

TABLE 1  
*E. coli* Strain K-12 Ribosomal Subunit Proteins Observed by MALDI-MS

Part A: 30S subunit						
Subunit	Sequence mass (Da)	Experimental mass (Da)	Error (Da)	Methionine lost?	Amino acid in position 2	Comment
S1	61158.3	—	n/a	n/a	T	Not observed
S2	26612.6	26610.5	-2.1	Yes	A	
S3	25852.0	25851.9	-0.1	Yes	G	
S4	23338.0	23339.5	+1.5	Yes	A	
S5	17472.3	17514.8	+42.5	Yes	A	Acetylated (A1)
S6	15187.1	15187.2	+0.1	No	R	
S7	19888.0	19888.7	+0.7	Yes	P	
S8	13995.4	13993.2	-2.2	Yes	S	
S9	14725.1	14723.3	-1.8	Yes	A	
S10	11735.6	11734.5	-1.1	No	Q	
S11	13713.8	13727.7	+13.9	Yes	A	Methylated (A1)
S12	13605.9	13651.3	+45.4	Yes	A	$\beta$ -Methylthiolated (D88)
S13	12968.3	12968.1	-0.2	Yes	A	
S14	11449.3	11449.3	0.0	Yes	A	
S15	10137.6	10137.6	0.0	Yes	S	
S16	9190.6	9190.5	-0.1	No	V	
S17	9573.3	9573.0	-0.3	Yes	T	
S18	8855.3	8897.0	+41.7	Yes	A	Acetylated (A1)
S19	10299.1	10299.6	+0.5	Yes	P	
S20	9553.2	9553.6	+0.4	Yes	A	Same as L26
S21	8368.8	8368.8	0.0	Yes	P	
S22	5095.8	5095.9	+0.1	No	K	
Part B: 50S subunit						
Subunit	Sequence mass (Da)	Experimental mass (Da)	Error (Da)	Methionine lost?	Amino acid in position 2	Comment
L1	24598.6	24598.9	+0.3	Yes	A	
L2	29729.4	29732.3	+2.9	Yes	A	Weak
L3	22243.6	22257.2	+13.6	No	I	Methylated (Q150)
L4	22086.6	22086.2	-0.4	No	E	
L5	20170.5	20169.8	-0.7	Yes	A	
L6	18772.7	18772.7	0.0	Yes	S	
L7	12164.1	12206.7	+42.6	Yes	S	Acetylated (S1)
L9	15769.1	15769.7	+0.6	No	Q	
L10	17580.5	17581.1	+0.6	Yes	A	
L11	14744.3	14870.2	+125.9	Yes	A	Methylated (9 times)
L12	12164.1	12174.4	+10.3	Yes	S	Methylated (K81)
L13	16018.6	16018.0	-0.6	No	K	
L14	13541.1	13540.2	-0.9	No	I	
L15	14980.5	14980.1	-0.4	No	R	
L16	15281.3	15326.2	+44.9	No	L	unknown mod. (R81)
L17	14364.7	14364.7	0.0	No	R	
L18	12769.7	12769.8	+0.1	No	D	
L19	13002.1	13001.7	-0.4	No	S	
L20	13365.8	13366.9	+1.2	Yes	A	Weak
L21	11564.4	11562.7	-1.7	No	Y	
L22	12226.4	12225.3	-1.1	No	E	
L23	11199.2	11198.0	-1.2	No	I	Shoulder on L24
L24	11185.1	11186.5	+1.4	Yes	A	
L25	10693.5	10693.4	-0.1	No	F	
L26	9553.2	9553.6	+0.4	Yes	A	Same as S20
L27	8993.3	8993.5	+0.2	Yes	A	
L28	8875.3	8875.0	-0.3	Yes	S	
L29	7273.5	7273.4	-0.1	No	K	
L30	6410.6	6410.3	-0.3	Yes	A	
L31	7871.1	7871.0	-0.1	No	K	
L31 frag	6971.1	6971.1	0.0	No	K	-RFNIPGSK (C-term)
L32	6315.2	6315.1	-0.1	Yes	A	
L33	6240.4	6254.1	+13.7	Yes	A	Methylated (A1)
L34	5380.4	5380.5	+0.1	No	K	
L35	7157.8	7158.0	+0.2	Yes	P	
L36	4364.4	4364.2	-0.2	No	K	

Note. L1, L3, L6, L9, L10, L17, L18, L25, L27, L29, L30, L31, L31 frag., and L33 were used as internal calibrants.

<sup>a</sup> Sequence mass is calculated by accounting for N-terminal methionine loss, but does not include any other modifications. S5, S11, S14, S15, S16, S19, S21, and S22 were used as internal calibrants.