%)	73	84
38	A1	127/131 (97%)	124 (98%)	3 (2%)	49	69
39	A2	97/109 (89%)	96 (99%)	1 (1%)	76	86
40	A4	60/60 (100%)	57 (95%)	3 (5%)	24	49
41	A6	83/83 (100%)	76 (92%)	7 (8%)	11	33
42	A7	90/96 (94%)	87 (97%)	3 (3%)	38	61
43	AN	135/135 (100%)	130 (96%)	5 (4%)	34	58
44	A8	114/114 (100%)	108 (95%)	6 (5%)	22	47
45	A9	90/90 (100%)	86 (96%)	4 (4%)	28	53
46	Aa	89/89 (100%)	85 (96%)	4 (4%)	27	52
47	Ab	82/92 (89%)	81 (99%)	1 (1%)	71	83
48	Ad	69/73 (94%)	68 (99%)	1 (1%)	67	80
49	Ae	40/47 (85%)	38 (95%)	2 (5%)	24	49
50	Af	45/45 (100%)	45 (100%)	0	100	100
51	AP	179/179 (100%)	175 (98%)	4 (2%)	52	71
52	Ah	70/70 (100%)	70 (100%)	0	100	100
53	Ai	87/87 (100%)	87 (100%)	0	100	100
54	AI	189/195 (97%)	183 (97%)	6 (3%)	39	61
55	AJ	204/224 (91%)	200 (98%)	4 (2%)	55	74
56	Ac	74/74 (100%)	68 (92%)	6 (8%)	11	35
57	AK	181/181 (100%)	178 (98%)	3 (2%)	60	78
58	AM	106/106 (100%)	104 (98%)	2 (2%)	57	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	AS	158/158 (100%)	151 (96%)	7 (4%)	28	53
60	AO	121/121 (100%)	119 (98%)	2 (2%)	60	78
61	AQ	165/176 (94%)	160 (97%)	5 (3%)	41	63
62	AR	215/250 (86%)	208 (97%)	7 (3%)	38	61
63	AW	128/128 (100%)	126 (98%)	2 (2%)	62	79
64	AY	90/90 (100%)	88 (98%)	2 (2%)	52	71
65	AT	162/162 (100%)	161 (99%)	1 (1%)	86	92
66	AZ	111/111 (100%)	111 (100%)	0	100	100
67	A3	110/110 (100%)	108 (98%)	2 (2%)	59	77
68	A5	201/201 (100%)	196 (98%)	5 (2%)	47	68
69	AD	191/191 (100%)	185 (97%)	6 (3%)	40	62
70	AE	335/335 (100%)	329 (98%)	6 (2%)	59	77
71	AF	336/336 (100%)	327 (97%)	9 (3%)	44	65
72	AG	110/142 (78%)	106 (96%)	4 (4%)	35	59
73	AU	162/162 (100%)	158 (98%)	4 (2%)	47	68
74	AH	168/168 (100%)	164 (98%)	4 (2%)	49	69
75	AV	140/140 (100%)	137 (98%)	3 (2%)	53	72
76	Ag	34/34 (100%)	33 (97%)	1 (3%)	42	64
77	AX	92/92 (100%)	91 (99%)	1 (1%)	73	84
78	A0	53/53 (100%)	52 (98%)	1 (2%)	57	75
All	All	9096/9417 (97%)	8847 (97%)	249 (3%)	48	65

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

Mol	Chain	Res	Type
39	A2	94	GLN
70	AE	361	LYS
45	A9	136	TYR
70	AE	269	TYR
73	AU	107	THR

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

Mol	Chain	Res	Type
60	AO	119	ASN
71	AF	286	ASN
63	AW	25	HIS
68	A5	232	HIS
73	AU	162	HIS

5.3.3 RNA [i](#)

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

5 of 1544 RNA backbone outliers are listed below:

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

5 of 289 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	AA	2886	A
36	AB	39	C
34	AA	3034	A
34	AA	3505	U
34	AA	62	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
63	AW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	154:ASN	C	197:UNK	N	30.56

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-6454. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution

This section was not generated.

7.2 Volume estimate versus contour level

This section was not generated.

7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.