



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:50 PM BST

PDB ID : 3J0O
EMDB ID: : EMD-5327
Title : Core of mammalian 80S pre-ribosome in complex with tRNAs fitted to a 9A cryo-EM map: classic PRE state 2
Authors : Budkevich, T.; Giesebrecht, J.; Altman, R.; Munro, J.; Mielke, T.; Nierhaus, K.; Blanchard, S.; Spahn, C.M.
Deposited on : 2011-10-05
Resolution : 9.00 Å(reported)
Based on PDB ID : 2XZM, 2WDK, 3O58

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) : trunk27241

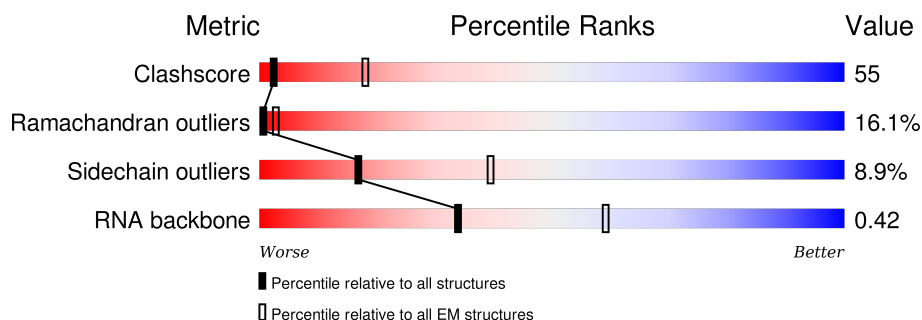
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 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.







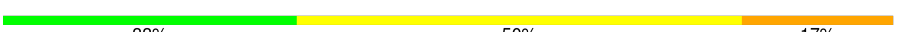
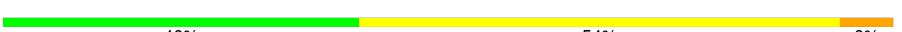
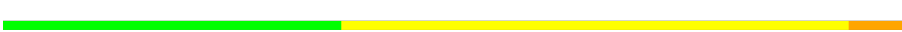





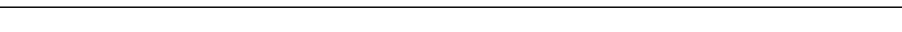

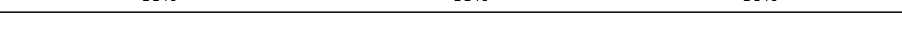

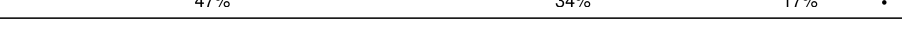

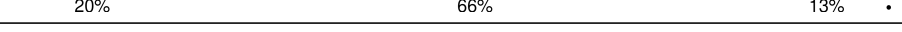
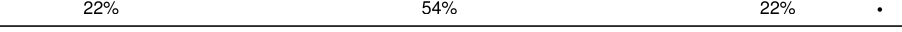
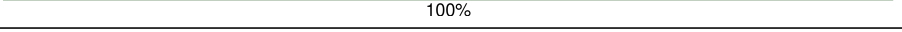
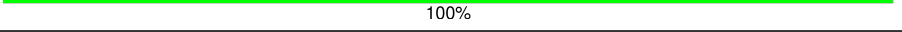
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	48	65% 23% 8% .
2	b	12	67% 33%
3	c	17	71% 29%
4	d	7	71% 14% 14%
5	e	4	100%
6	E	5	60% 20% 20%
7	f	21	76% 24%
8	g	31	71% 23% 6%

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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	2	112	
17	3	12	
18	4	14	
19	5	6	
20	6	19	
21	7	50	
22	8	20	
23	B	213	
24	F	95	
25	V	76	
25	W	76	
25	Y	76	
26	v	3	
26	y	3	
27	w	2	

2 Entry composition [i](#)

There are 27 unique types of molecules in this entry. The entry contains 22450 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	2	112	Total	C	N	O	P	0	0
			2392	1070	435	775	112		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	3	12	Total	C	N	O	P	0	0
			259	116	50	81	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	4	14	Total	C	N	O	P	0	0
			306	135	59	98	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	5	6	Total	C	N	O	P	0	0
			127	57	23	41	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	6	19	Total	C	N	O	P	0	0
			417	187	88	123	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	7	50	Total	C	N	O	P	0	0
			1054	471	173	360	50		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	8	20	Total	C	N	O	P	0	0
			431	192	80	139	20		

- Molecule 23 is a protein called Ribosomal protein L10a.

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

- Molecule 24 is a protein called Ribosomal protein L36a.

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

- Molecule 25 is a RNA chain called tRNA.

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

- Molecule 26 is a RNA chain called mRNA fragment.

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

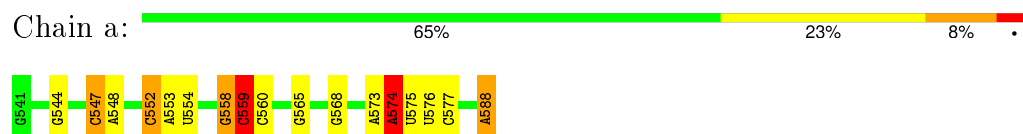
- Molecule 27 is a RNA chain called mRNA fragment.

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

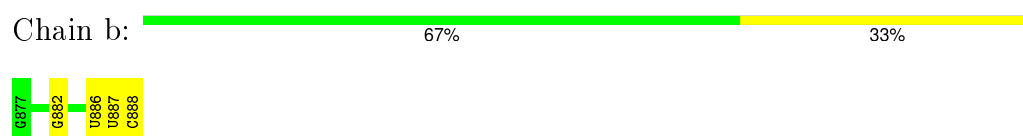
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

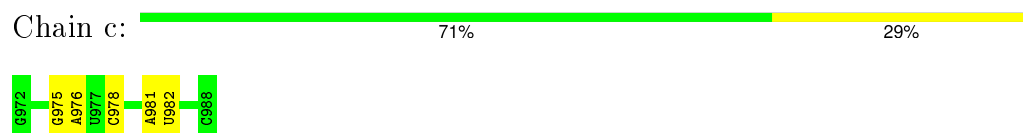
- Molecule 1: 40S ribosomal RNA fragment



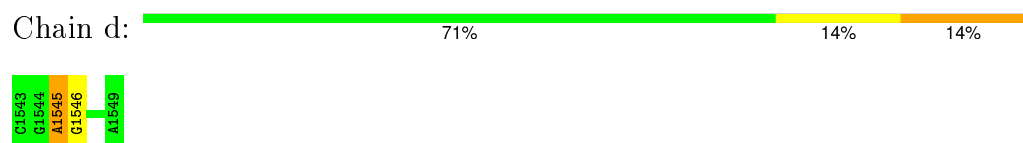
- Molecule 2: 40S ribosomal RNA fragment



- 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



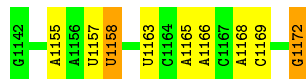
- Molecule 7: 40S ribosomal RNA fragment

Chain f:  76% 24%



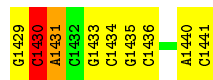
- Molecule 8: 40S ribosomal RNA fragment

Chain g:  71% 23% 6%




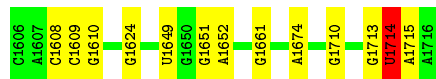
- Molecule 9: 40S ribosomal RNA fragment

Chain G:  31% 54% 8% 8%



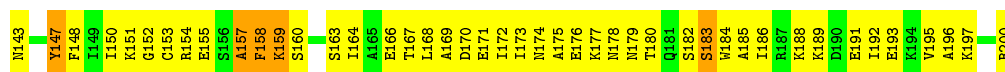
- Molecule 10: 40S ribosomal RNA fragment

Chain h:  88% 11%




- Molecule 11: Ribosomal protein S5

Chain T:  26% 61% 11%

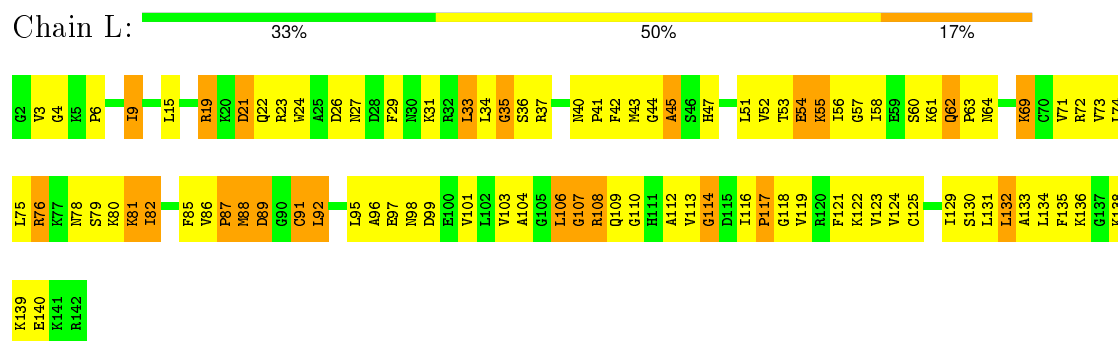


- Molecule 12: Ribosomal protein S14

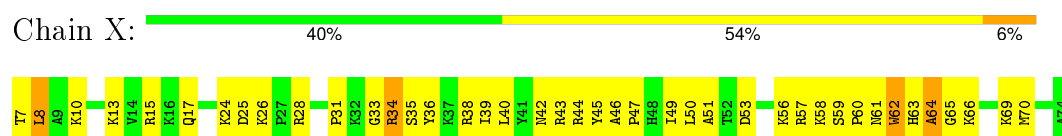
Chain K:  31% 54% 14%



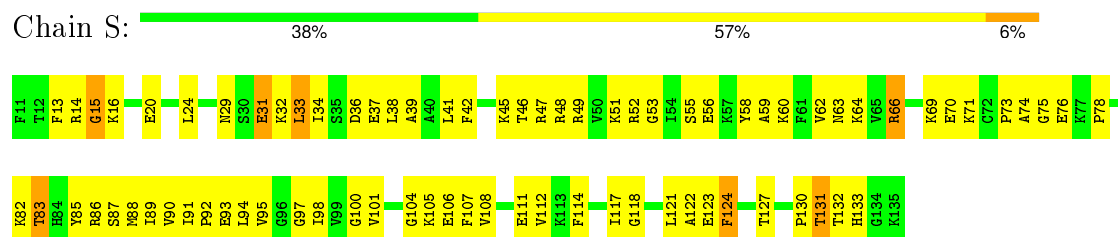
- Molecule 13: Ribosomal protein S23



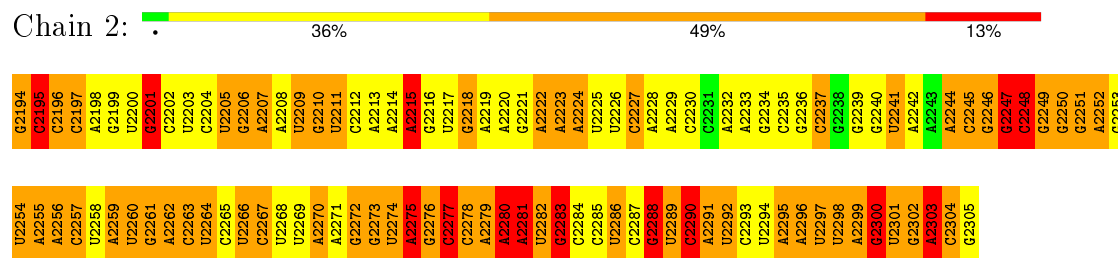
- Molecule 14: Ribosomal protein S30



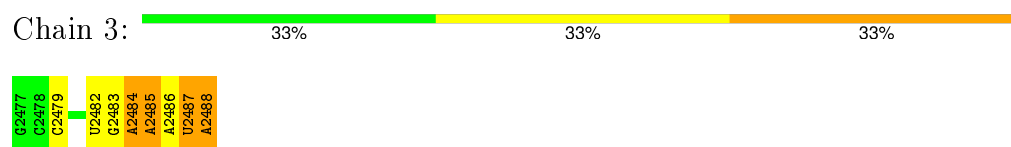
- Molecule 15: Ribosomal protein S15



- Molecule 16: 60S ribosomal RNA fragment



- Molecule 17: 60S ribosomal RNA fragment



- Molecule 18: 60S ribosomal RNA fragment



G2614
G2615
G2616
U2617
G2618
G2619
G2620
G2621
G2622
G2623
G2624
G2625
A2626
G2627

- Molecule 19: 60S ribosomal RNA fragment

Chain 5: 33% 67%

G2653
G2654
U2655
A2656
A2657
G2658

- Molecule 20: 60S ribosomal RNA fragment

Chain 6: 21% 42% 37%

A2689
G2690
A2691
U2692
G2693
A2694
A2695
A2696
A2697
G2698
G2699
G2700
U2701
A2702
A2703
A2704
A2705
G2706
G2707

- Molecule 21: 60S ribosomal RNA fragment

Chain 7: 30% 54% 16%

G2824
G2825
U2826
U2827
G2828
U2829
G2830
G2831
G2832
A2833
G2834
G2835
U2836
A2837
A2838
G2839
G2840
G2841
U2842
U2843
G2844
A2845
U2846
A2847
G2848
G2849
G2850
A2851
G2852
A2853
U2854
U2855
U2856
G2857
U2858
U2859
U2860
U2861
U2862
G2863
A2864
U2865
U2866
G2867
U2868
U2869
G2870
G2871
A2872
U2873

- Molecule 22: 60S ribosomal RNA fragment

Chain 8: 35% 35% 30%

G2957
A2958
G2959
G2960
G2961
U2962
G2963
G2964
U2965
G2966
A2967
G2968
G2969
G2970
A2971
G2972
G2973
U2974
U2975
A2976

- Molecule 23: Ribosomal protein L10a

Chain B: 55% 36% 8%

I4
I5
H12
E22
T23
K24
K25
K26
N27
V32
V36
K39
K40
Y41
D42
P43
Q44
R45
P46
N57
P58
R60
P61
I65
C66
I67
F68
G69
D73
A77
K92
K95
N96
I100
K101
K102
L103
S104
K105
K106

Y107
M108
A109
A112
V115
L116
L117
V120
P121
R122
L123
L124
R125
P126
S209
M210
L128
S129
K130
A131
G132
P135
T136
P137
D143
K44
Y145
V148
V151
R152
S153
T154
I155
K156
L165
A166
V167
A168
V169
M174
D177
V178
N181
Q182
S186
Y187
N188
F189
F190

W191
S192
L193
L194
K195
K196
W197
V201
G202
S203
L204
K195
V205
V206
K207
S208
R18
S209
M210
G211
P212
A213
L216

- Molecule 24: Ribosomal protein L36a

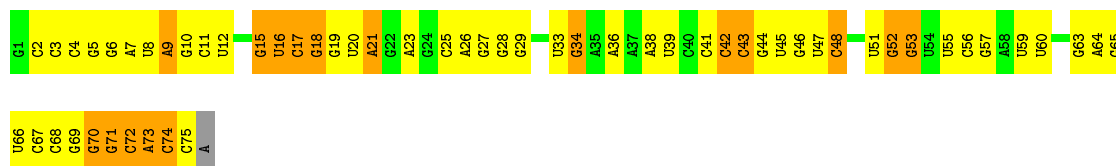
Chain F: 47% 34% 17%

V2
M3
V4
P5
K6
K9
T10
Y11
C12
K13
G14
K15
T16
C17
R18
K19
H20
T21
Q22
H23
A33
S34
Q38
G39
K40
R41
R42
L144
Y43
D44
R45
K46
Q47
S48
G52
Q53
T54
K55
P56
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C74
V75
K76
C77
K78
T79
R80
A81
Q82



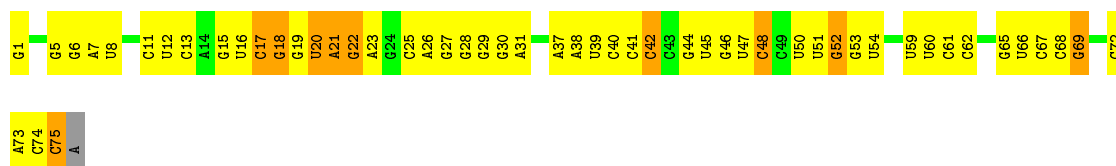
- Molecule 25: tRNA

Chain Y: 22% 54% 22%



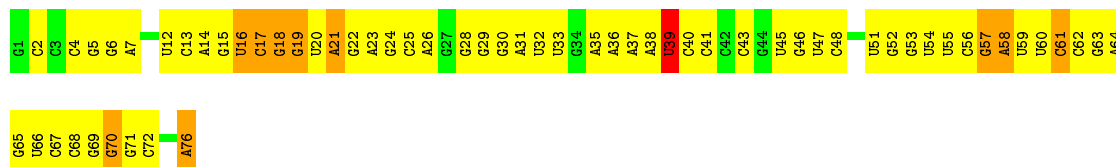
- Molecule 25: tRNA

Chain V: 29% 57% 13%



- Molecule 25: tRNA

Chain W: 20% 66% 13%



- Molecule 26: mRNA fragment

Chain y: 100%

There are no outlier residues recorded for this chain.

- Molecule 26: mRNA fragment

Chain v: 100%

There are no outlier residues recorded for this chain.

- Molecule 27: 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 images	81946	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	39000	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	0.38	0/1003	0.65	1/1342 (0.1%)
16	2	1.10	3/2677 (0.1%)	1.68	69/4170 (1.7%)
17	3	0.19	0/290	0.43	0/450
18	4	0.67	0/342	1.31	5/533 (0.9%)
19	5	0.69	0/141	1.32	1/217 (0.5%)
2	b	0.55	0/291	0.79	0/452
20	6	1.25	0/470	2.08	30/732 (4.1%)
21	7	1.06	2/1174 (0.2%)	2.34	33/1825 (1.8%)
22	8	1.45	4/482 (0.8%)	1.89	23/750 (3.1%)
23	B	0.34	0/1054	0.63	9/1468 (0.6%)
24	F	0.47	0/466	0.68	2/646 (0.3%)
25	V	0.44	0/1784	0.75	0/2780
25	W	0.43	0/1809	0.71	0/2819
25	Y	0.47	0/1784	0.74	0/2780
26	v	0.51	0/65	0.65	0/98
26	y	0.39	0/65	0.68	0/98
27	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	0.55	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	10/24379 (0.0%)	1.11	184/36535 (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
25	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 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	7	2845	A	C6-N1	-11.01	1.27	1.35
22	8	2969	A	N9-C4	-7.42	1.33	1.37
16	2	2283	G	N9-C8	6.14	1.42	1.37
22	8	2961	G	N9-C4	6.09	1.42	1.38
22	8	2958	A	N9-C4	-5.70	1.34	1.37

The worst 5 of 184 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	7	2845	A	N1-C6-N6	39.35	142.21	118.60
21	7	2845	A	C6-N1-C2	38.59	141.75	118.60
21	7	2845	A	C5-C6-N1	-34.02	100.69	117.70
21	7	2845	A	N1-C2-N3	-22.73	117.94	129.30
20	6	2689	A	C8-N9-C4	-13.86	100.26	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	6	0
7	f	452	0	226	0	0
8	g	660	0	335	0	0
9	G	276	0	141	15	0
10	h	2368	0	1197	0	0
11	T	1520	0	1569	195	0
12	K	1063	0	1088	111	0
13	L	1097	0	1169	105	0
14	X	554	0	604	42	0
15	S	985	0	1026	95	0
16	2	2392	0	1208	438	0
17	3	259	0	131	13	0
18	4	306	0	154	63	0
19	5	127	0	66	25	0
20	6	417	0	209	77	0
21	7	1054	0	532	177	0
22	8	431	0	216	51	0
23	B	1055	0	453	31	0
24	F	467	0	208	32	0
25	V	1597	0	807	69	0
25	W	1619	0	821	120	0
25	Y	1597	0	811	87	0
26	v	60	0	31	0	0
26	y	60	0	31	0	0
27	w	44	0	23	0	0
All	All	22450	0	14069	1641	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 55.

The worst 5 of 1641 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)
19:5:2657:A:C2	20:6:2694:A:N3	1.73	1.45
18:4:2619:G:OP1	21:7:2866:U:C6	1.79	1.35
18:4:2619:G:OP1	21:7:2866:U:C4	1.80	1.34
18:4:2618:G:H2'	21:7:2865:U:P	1.69	1.33
18:4:2618:G:C2'	21:7:2865:U:P	2.22	1.28

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	18
12	K	138/140 (99%)	96 (70%)	28 (20%)	14 (10%)	1	14
13	L	139/141 (99%)	106 (76%)	17 (12%)	16 (12%)	0	9
14	X	66/68 (97%)	48 (73%)	12 (18%)	6 (9%)	1	17
15	S	123/125 (98%)	91 (74%)	25 (20%)	7 (6%)	2	28
23	B	211/213 (99%)	76 (36%)	67 (32%)	68 (32%)	0	0
24	F	93/95 (98%)	37 (40%)	28 (30%)	28 (30%)	0	0
All	All	960/974 (99%)	595 (62%)	210 (22%)	155 (16%)	1	5

5 of 155 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
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%)	10	39
12	K	112/112 (100%)	96 (86%)	16 (14%)	4	25
13	L	113/113 (100%)	101 (89%)	12 (11%)	8	36
14	X	57/57 (100%)	55 (96%)	2 (4%)	43	74
15	S	105/105 (100%)	102 (97%)	3 (3%)	50	78
All	All	550/550 (100%)	501 (91%)	49 (9%)	17	44

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 13 such sidechains are listed below:

Mol	Chain	Res	Type
11	T	143	ASN
11	T	199	ASN
14	X	42	ASN
11	T	102	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	2	111/112 (99%)	54 (48%)	9 (8%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
17	3	11/12 (91%)	6 (54%)	1 (9%)
18	4	13/14 (92%)	5 (38%)	1 (7%)
19	5	5/6 (83%)	4 (80%)	1 (20%)
2	b	11/12 (91%)	4 (36%)	0
20	6	18/19 (94%)	13 (72%)	1 (5%)
21	7	49/50 (98%)	29 (59%)	5 (10%)
22	8	19/20 (95%)	8 (42%)	0
25	V	74/76 (97%)	15 (20%)	0
25	W	75/76 (98%)	13 (17%)	0
25	Y	74/76 (97%)	20 (27%)	1 (1%)
26	v	2/3 (66%)	0	0
26	y	2/3 (66%)	0	0
27	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%)	1 (25%)
7	f	20/21 (95%)	5 (25%)	0
8	g	30/31 (96%)	8 (26%)	0
9	G	12/13 (92%)	2 (16%)	1 (8%)
All	All	713/738 (96%)	220 (30%)	21 (2%)

5 of 220 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

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	2	2290	C
17	3	2487	U
21	7	2851	A
16	2	2281	A
21	7	2859	U

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 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.