



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 11:25 am GMT

PDB ID : 3J0L
EMDB ID: : EMD-5326
Title : Core of mammalian 80S pre-ribosome in complex with tRNAs fitted to a 9.8A cryo-EM map: classic PRE state 1
Authors : Budkevich, T.; Giesebrecht, J.; Altman, R.; Munro, J.; Mielke, T.; Nierhaus, K.; Blanchard, S.; Spahn, C.M.
Deposited on : 2011-10-04
Resolution : 9.80 Å(reported)
Based on PDB ID : 2XZM, 2WDK, 3O58

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

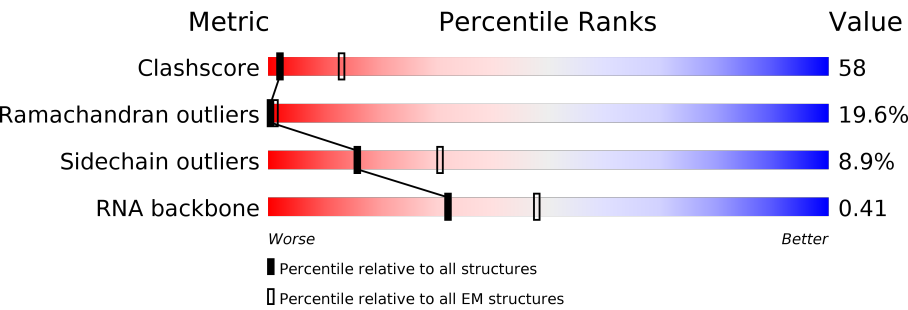
MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

1 Overall quality at a glance i

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

The reported resolution of this entry is 9.80 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.



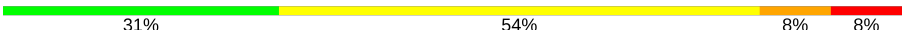


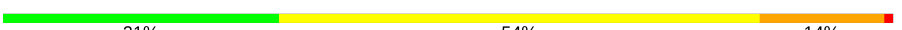
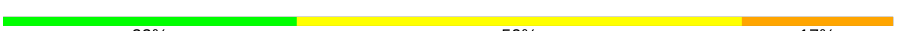
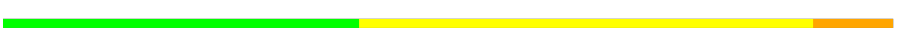






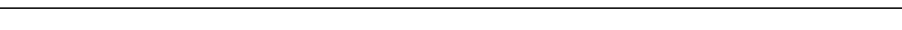


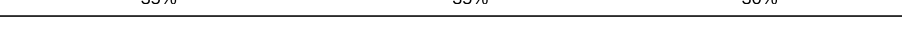

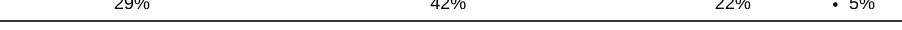


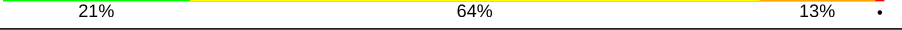
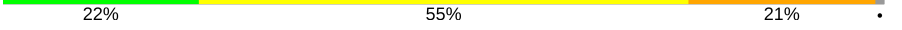
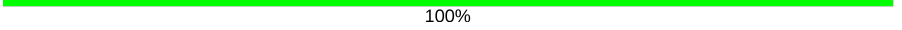
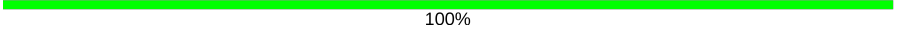
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	48	<div><div>65%</div><div>23%</div><div>8%</div><div>.</div></div>
2	b	12	<div><div>67%</div><div>33%</div></div>
3	c	17	<div><div>71%</div><div>29%</div></div>
4	d	7	<div><div>71%</div><div>14%</div><div>14%</div></div>
5	e	4	<div><div>100%</div></div>
6	E	5	<div><div>60%</div><div>40%</div></div>
7	f	21	<div><div>76%</div><div>24%</div></div>
8	g	31	<div><div>71%</div><div>23%</div><div>6%</div></div>

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Mol	Chain	Length	Quality of chain
9	G	13	
10	h	111	
11	T	192	
12	K	140	
13	L	141	
14	X	68	
15	S	125	
16	1	50	
17	2	112	
18	3	12	
19	4	14	
20	5	6	
21	6	19	
22	7	50	
23	8	20	
24	B	213	
25	J	219	
26	F	95	
27	V	76	
27	W	76	
27	Y	76	
28	v	3	
28	y	3	
29	w	2	

2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 24541 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 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	48	Total	C	N	O	P	0	0
			1029	459	190	332	48		

- Molecule 2 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	12	Total	C	N	O	P	0	0
			260	116	49	83	12		

- Molecule 3 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	17	Total	C	N	O	P	0	0
			362	162	66	117	17		

- Molecule 4 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	7	Total	C	N	O	P	0	0
			155	69	33	46	7		

- Molecule 5 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	4	Total	C	N	O	P	0	0
			84	38	16	26	4		

- Molecule 6 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	5	Total	C	N	O	P	0	0
			100	45	13	37	5		

- Molecule 7 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	f	21	Total	C	N	O	P	0	0
			452	200	79	152	21		

- Molecule 8 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	g	31	Total	C	N	O	P	0	0
			660	295	118	216	31		

- Molecule 9 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	13	Total	C	N	O	P	0	0
			276	123	49	91	13		

- Molecule 10 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	h	111	Total	C	N	O	P	0	0
			2368	1060	431	766	111		

- Molecule 11 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	T	192	Total	C	N	O	S	0	0
			1520	961	281	270	8		

- Molecule 12 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	140	Total	C	N	O	S	0	0
			1063	654	206	197	6		

- Molecule 13 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	141	Total	C	N	O	S	0	0
			1097	691	221	180	5		

- Molecule 14 is a protein called Ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	X	68	Total	C	N	O	S	0	0
			554	350	113	90	1		

- Molecule 15 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	125	Total	C	N	O	S	0	0
			985	632	173	176	4		

- Molecule 16 is a RNA chain called 60S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	1	50	Total	C	N	O	P	0	0
			1064	476	188	350	50		

- Molecule 17 is a RNA chain called 60S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	2	112	Total	C	N	O	P	0	0
			2392	1070	435	775	112		

- Molecule 18 is a RNA chain called 60S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	3	12	Total	C	N	O	P	0	0
			259	116	50	81	12		

- Molecule 19 is a RNA chain called 60S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	4	14	Total	C	N	O	P	0	0
			306	135	59	98	14		

- Molecule 20 is a RNA chain called 60S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	5	6	Total	C	N	O	P	0	0
			127	57	23	41	6		

- Molecule 21 is a RNA chain called 60S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	6	19	Total	C	N	O	P	0	0
			417	187	88	123	19		

- Molecule 22 is a RNA chain called 60S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	7	50	Total	C	N	O	P	0	0
			1054	471	173	360	50		

- Molecule 23 is a RNA chain called 60S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	8	20	Total	C	N	O	P	0	0
			431	192	80	139	20		

- Molecule 24 is a protein called Ribosomal protein L10a.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	B	213	Total	C	N	O	0	0
			1055	629	213	213		

- Molecule 25 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	J	208	Total	C	N	O	0	0
			1027	611	208	208		

- Molecule 26 is a protein called Ribosomal protein L36a.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	F	95	Total	C	N	O	0	0
			467	277	95	95		

- Molecule 27 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	75	Total	C	N	O	P	0	0
			1597	713	285	525	74		
27	V	75	Total	C	N	O	P	0	0
			1597	713	285	525	74		
27	W	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 28 is a RNA chain called mRNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	y	3	Total	C	N	O	P	0	0
			60	27	7	23	3		
28	v	3	Total	C	N	O	P	0	0
			60	27	7	23	3		

- Molecule 29 is a RNA chain called mRNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	w	2	Total	C	N	O	P	0	0
			44	20	10	12	2		

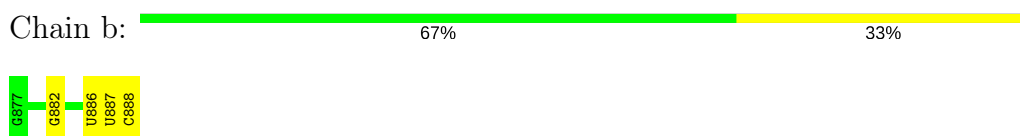
3 Residue-property plots [i](#)

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

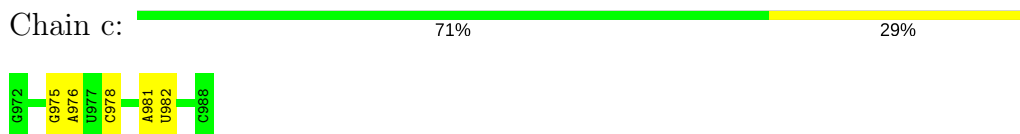
- Molecule 1: 40S ribosomal RNA fragment



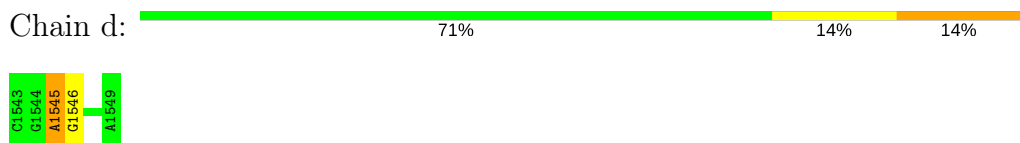
- Molecule 2: 40S ribosomal RNA fragment



- Molecule 3: 40S ribosomal RNA fragment



- Molecule 4: 40S ribosomal RNA fragment



- Molecule 5: 40S ribosomal RNA fragment

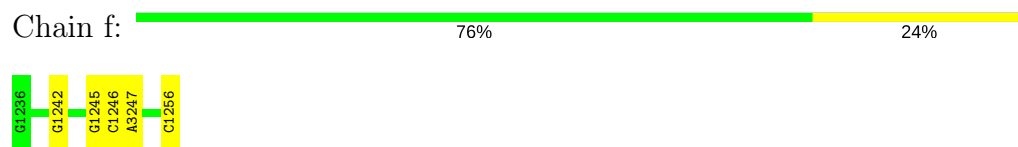


There are no outlier residues recorded for this chain.

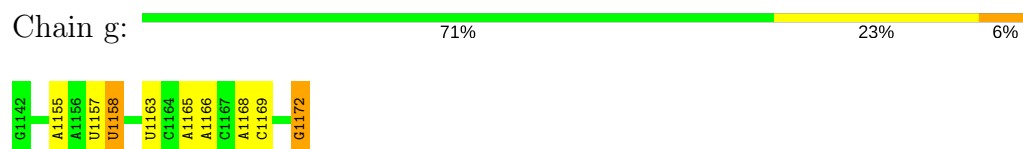
- Molecule 6: 40S ribosomal RNA fragment



- Molecule 7: 40S ribosomal RNA fragment



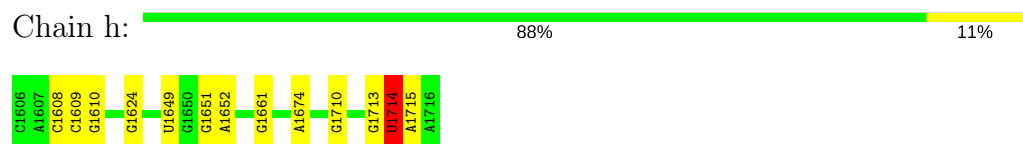
- Molecule 8: 40S ribosomal RNA fragment



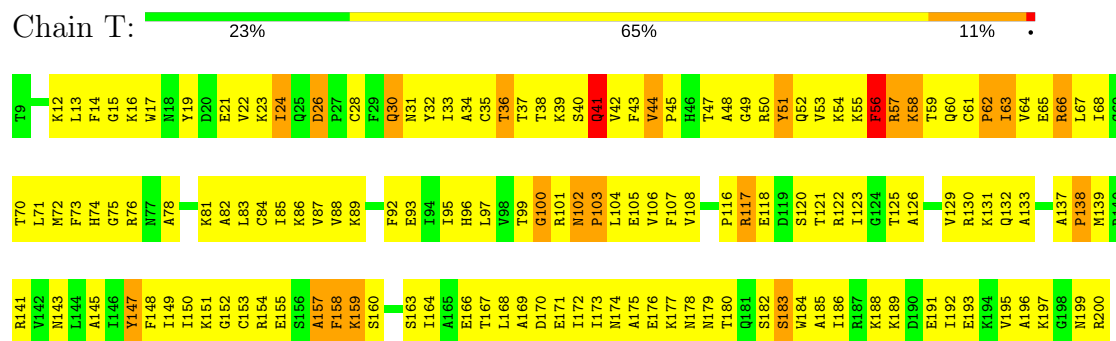
- Molecule 9: 40S ribosomal RNA fragment



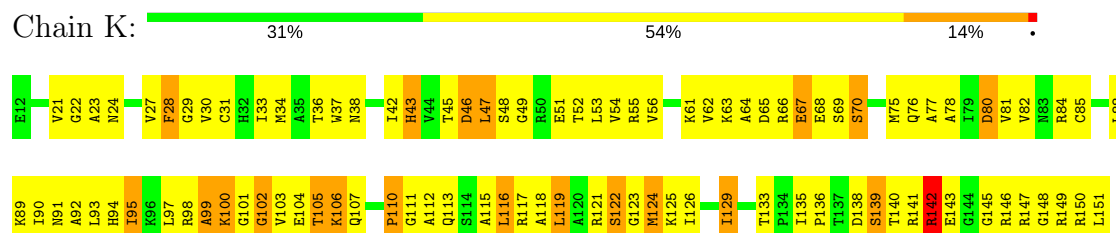
- Molecule 10: 40S ribosomal RNA fragment



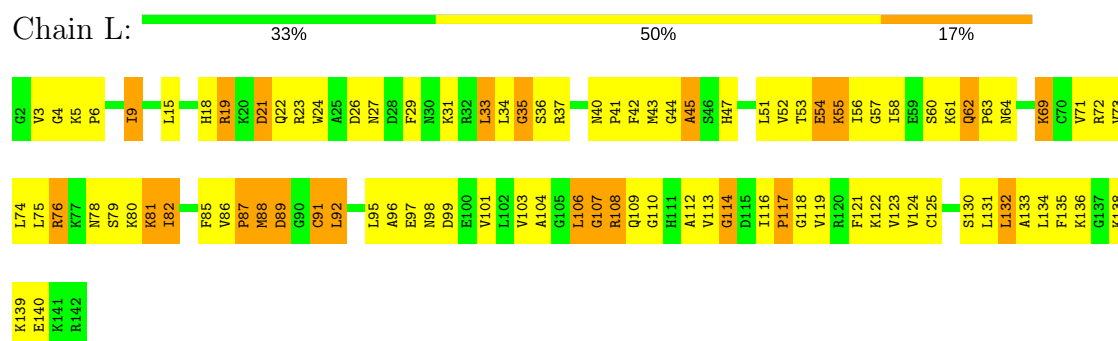
- Molecule 11: Ribosomal protein S5



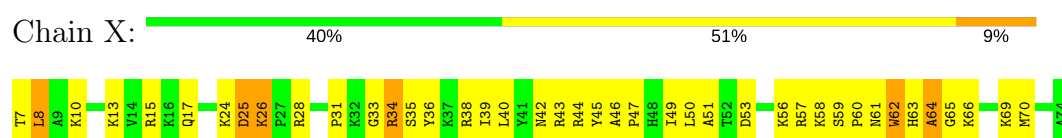
- Molecule 12: Ribosomal protein S14



- Molecule 13: Ribosomal protein S23



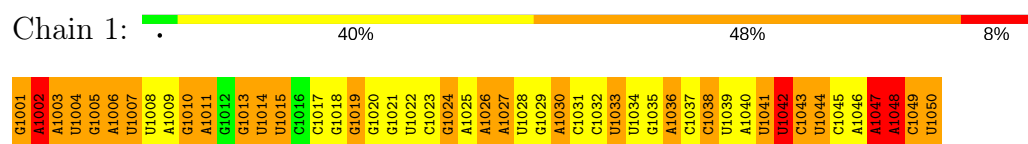
- Molecule 14: Ribosomal protein S30



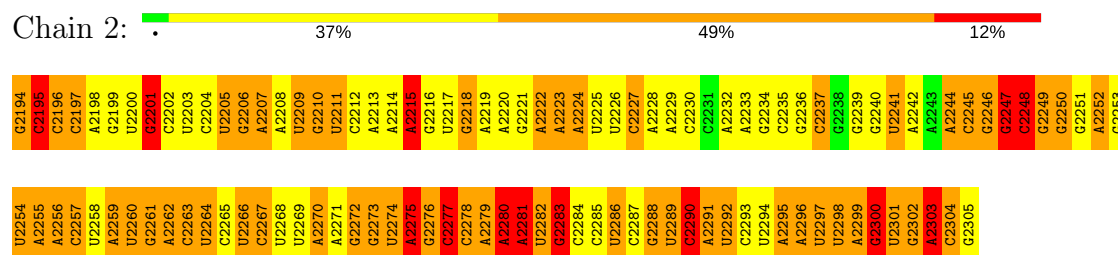
- Molecule 15: Ribosomal protein S15



- Molecule 16: 60S ribosomal RNA fragment



- Molecule 17: 60S ribosomal RNA fragment



- Molecule 18: 60S ribosomal RNA fragment





- Molecule 19: 60S ribosomal RNA fragment

Chain 4: 71% 21% 7%



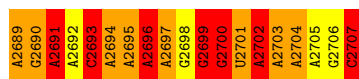
- Molecule 20: 60S ribosomal RNA fragment

Chain 5: 33% 67%



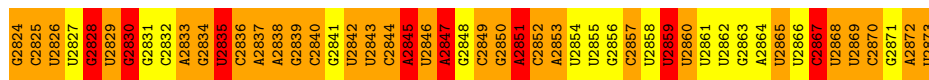
- Molecule 21: 60S ribosomal RNA fragment

Chain 6: 21% 42% 37%



- Molecule 22: 60S ribosomal RNA fragment

Chain 7: 30% 54% 16%



- Molecule 23: 60S ribosomal RNA fragment

Chain 8: 35% 35% 30%

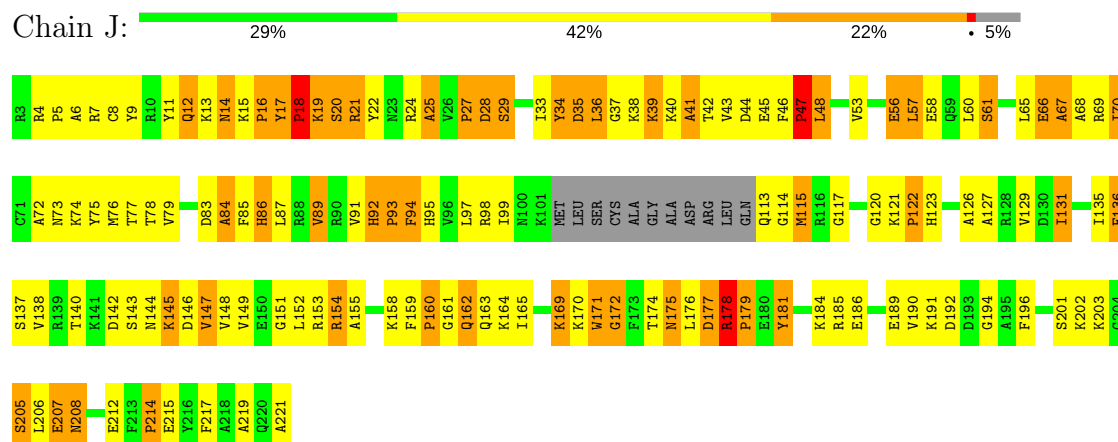


- Molecule 24: Ribosomal protein L10a

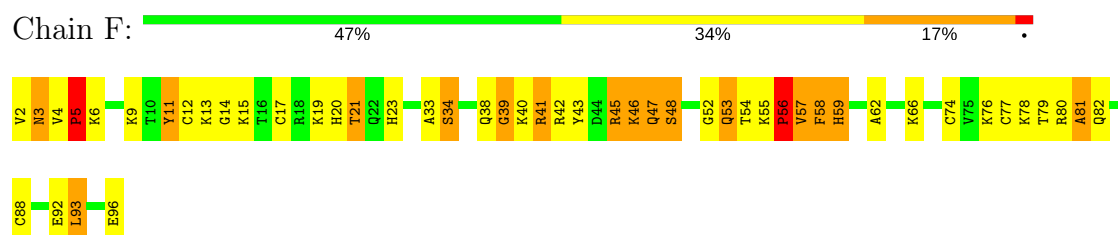
Chain B: 55% 36% 8%



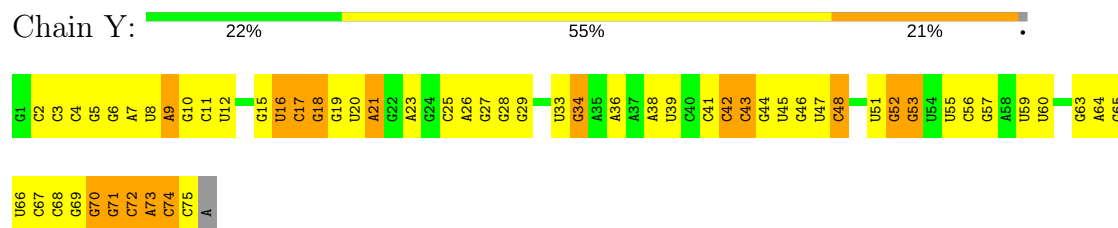
- Molecule 25: Ribosomal protein L10



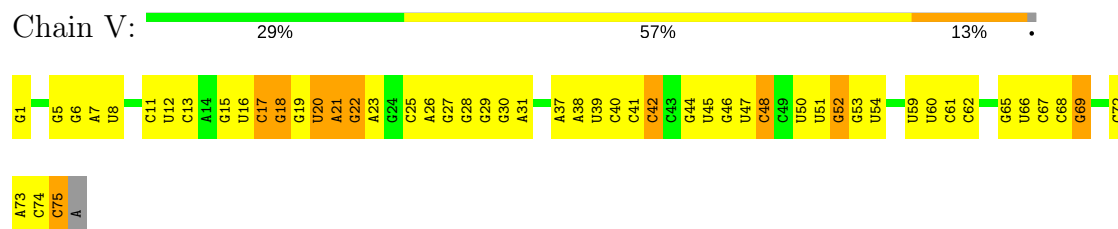
- Molecule 26: Ribosomal protein L36a



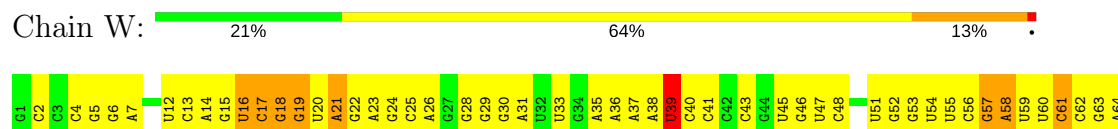
- Molecule 27: tRNA



- Molecule 27: tRNA



- Molecule 27: tRNA





- Molecule 28: mRNA fragment

Chain y:  100%

There are no outlier residues recorded for this chain.

- Molecule 28: mRNA fragment

Chain v:  100%

There are no outlier residues recorded for this chain.

- Molecule 29: mRNA fragment

Chain w:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	30448	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTF CORRECTION OF EACH DEFOCUS GROUP VOLUME PRIOR TO BACK PROJECTION	Depositor
Microscope	FEI POLARA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	65520	Depositor
Image detector	KODAK SO163 FILM	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	0.75	1/1151 (0.1%)	1.00	7/1793 (0.4%)
10	h	0.48	0/2650	0.75	1/4127 (0.0%)
11	T	0.45	0/1546	0.71	0/2079
12	K	0.42	0/1078	0.73	0/1452
13	L	0.41	0/1114	0.73	0/1485
14	X	0.36	0/566	0.70	0/753
15	S	0.37	0/1003	0.65	1/1342 (0.1%)
16	1	0.72	1/1189 (0.1%)	1.28	21/1850 (1.1%)
17	2	1.10	3/2677 (0.1%)	1.68	69/4170 (1.7%)
18	3	0.19	0/290	0.43	0/450
19	4	0.67	0/342	1.30	5/533 (0.9%)
2	b	0.55	0/291	0.79	0/452
20	5	0.69	0/141	1.32	1/217 (0.5%)
21	6	1.25	0/470	2.07	30/732 (4.1%)
22	7	1.06	2/1174 (0.2%)	2.34	33/1825 (1.8%)
23	8	1.45	4/482 (0.8%)	1.89	22/750 (2.9%)
24	B	0.34	0/1054	0.63	9/1468 (0.6%)
25	J	0.66	0/1025	0.89	8/1424 (0.6%)
26	F	0.47	0/466	0.68	2/646 (0.3%)
27	V	0.44	0/1784	0.75	0/2780
27	W	0.43	0/1809	0.71	0/2819
27	Y	0.47	0/1784	0.74	0/2780
28	v	0.51	0/65	0.65	0/98
28	y	0.39	0/65	0.68	0/98
29	w	0.40	0/49	0.79	0/74
3	c	0.66	0/404	0.92	1/627 (0.2%)
4	d	0.51	0/174	0.86	0/270
5	e	0.46	0/93	0.62	0/142
6	E	0.54	0/109	0.86	0/166
7	f	0.65	0/504	0.89	0/785
8	g	0.66	0/737	0.88	2/1146 (0.2%)
9	G	0.54	0/307	0.82	0/476
All	All	0.67	11/26593 (0.0%)	1.11	212/39809 (0.5%)

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	4
10	h	0	2
27	W	0	2
4	d	0	1
6	E	0	1
8	g	0	2
9	G	0	1
All	All	0	13

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	7	2845	A	C6-N1	-11.05	1.27	1.35
23	8	2969	A	N9-C4	-7.32	1.33	1.37
17	2	2283	G	N9-C8	6.16	1.42	1.37
23	8	2961	G	N9-C4	6.14	1.42	1.38
23	8	2958	A	N9-C4	-5.64	1.34	1.37

The worst 5 of 212 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	7	2845	A	N1-C6-N6	39.32	142.19	118.60
22	7	2845	A	C6-N1-C2	38.63	141.78	118.60
22	7	2845	A	C5-C6-N1	-34.02	100.69	117.70
22	7	2845	A	N1-C2-N3	-22.80	117.90	129.30
21	6	2689	A	C8-N9-C4	-13.78	100.29	105.80

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	a	547	C	Sidechain
1	a	558	G	Sidechain
1	a	559	C	Sidechain
1	a	574	A	Sidechain
4	d	1545	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	1029	0	521	0	0
2	b	260	0	130	0	0
3	c	362	0	185	0	0
4	d	155	0	78	0	0
5	e	84	0	45	0	0
6	E	100	0	54	5	0
7	f	452	0	224	0	0
8	g	660	0	335	0	0
9	G	276	0	141	16	0
10	h	2368	0	1196	0	0
11	T	1520	0	1570	200	0
12	K	1063	0	1088	111	0
13	L	1097	0	1169	106	0
14	X	554	0	604	45	0
15	S	985	0	1026	94	0
16	1	1064	0	536	165	0
17	2	2392	0	1208	408	0
18	3	259	0	131	13	0
19	4	306	0	150	41	0
20	5	127	0	66	17	0
21	6	417	0	209	73	0
22	7	1054	0	532	148	0
23	8	431	0	217	43	0
24	B	1055	0	453	31	0
25	J	1027	0	467	164	0
26	F	467	0	208	32	0
27	V	1597	0	807	68	0
27	W	1619	0	821	116	0
27	Y	1597	0	811	66	0
28	v	60	0	31	0	0
28	y	60	0	31	0	0
29	w	44	0	23	0	0
All	All	24541	0	15067	1854	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 58.

The worst 5 of 1854 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)
16:1:1010:G:H2'	25:J:40:LYS:CB	1.41	1.47
16:1:1048:A:C8	25:J:21:ARG:CB	2.01	1.41
25:J:177:ASP:HA	25:J:179:PRO:N	1.35	1.37
16:1:1010:G:N3	25:J:40:LYS:N	1.74	1.35
16:1:1048:A:N7	25:J:21:ARG:CB	1.91	1.33

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	
11	T	190/192 (99%)	141 (74%)	33 (17%)	16 (8%)	1	15
12	K	138/140 (99%)	96 (70%)	28 (20%)	14 (10%)	1	12
13	L	139/141 (99%)	106 (76%)	17 (12%)	16 (12%)	0	8
14	X	66/68 (97%)	48 (73%)	12 (18%)	6 (9%)	1	15
15	S	123/125 (98%)	91 (74%)	25 (20%)	7 (6%)	2	24
24	B	211/213 (99%)	76 (36%)	67 (32%)	68 (32%)	0	0
25	J	204/219 (93%)	80 (39%)	51 (25%)	73 (36%)	0	0
26	F	93/95 (98%)	37 (40%)	28 (30%)	28 (30%)	0	0
All	All	1164/1193 (98%)	675 (58%)	261 (22%)	228 (20%)	0	3

5 of 228 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	T	56	PHE
11	T	60	GLN
11	T	63	ILE
11	T	75	GLY

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Mol	Chain	Res	Type
11	T	158	PHE

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	
11	T	163/163 (100%)	147 (90%)	16 (10%)	9	34
12	K	112/112 (100%)	96 (86%)	16 (14%)	4	22
13	L	113/113 (100%)	101 (89%)	12 (11%)	8	31
14	X	57/57 (100%)	55 (96%)	2 (4%)	41	69
15	S	105/105 (100%)	102 (97%)	3 (3%)	48	73
All	All	550/550 (100%)	501 (91%)	49 (9%)	16	39

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	K	85	CYS
12	K	119	LEU
14	X	62	TRP
12	K	113	GLN
12	K	129	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
11	T	199	ASN
12	K	38	ASN
14	X	42	ASN
11	T	143	ASN
13	L	98	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	47/48 (97%)	15 (31%)	0
10	h	110/111 (99%)	12 (10%)	0
16	1	49/50 (98%)	23 (46%)	0
17	2	111/112 (99%)	54 (48%)	0
18	3	11/12 (91%)	6 (54%)	0
19	4	13/14 (92%)	5 (38%)	0
2	b	11/12 (91%)	4 (36%)	0
20	5	5/6 (83%)	4 (80%)	0
21	6	18/19 (94%)	13 (72%)	0
22	7	49/50 (98%)	29 (59%)	0
23	8	19/20 (95%)	8 (42%)	0
27	V	74/76 (97%)	15 (20%)	0
27	W	75/76 (98%)	13 (17%)	0
27	Y	74/76 (97%)	20 (27%)	0
28	v	2/3 (66%)	0	0
28	y	2/3 (66%)	0	0
29	w	1/2 (50%)	0	0
3	c	16/17 (94%)	4 (25%)	0
4	d	6/7 (85%)	2 (33%)	0
5	e	3/4 (75%)	0	0
6	E	4/5 (80%)	1 (25%)	0
7	f	20/21 (95%)	5 (25%)	0
8	g	30/31 (96%)	8 (26%)	0
9	G	12/13 (92%)	2 (16%)	0
All	All	762/788 (96%)	243 (31%)	0

5 of 243 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	544	G
1	a	547	C
1	a	548	A
1	a	552	C
1	a	553	A

There are no RNA pucker outliers to report.

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.