



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:46 PM BST

PDB ID : 3J79
EMDB ID: : EMD-2660
Title : Cryo-EM structure of the Plasmodium falciparum 80S ribosome bound to the anti-protozoan drug emetine, large subunit
Authors : Wong, W.; Bai, X.C.; Brown, A.; Fernandez, I.S.; Hanssen, E.; Condron, M.; Tan, Y.H.; Baum, J.; Scheres, S.H.W.
Deposited on : 2014-06-02
Resolution : 3.20 Å(reported)

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>

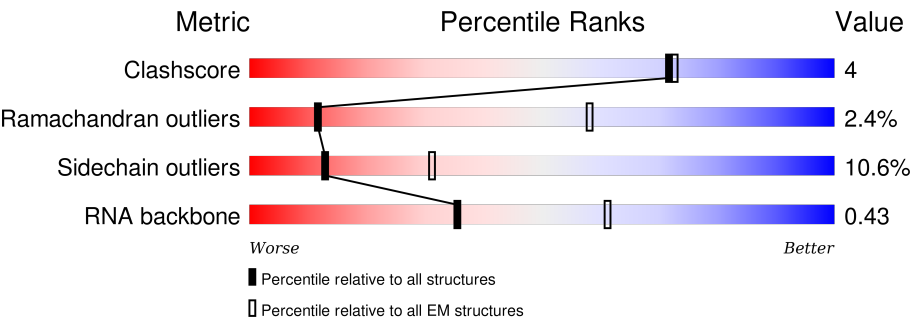
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 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.














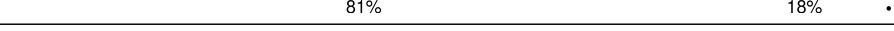




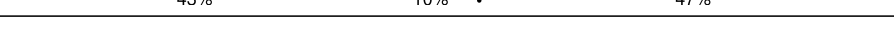


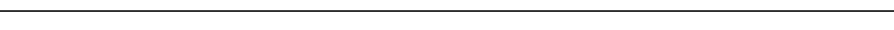

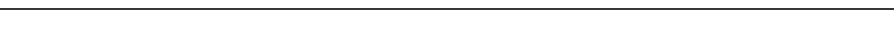
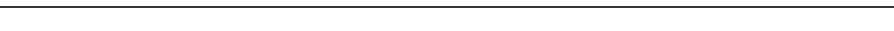


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	3788	<div><div>53%</div><div>27%</div><div>5%</div><div>16%</div></div>
2	B	119	<div><div>75%</div><div>20%</div><div>.</div><div>.</div></div>
3	C	159	<div><div>55%</div><div>33%</div><div>6%</div><div>5%</div></div>
4	D	260	<div><div>79%</div><div>13%</div><div>5%</div></div>
5	E	386	<div><div>79%</div><div>17%</div><div>.</div><div>.</div></div>
6	F	411	<div><div>76%</div><div>16%</div><div>5%</div></div>
7	G	173	<div><div>52%</div><div>17%</div><div>.</div><div>28%</div></div>
8	H	190	<div><div>70%</div><div>25%</div><div>.</div><div>.</div><div>.</div></div>











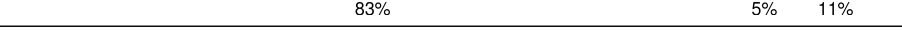

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Mol	Chain	Length	Quality of chain
9	I	221	
10	J	283	
11	K	202	
12	L	215	
13	M	139	
14	N	165	
15	O	148	
16	P	205	
17	Q	219	
18	R	294	
19	S	187	
20	T	182	
21	U	184	
22	V	161	
23	W	203	
24	X	139	
25	Y	190	
26	Z	126	
27	0	162	
28	1	146	
29	2	127	
30	3	124	
31	4	67	
32	5	257	
33	6	108	

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Mol	Chain	Length	Quality of chain
34	7	120	
35	8	131	
36	9	140	
37	a	150	
38	b	112	
39	c	92	
40	d	87	
41	e	51	
42	f	128	
43	g	39	
44	h	96	
45	i	104	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 124514 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3191	Total	C	N	O	P	0	0
			67935	30426	12044	22274	3191		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	118	Total	C	N	O	P	0	0
			2525	1128	461	818	118		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	151	Total	C	N	O	P	0	0
			3224	1444	589	1040	151		

- Molecule 4 is a protein called 60S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	247	Total	C	N	O	S	0	0
			1866	1166	374	317	9		

- Molecule 5 is a protein called 60S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	380	Total	C	N	O	S	0	0
			3061	1948	575	521	17		

- Molecule 6 is a protein called 60S ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	390	Total	C	N	O	S	0	0
			3094	1962	594	527	11		

- Molecule 7 is a protein called 60S ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	124	Total	C	N	O	S	0	0
			1010	636	197	171	6		

- Molecule 8 is a protein called 60S ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	185	Total	C	N	O	S	0	0
			1460	938	261	255	6		

- Molecule 9 is a protein called 60S ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	207	Total	C	N	O	S	0	0
			1684	1096	298	285	5		

- Molecule 10 is a protein called 60S ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	229	Total	C	N	O	S	0	0
			1873	1210	337	319	7		

- Molecule 11 is a protein called 60S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	201	Total	C	N	O	S	0	0
			1659	1064	311	276	8		

- Molecule 12 is a protein called 60S ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	211	Total	C	N	O	S	0	0
			1761	1119	349	290	3		

- Molecule 13 is a protein called 60S ribosomal protein uL14.

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

- Molecule 14 is a protein called 60S ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	146	Total	C	N	O	S	0	0
			1197	779	210	202	6		

- Molecule 15 is a protein called 60S ribosomal protein uL15.

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

- Molecule 16 is a protein called 60S ribosomal protein eL15.

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

- Molecule 17 is a protein called 60S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	189	Total	C	N	O	S	0	0
			1544	984	291	261	8		

- Molecule 18 is a protein called 60S ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	252	Total	C	N	O	S	0	0
			2045	1297	384	358	6		

- Molecule 19 is a protein called 60S ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	186	Total	C	N	O	S	0	0
			1502	958	299	240	5		

- Molecule 20 is a protein called 60S ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	181	Total	C	N	O	S	0	0
			1505	949	308	244	4		

- Molecule 21 is a protein called 60S ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	180	Total	C	N	O	S	0	0
			1496	946	289	254	7		

- Molecule 22 is a protein called 60S ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	155	Total	C	N	O	S	0	0
			1275	814	241	214	6		

- Molecule 23 is a protein called 60S ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	170	Total	C	N	O	S	0	0
			1318	824	266	221	7		

- Molecule 24 is a protein called 60S ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	97	Total	C	N	O	S	0	0
			824	548	135	139	2		

- Molecule 25 is a protein called 60S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	101	Total	C	N	O	S	0	0
			796	502	144	144	6		

- Molecule 26 is a protein called 60S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	121	Total	C	N	O	S	0	0
			1000	626	206	165	3		

- Molecule 27 is a protein called 60S ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	0	62	Total	C	N	O	S	0	0
			521	336	97	87	1		

- Molecule 28 is a protein called 60S ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 29 is a protein called 60S ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2	104	Total	C	N	O	S	0	0
			830	529	151	147	3		

- Molecule 30 is a protein called 60S ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	3	119	Total	C	N	O	S	0	0
			994	635	194	163	2		

- Molecule 31 is a protein called 60S ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 32 is a protein called 60S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 33 is a protein called 60S ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	6	98	Total	C	N	O	S	0	0
			740	462	132	139	7		

- Molecule 34 is a protein called 60S ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	7	96	Total	C	N	O	S	0	0
			793	508	151	129	5		

- Molecule 35 is a protein called 60S ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	8	125	Total	C	N	O	S	0	0
			1036	660	206	163	7		

- Molecule 36 is a protein called 60S ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	9	103	Total	C	N	O	S	0	0
			844	543	163	135	3		

- Molecule 37 is a protein called 60S ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	106	Total	C	N	O	S	0	0
			858	530	184	138	6		

- Molecule 38 is a protein called 60S ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	b	95	Total	C	N	O		0	0
			756	477	150	129			

- Molecule 39 is a protein called 60S ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	89	Total	C	N	O	S	0	0
			705	439	150	111	5		

- Molecule 40 is a protein called 60S ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	d	72	Total	C	N	O	S	0	0
			603	395	107	99	2		

- Molecule 41 is a protein called 60S ribosomal protein eL39.

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

- Molecule 42 is a protein called 60S ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	51	Total	C	N	O	S	0	0
			413	255	87	66	5		

- Molecule 43 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	37	Total	C	N	O	S	0	0
			342	210	86	44	2		

- Molecule 44 is a protein called 60S ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	h	85	Total	C	N	O	S	0	0
			658	417	127	107	7		

- Molecule 45 is a protein called 60S ribosomal protein eL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	i	95	Total	C	N	O	S	0	0
			778	490	152	127	9		

- Molecule 46 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
46	B	3	Total	Mg	0
			3	3	
46	A	153	Total	Mg	0
			153	153	
46	Q	1	Total	Mg	0
			1	1	
46	C	5	Total	Mg	0
			5	5	
46	M	1	Total	Mg	0
			1	1	

- Molecule 47 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	h	1	Total	Zn	0
			1	1	
47	a	1	Total	Zn	0
			1	1	

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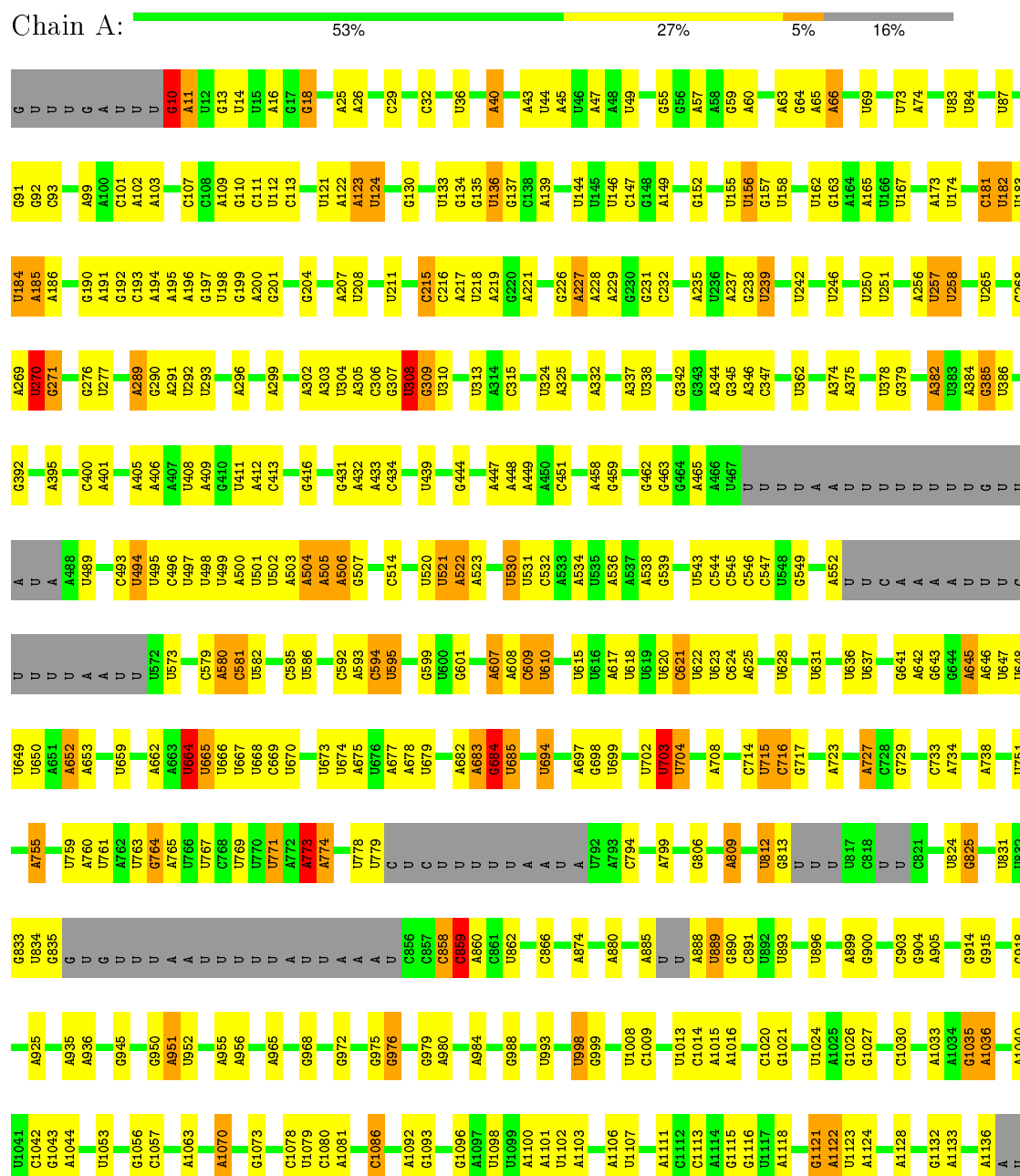
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Mol	Chain	Residues	Atoms		AltConf
47	c	1	Total 1	Zn 1	0
47	f	1	Total 1	Zn 1	0
47	i	1	Total 1	Zn 1	0

3 Residue-property plots

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

• Molecule 1: 28S ribosomal RNA






G3600	U2711	A	C	G3029	A3138	A3269	A3362	U3475	G3574	G	A3735
C2601	A2712	C	C	A3030	C3139	A3270	U3363	A3476	U3575	A3645	A3736
U2602	G2728	A	G	A3033	U3140	G3271	A3364	A3477	A3576	C3654	U3737
U2603	G2729	G	G	A3035	G3141	G3272	A3365	A3478	A3577	U3655	G3738
A2606	G2730	U	U	A3036	U3146	G3277	U	U3483	G3580	U3656	A3739
U2607	A2733	A	A	A3038	G3155	U3282	U	U3488	A3581	A3657	A3741
G2608	G2734	A	A	G3039	U3158	U3287	U	U3493	G3582	G3658	G3742
C2624	G2735	A	A	A3042	G3159	C3287	A	G3493	A3583	U3659	U
U2627	A2736	U	U	A3045	A3160	U3292	U3373	G3500	A3584	A3660	U
U2628	G2737	C	C	C3046	A3161	A3293	U3374	G3501	A3585	U3662	G
U2629	U2738	C	C	A3066	A3162	A3295	A3375	C3502	U3586	A3663	U
	U2739	A	A	G3067		U3294	A3376		A3590	G3664	U2748
	A2740	U	U	A3068	C3169	A3295	C3378	A3507	U3591	U3665	C3752
C2632	A2741	U	U	G3073	G3173	G3296	U3379	A3510	U3592	G3667	G3753
U2633	G2742	C	C	U3074	C3174	G3297	U3380	C3510	G3593	U3668	A3754
A2634		U	U	A3075	A3175	A3300	U3381	A3515	G3594	U3669	
	G2745	G	G	G3076	A3176	C3301	U3382	A3516	C3595	U3670	G3761
U2640	U2746	A	A	A3079	C3180	G3304	U3383		C3596	A3671	U3767
A2649	G2747	U	U	A3086		A3305	U3387	G3524	U	A3675	
A2650	U	A	A	A3087	G3183	G3306	U3388	A3525	U	C3676	C3770
A2651	G2748	U	U	G3088	C3184	U3309	G3389	U3526	U	A3677	
A2656	A	U	U	U2970	C3195	G3309	U3390	U3527	U		A3774
		U	U	U2883			G3391	A3528	G3606	A3680	G3775
A2665		A	A	A2885	U9091	G3313	U3398	A3529	U	G3683	U3776
A2666	G2749	U	U	U2886	G3092	G3316	G3414	U3537	A3611	U	G3777
A2667		G	G	U2887	C3093	A3317	A3415	A3538	U3612	A	U3778
G2668		G	G	U2888	C3094	A3317	G3416	U	A3613	U	A3780
		U	U		C3095	A3328	G3417	U	U3614	U	G3782
C2671		U	U		U3096	A3329	A3418	C	A3615	G3688	A3783
		A	A		G3100	A3330	A3421	U	A3617	A3690	
C2676		U	U		C3103	U3334		U3545	U3618		U3786
A2677		A	A		A3108	U3340	G3426		U3619	G3697	U
A2678		G	G			A3341	A3434	G3553	A3623	U3698	
A2679		A	A		U3111	C3342	A3435	U3554	C3624	U3699	
A2680		A	A		U3112	C3343	A3436	U3555	C3625	G3700	
U2681		C	C		U3113	C3344	G3439	U	A3626	A3701	
C2682		A	A			U3345	U3439	C	C3627		A3704
A2683		U	U		A3116	A3346	C3442	U	U3628	A3707	
G2684		A	A		A3117	C3347	A3443	U	U3629	U3708	
C2685		U	U		A3118	U3348	G3444	U	U3630		A100
G2686		A	A		A3119	G3349	C3445	U	U3631	U3710	A101
G2687		U	U		C3123	A3350		U	U3632	U3711	A102
		U	U		G3124	A3353	A3458	U	U3633	G3712	A103
A2690		U	U		U3125	A3354	A3459	U	C3634		G110
A2694		A	A		A3126	U3355	C3460	U	G3635	C3716	A118
A2695		U	U		A3127	U3356	G3463	C	U3636	U3726	G119
G2696		C	C		U3130	U3357	U3464	U	A3637	A3727	
A2697		U	U		A3131	G3358	U3464	U	G3639	A3728	
		U	U		U3025	U3359	A3471	U	C3640		U2704
		U	U		G3026	U3360	G3474	U	U3641	U3732	G2705
		A	A		A3028	U3361		U3573	G	G3733	
		U	U						U	A3734	G

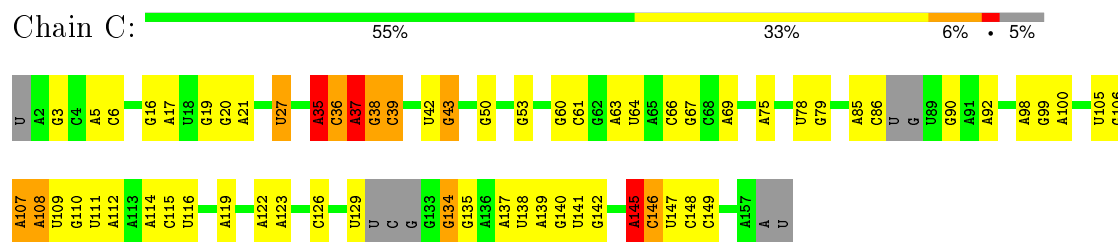
- Molecule 2: 5S ribosomal RNA

Chain B:

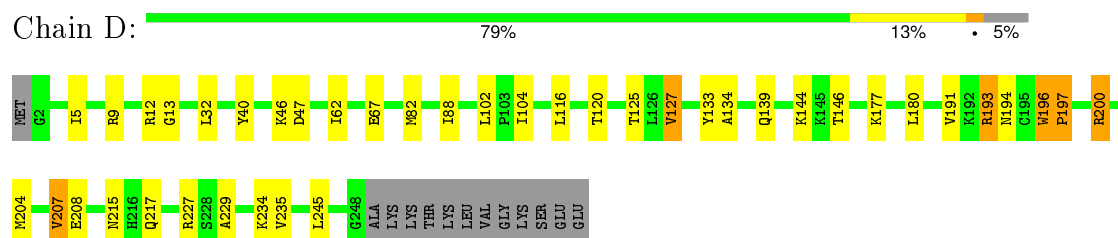


U	G2	A13	G22	A23	C26	G31	A32	U33	U38	G51	U52	A63	G71	U72	A74	G75	U76	G89	G97	A100	C102	A103	G110	A118	G119
	A3	C4	U5	G6	U7	A13	U18	A27	G31	U33	U38	A63	G71	U72	A74	G75	U76	G89	G97	A100	C102	A103	G110	A118	G119

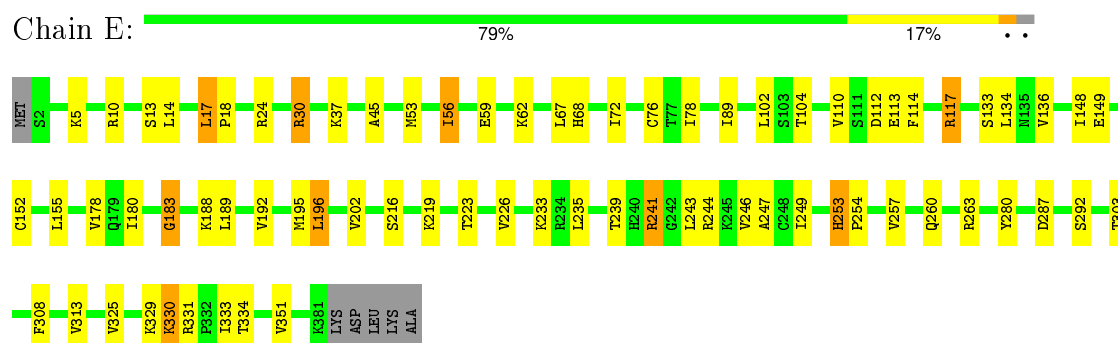
- Molecule 3: 5.8S ribosomal RNA



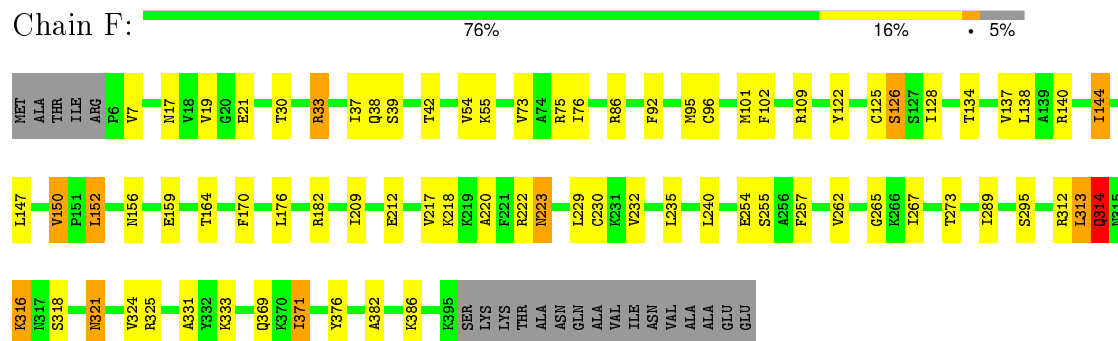
• Molecule 4: 60S ribosomal protein uL2



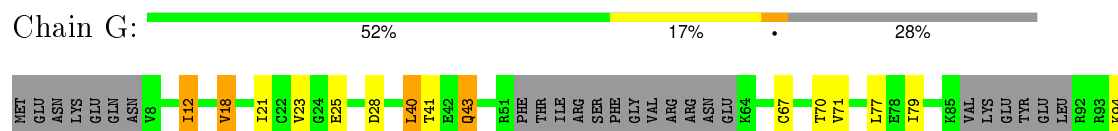
• Molecule 5: 60S ribosomal protein uL3



• Molecule 6: 60S ribosomal protein uL4



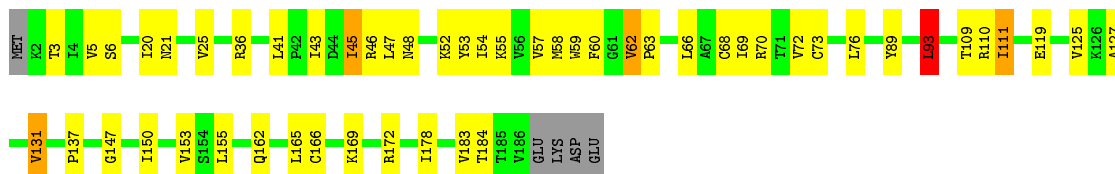
• Molecule 7: 60S ribosomal protein uL5





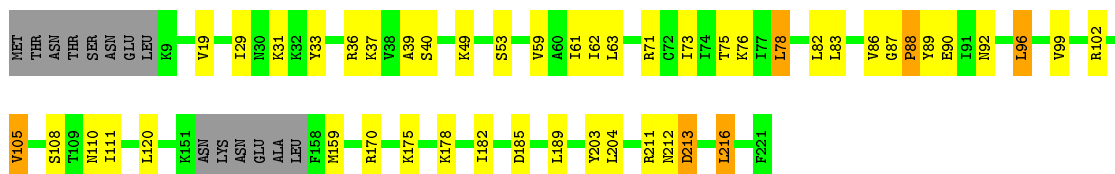
- Molecule 8: 60S ribosomal protein uL6

Chain H: 70% 25%



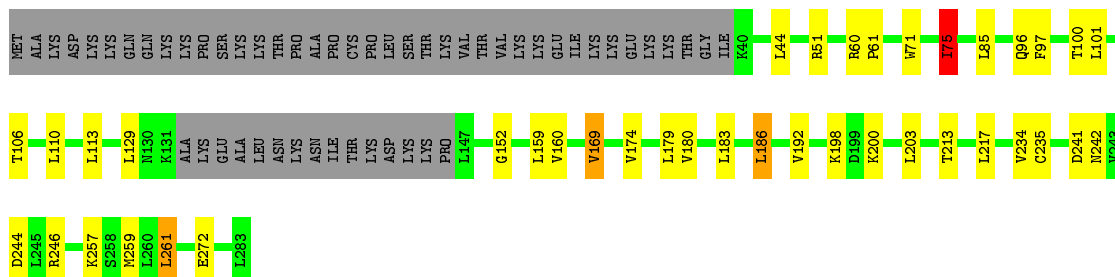
- Molecule 9: 60S ribosomal protein eL6

Chain I: 72% 19% 6%



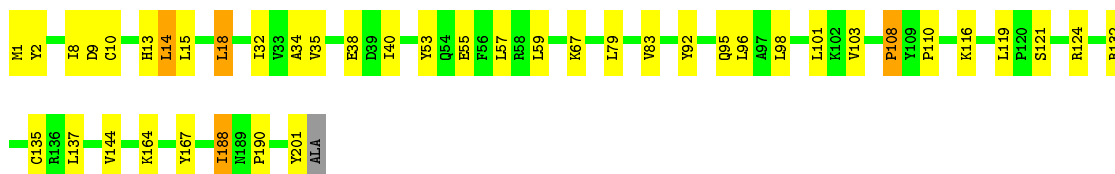
- Molecule 10: 60S ribosomal protein eL8

Chain J: 67% 13% 19%



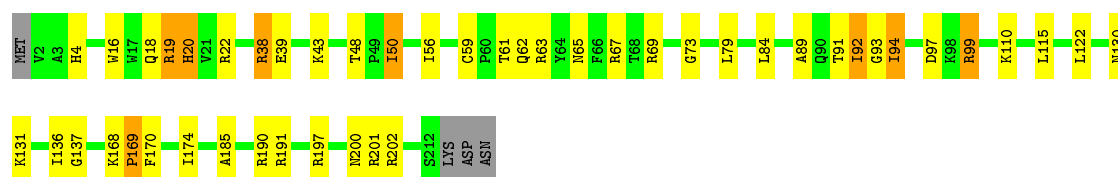
- Molecule 11: 60S ribosomal protein uL13

Chain K: 79% 19%



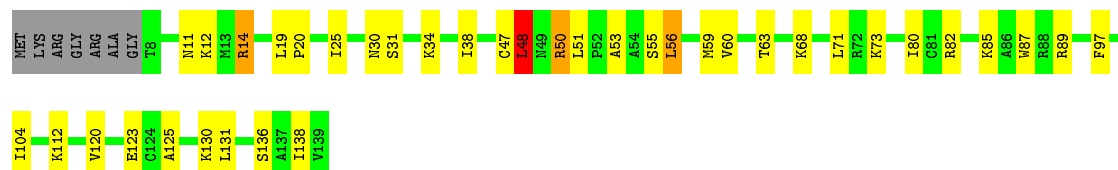
- Molecule 12: 60S ribosomal protein eL13

Chain L: 76% 18%



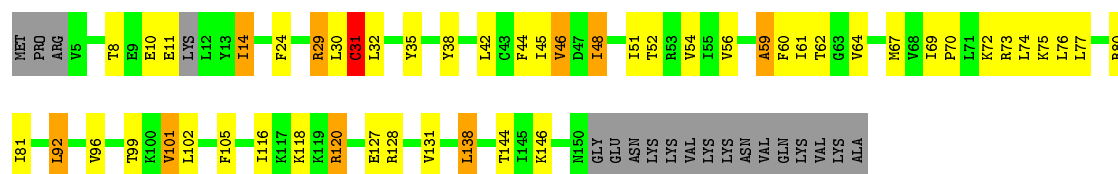
- Molecule 13: 60S ribosomal protein uL14

Chain M: 68% 24% 5%



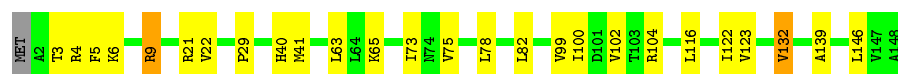
- Molecule 14: 60S ribosomal protein eL14

Chain N: 58% 25% 5% 12%



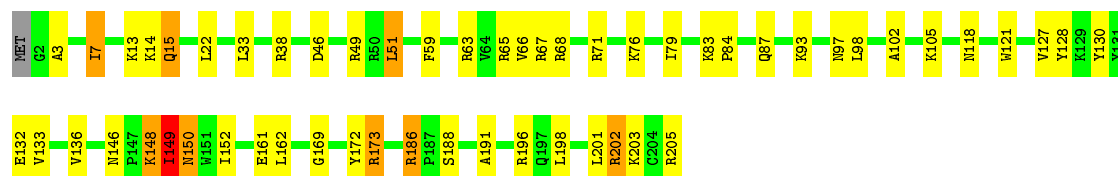
- Molecule 15: 60S ribosomal protein uL15

Chain O: 82% 16%



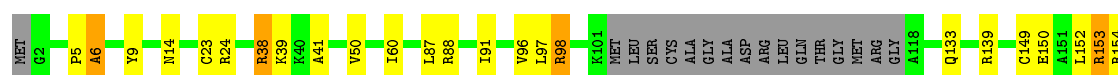
- Molecule 16: 60S ribosomal protein eL15

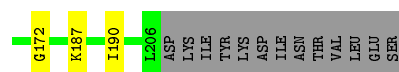
Chain P: 73% 22%



- Molecule 17: 60S ribosomal protein uL16

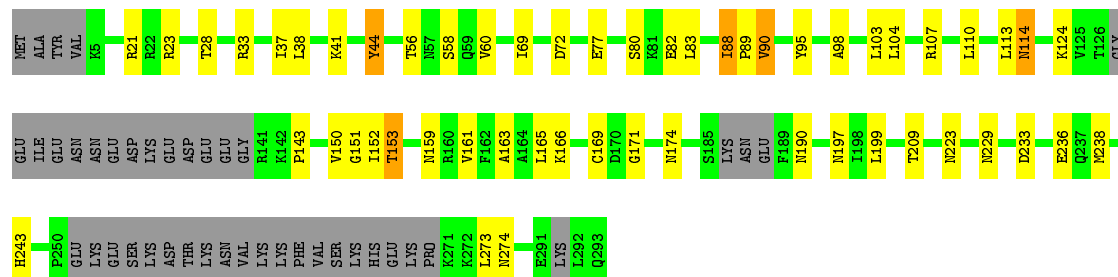
Chain Q: 74% 11% 14%





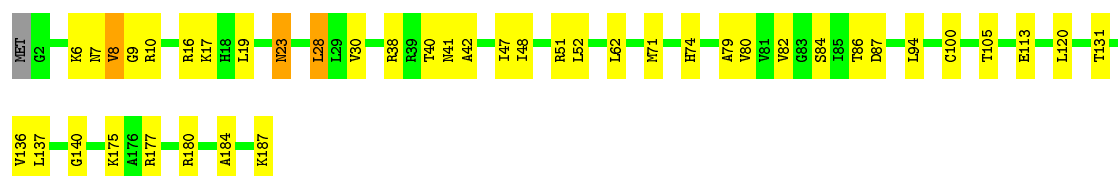
• Molecule 18: 60S ribosomal protein uL18

Chain R: 67% 17% 14%



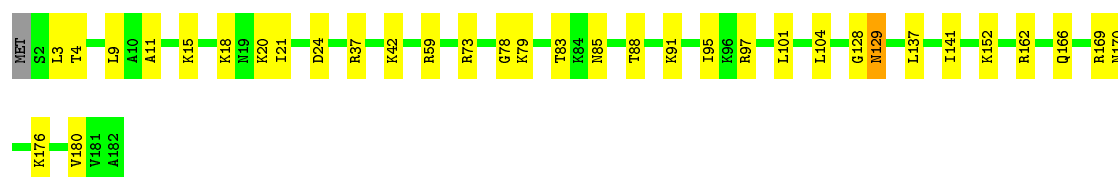
• Molecule 19: 60S ribosomal protein eL18

Chain S: 77% 21% ..



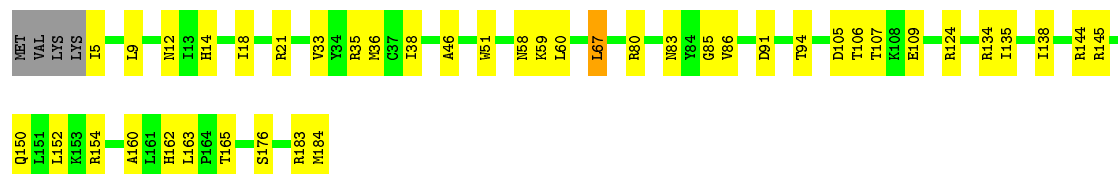
• Molecule 20: 60S ribosomal protein eL19

Chain T: 81% 18% ..



• Molecule 21: 60S ribosomal protein eL20

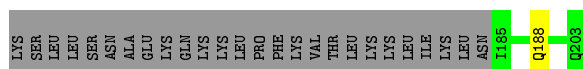
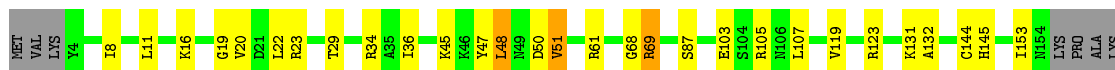
Chain U: 75% 22% ..



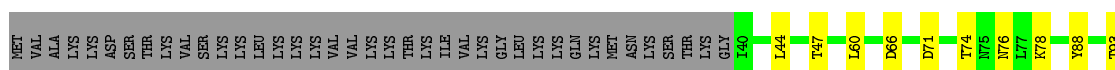
• Molecule 22: 60S ribosomal protein eL21

Chain V: 84% 12% ..

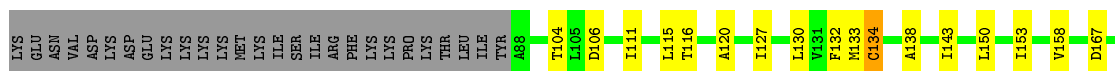
- Molecule 23: 60S ribosomal protein uL22



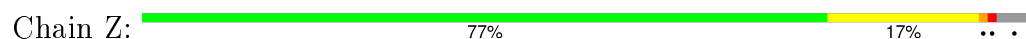
- Molecule 24: 60S ribosomal protein eL22



- Molecule 25: 60S ribosomal protein uL23



- Molecule 26: 60S ribosomal protein uL24




- Molecule 27: 60S ribosomal protein eL24



SER
LYS
MET
HIS
LYS
MET
MET
LYS
LYS

- Molecule 28: 60S ribosomal protein eL27

Chain 1:  80% 15% . .

MET G2 K3 K4 L5 K9 V10 I11 I12 I13 A19 A23 V26 L42 V43 K61 I62 V63 I72 K73 C74 I80 I81 P82 N106 K107 K108 V111 L114 I117 L123 E124 P125 V126 ASN LYS LYS THR GLY E132 F146

- Molecule 29: 60S ribosomal protein eL28

Chain 2:  72% 8% 18% .


MET S2 N3 N23 G36 D34 N37 V38 N39 V57 K60 K69 THR SER LYS GLU SER ASN VAL V77 K82 ALA LYS ASN P86 H96 G97 S98 PHE GLU LYS ALA K103 L108 Y119 GLU THR SER HIS LYS LYS THR ASN

- Molecule 30: 60S ribosomal protein uL29

Chain 3:  75% 17% . .

MET SER N3 V4 L18 L24 L31 K42 P37 N43 I46 N52 V53 A54 R55 N61 R64 K65 R66 E67 L68 K76 F77 L82 R83 T87 K90 K97 Q98 L104 L119 V121 HIS LYS GLU

- Molecule 31: 60S ribosomal protein eL29

Chain 4:  82% 16% .

MET K2 N13 G20 I21 K28 D36 P37 N38 F39 Q51 K62 Q63 R67

- Molecule 32: 60S ribosomal protein uL30

Chain 5:  67% 19% 13% .

MET ALA ASP ARG TYR GLU ASN GLN VAL ASN GLU LEU GLY LYS SER MET THR SER LEU ARG ALA LYS VAL ASN LYS LYS LEU LYS GLN ALA A35 K49 L53 R54 T57 L58 R59 R79 E89 F94 R97 L98 K107 V111 L115 R116

L117 V124 V128 N129 E134 K137 P141 T144 Y147 P148 T149 L156 L157 R160 V168 A172 I176 Q177 D181 I182 Y189 N190 V191 E195 L201 C204 V207 K210 R224 R231 E232 A233 E236 W242 E246

I249 N250 I253 I257

- Molecule 33: 60S ribosomal protein eL30

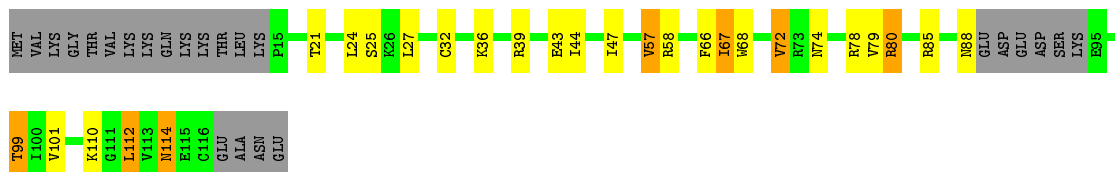
Chain 6:  62% 26% 9% .

MET ALA LYS LYS SER LYS SER LYS S8 L17 Q18 L19 V20 M21 K22 F28 C33 L37 L44 V45 I46 M50 C51 S53 S54 I54 Q55 V58 I59 Y62 L65 S66 K67 H71 H77 L80 C84 G85 R89 I90 S91 V94 I95 S101 D102



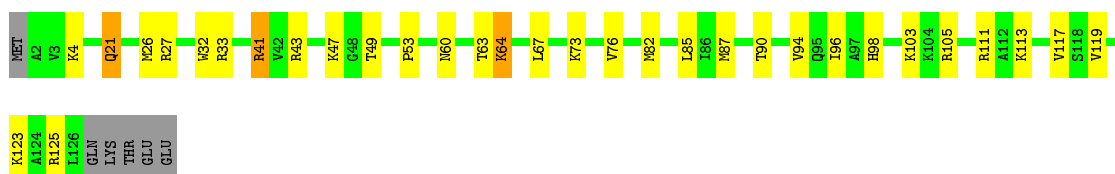
- Molecule 34: 60S ribosomal protein eL31

Chain 7: 58% 17% 6% 20%



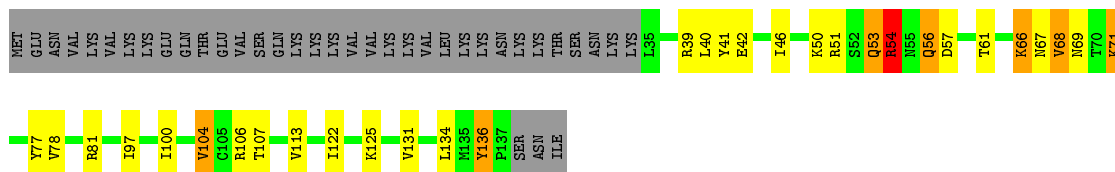
- Molecule 35: 60S ribosomal protein eL32

Chain 8: 71% 22% 5%



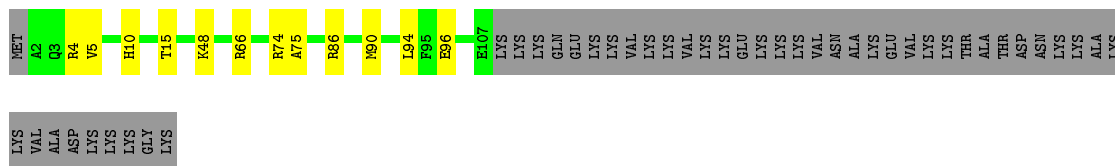
- Molecule 36: 60S ribosomal protein eL33

Chain 9: 51% 16% 5% 26%



- Molecule 37: 60S ribosomal protein eL34

Chain a: 63% 8% 29%




- Molecule 38: 60S ribosomal protein eL36

Chain b: 79% 5% 15%



- Molecule 39: 60S ribosomal protein eL37

Chain c:  83% 14%



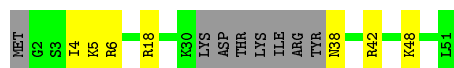
- Molecule 40: 60S ribosomal protein eL38

Chain d:  75% 8% 17%



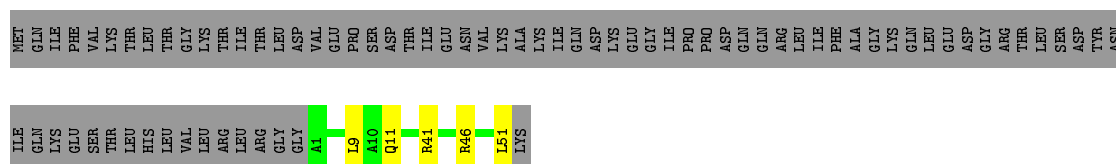
- Molecule 41: 60S ribosomal protein eL39

Chain e:  71% 14% 16%




- Molecule 42: 60S ribosomal protein eL40

Chain f:  36% 60%




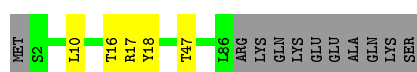
- Molecule 43: 60S ribosomal protein eL41

Chain g:  90% 5% 5%




- Molecule 44: 60S ribosomal protein eL43

Chain h:  83% 5% 11%



- Molecule 45: 60S ribosomal protein eL44

Chain i:  81% 11% 9%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	105247	Depositor
Resolution determination method	FSC 0.143 gold-standard	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3800	Depositor
Magnification	78000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0.30	1/75991 (0.0%)	0.73	35/118299 (0.0%)
10	J	0.41	0/1901	0.74	0/2537
11	K	0.45	0/1689	0.81	0/2260
12	L	0.44	0/1793	0.80	0/2387
13	M	0.45	0/1012	0.73	0/1363
14	N	0.45	0/1213	0.81	0/1616
15	O	0.44	0/1199	0.76	0/1597
16	P	0.44	0/1735	0.83	2/2320 (0.1%)
17	Q	0.41	0/1579	0.73	0/2113
18	R	0.43	0/2074	0.79	0/2773
19	S	0.43	0/1530	0.80	0/2040
2	B	0.26	0/2826	0.69	0/4404
20	T	0.46	0/1521	0.80	0/2012
21	U	0.43	0/1526	0.73	0/2043
22	V	0.40	0/1300	0.70	0/1732
23	W	0.45	0/1338	0.78	0/1793
24	X	0.40	0/841	0.66	0/1125
25	Y	0.41	0/805	0.74	0/1074
26	Z	0.39	0/1012	0.78	1/1339 (0.1%)
27	0	0.46	0/533	0.76	0/711
28	1	0.37	0/1151	0.68	0/1531
29	2	0.41	0/839	0.64	0/1114
3	C	0.28	0/3608	0.74	4/5615 (0.1%)
30	3	0.44	0/1004	0.82	0/1329
31	4	0.43	0/564	0.77	0/737
32	5	0.45	0/1917	0.83	0/2562
33	6	0.42	0/748	0.83	0/1001
34	7	0.44	0/805	0.82	0/1073
35	8	0.45	0/1053	0.79	0/1399
36	9	0.48	0/864	0.87	0/1160
37	a	0.38	0/871	0.77	0/1161
38	b	0.46	0/762	0.83	0/1008

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	c	0.47	0/718	0.84	0/946
4	D	0.48	0/1901	0.82	1/2544 (0.0%)
40	d	0.42	0/611	0.71	0/812
41	e	0.48	0/396	0.84	0/521
42	f	0.45	0/418	0.83	0/556
43	g	0.45	0/347	0.95	0/448
44	h	0.43	0/667	0.73	0/887
45	i	0.41	0/788	0.71	0/1032
5	E	0.43	0/3129	0.74	0/4195
6	F	0.42	0/3144	0.80	2/4205 (0.0%)
7	G	0.43	0/1020	0.80	0/1349
8	H	0.42	0/1485	0.77	1/2009 (0.0%)
9	I	0.41	0/1707	0.75	0/2274
All	All	0.36	1/133935 (0.0%)	0.75	46/197006 (0.0%)

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
11	K	0	1
14	N	0	1
23	W	0	1
32	5	0	1
33	6	0	1
36	9	0	1
39	c	0	1
4	D	0	1
5	E	0	3
6	F	0	1
9	I	0	1
All	All	0	13

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2463	U	O3'-P	-5.46	1.54	1.61

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1805	U	C2'-C3'-O3'	8.69	128.62	109.50
1	A	289	A	C2'-C3'-O3'	8.40	127.98	109.50
3	C	145	A	C2'-C3'-O3'	8.31	127.79	109.50
3	C	37	A	C2'-C3'-O3'	8.03	127.16	109.50
1	A	652	A	C2'-C3'-O3'	7.52	126.05	109.50

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	196	TRP	Peptide
5	E	17	LEU	Peptide
5	E	195	MET	Peptide
5	E	253	HIS	Peptide
6	F	150	VAL	Peptide

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	67935	0	34190	456	0
2	B	2525	0	1274	7	0
3	C	3224	0	1630	20	0
4	D	1866	0	1964	18	0
5	E	3061	0	3205	40	0
6	F	3094	0	3333	37	0
7	G	1010	0	1073	14	0
8	H	1460	0	1532	19	0
9	I	1684	0	1849	15	0
10	J	1873	0	2055	10	0
11	K	1659	0	1782	18	0
12	L	1761	0	1895	20	0
13	M	996	0	1044	17	0
14	N	1197	0	1312	28	0
15	O	1172	0	1230	16	0
16	P	1697	0	1802	30	0
17	Q	1544	0	1582	11	0
18	R	2045	0	2129	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	S	1502	0	1636	17	0
20	T	1505	0	1671	14	0
21	U	1496	0	1556	21	0
22	V	1275	0	1355	7	0
23	W	1318	0	1319	10	0
24	X	824	0	882	4	0
25	Y	796	0	850	12	0
26	Z	1000	0	1099	4	0
27	0	521	0	539	6	0
28	1	1134	0	1245	9	0
29	2	830	0	887	3	0
30	3	994	0	1121	9	0
31	4	555	0	599	1	0
32	5	1879	0	2005	21	0
33	6	740	0	763	9	0
34	7	793	0	869	10	0
35	8	1036	0	1139	12	0
36	9	844	0	886	14	0
37	a	858	0	911	0	0
38	b	756	0	842	0	0
39	c	705	0	754	0	0
40	d	603	0	686	0	0
41	e	388	0	421	0	0
42	f	413	0	449	0	0
43	g	342	0	388	0	0
44	h	658	0	724	0	0
45	i	778	0	857	0	0
46	A	153	0	0	0	0
46	B	3	0	0	0	0
46	C	5	0	0	0	0
46	M	1	0	0	0	0
46	Q	1	0	0	0	0
47	a	1	0	0	0	0
47	c	1	0	0	0	0
47	f	1	0	0	0	0
47	h	1	0	0	0	0
47	i	1	0	0	0	0
All	All	124514	0	91334	867	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 4.

The worst 5 of 867 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)
1:A:3626:A:C6	1:A:3660:A:C6	2.12	1.37
1:A:3626:A:C2	1:A:3660:A:C2	2.31	1.19
1:A:3123:C:O2	12:L:202:ARG:NH2	1.80	1.14
1:A:3626:A:C5	1:A:3660:A:C6	2.38	1.12
1:A:3016:G:O6	1:A:3019:A:N6	1.87	1.07

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	
4	D	245/260 (94%)	225 (92%)	15 (6%)	5 (2%)	9	48
5	E	378/386 (98%)	345 (91%)	26 (7%)	7 (2%)	10	50
6	F	388/411 (94%)	359 (92%)	20 (5%)	9 (2%)	8	44
7	G	116/173 (67%)	106 (91%)	7 (6%)	3 (3%)	7	40
8	H	183/190 (96%)	150 (82%)	26 (14%)	7 (4%)	4	28
9	I	203/221 (92%)	179 (88%)	15 (7%)	9 (4%)	3	24
10	J	225/283 (80%)	203 (90%)	16 (7%)	6 (3%)	6	39
11	K	199/202 (98%)	185 (93%)	10 (5%)	4 (2%)	9	48
12	L	209/215 (97%)	183 (88%)	17 (8%)	9 (4%)	3	25
13	M	130/139 (94%)	119 (92%)	8 (6%)	3 (2%)	8	44
14	N	144/165 (87%)	135 (94%)	5 (4%)	4 (3%)	6	37
15	O	145/148 (98%)	133 (92%)	12 (8%)	0	100	100
16	P	202/205 (98%)	185 (92%)	11 (5%)	6 (3%)	5	35
17	Q	185/219 (84%)	157 (85%)	22 (12%)	6 (3%)	5	33
18	R	244/294 (83%)	218 (89%)	17 (7%)	9 (4%)	4	29
19	S	184/187 (98%)	167 (91%)	12 (6%)	5 (3%)	6	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	T	179/182 (98%)	172 (96%)	4 (2%)	3 (2%)	11	52
21	U	178/184 (97%)	166 (93%)	9 (5%)	3 (2%)	11	52
22	V	153/161 (95%)	134 (88%)	13 (8%)	6 (4%)	4	28
23	W	166/203 (82%)	152 (92%)	13 (8%)	1 (1%)	30	75
24	X	95/139 (68%)	86 (90%)	6 (6%)	3 (3%)	5	33
25	Y	99/190 (52%)	93 (94%)	6 (6%)	0	100	100
26	Z	119/126 (94%)	102 (86%)	14 (12%)	3 (2%)	7	41
27	0	60/162 (37%)	55 (92%)	3 (5%)	2 (3%)	5	32
28	1	136/146 (93%)	125 (92%)	10 (7%)	1 (1%)	26	72
29	2	96/127 (76%)	85 (88%)	9 (9%)	2 (2%)	9	46
30	3	117/124 (94%)	104 (89%)	10 (8%)	3 (3%)	7	40
31	4	64/67 (96%)	56 (88%)	5 (8%)	3 (5%)	3	22
32	5	221/257 (86%)	197 (89%)	20 (9%)	4 (2%)	11	51
33	6	96/108 (89%)	92 (96%)	2 (2%)	2 (2%)	9	46
34	7	92/120 (77%)	88 (96%)	4 (4%)	0	100	100
35	8	123/131 (94%)	109 (89%)	10 (8%)	4 (3%)	5	32
36	9	101/140 (72%)	86 (85%)	12 (12%)	3 (3%)	5	35
37	a	104/150 (69%)	98 (94%)	4 (4%)	2 (2%)	10	50
38	b	91/112 (81%)	86 (94%)	3 (3%)	2 (2%)	8	45
39	c	87/92 (95%)	68 (78%)	15 (17%)	4 (5%)	3	23
40	d	68/87 (78%)	65 (96%)	3 (4%)	0	100	100
41	e	39/51 (76%)	38 (97%)	1 (3%)	0	100	100
42	f	49/128 (38%)	45 (92%)	4 (8%)	0	100	100
43	g	35/39 (90%)	31 (89%)	4 (11%)	0	100	100
44	h	83/96 (86%)	74 (89%)	8 (10%)	1 (1%)	16	60
45	i	93/104 (89%)	82 (88%)	7 (8%)	4 (4%)	3	25
All	All	6124/7124 (86%)	5538 (90%)	438 (7%)	148 (2%)	12	43

5 of 148 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	197	PRO
5	E	18	PRO

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Mol	Chain	Res	Type
6	F	102	PHE
7	G	130	HIS
7	G	143	ARG

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	
4	D	191/202 (95%)	174 (91%)	17 (9%)	12	44
5	E	335/340 (98%)	311 (93%)	24 (7%)	18	57
6	F	336/352 (96%)	306 (91%)	30 (9%)	12	44
7	G	110/155 (71%)	94 (86%)	16 (14%)	4	19
8	H	164/173 (95%)	139 (85%)	25 (15%)	3	17
9	I	189/203 (93%)	169 (89%)	20 (11%)	8	34
10	J	211/260 (81%)	189 (90%)	22 (10%)	9	35
11	K	181/182 (100%)	163 (90%)	18 (10%)	10	38
12	L	190/194 (98%)	168 (88%)	22 (12%)	7	30
13	M	106/110 (96%)	88 (83%)	18 (17%)	2	12
14	N	134/152 (88%)	112 (84%)	22 (16%)	3	13
15	O	121/122 (99%)	114 (94%)	7 (6%)	25	66
16	P	179/180 (99%)	162 (90%)	17 (10%)	11	40
17	Q	165/190 (87%)	156 (94%)	9 (6%)	27	68
18	R	214/254 (84%)	185 (86%)	29 (14%)	5	22
19	S	158/159 (99%)	141 (89%)	17 (11%)	8	33
20	T	161/163 (99%)	144 (89%)	17 (11%)	8	34
21	U	162/166 (98%)	148 (91%)	14 (9%)	13	46
22	V	140/144 (97%)	134 (96%)	6 (4%)	35	75
23	W	128/178 (72%)	113 (88%)	15 (12%)	7	30
24	X	92/131 (70%)	88 (96%)	4 (4%)	35	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	Y	90/177 (51%)	84 (93%)	6 (7%)	20	60
26	Z	111/115 (96%)	94 (85%)	17 (15%)	3	17
27	0	53/146 (36%)	47 (89%)	6 (11%)	7	31
28	1	127/132 (96%)	115 (91%)	12 (9%)	11	41
29	2	97/118 (82%)	91 (94%)	6 (6%)	23	64
30	3	110/115 (96%)	94 (86%)	16 (14%)	4	19
31	4	60/61 (98%)	54 (90%)	6 (10%)	9	37
32	5	201/231 (87%)	180 (90%)	21 (10%)	9	35
33	6	83/92 (90%)	69 (83%)	14 (17%)	2	13
34	7	90/112 (80%)	71 (79%)	19 (21%)	1	7
35	8	114/120 (95%)	97 (85%)	17 (15%)	4	17
36	9	90/127 (71%)	73 (81%)	17 (19%)	2	10
37	a	89/128 (70%)	79 (89%)	10 (11%)	7	32
38	b	82/97 (84%)	76 (93%)	6 (7%)	17	57
39	c	73/77 (95%)	65 (89%)	8 (11%)	8	33
40	d	69/83 (83%)	62 (90%)	7 (10%)	9	36
41	e	40/48 (83%)	33 (82%)	7 (18%)	2	12
42	f	45/114 (40%)	40 (89%)	5 (11%)	8	32
43	g	34/35 (97%)	32 (94%)	2 (6%)	24	65
44	h	70/80 (88%)	66 (94%)	4 (6%)	25	67
45	i	87/93 (94%)	80 (92%)	7 (8%)	15	52
All	All	5482/6311 (87%)	4900 (89%)	582 (11%)	13	34

5 of 582 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	Q	98	ARG
20	T	166	GLN
38	b	38	SER
18	R	44	TYR
18	R	274	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
18	R	197	ASN
20	T	129	ASN
39	c	51	ASN
18	R	223	ASN
19	S	23	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3163/3788 (83%)	934 (29%)	167 (5%)
2	B	117/119 (98%)	23 (19%)	1 (0%)
3	C	148/159 (93%)	43 (29%)	8 (5%)
All	All	3428/4066 (84%)	1000 (29%)	176 (5%)

5 of 1000 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	A
1	A	13	G
1	A	14	U
1	A	16	A
1	A	18	G

5 of 176 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1536	U
1	A	1990	A
1	A	3664	G
1	A	1538	U
1	A	1750	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 168 ligands modelled in this entry, 168 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.