

**Table 1**

The translational processivity and the corresponding nonsense suppression rate of codon UGA220 in wild-type and a variety of ribosome mutant strains

Ribosome character	Phenotype	+/- Sm	Processivity	Suppression rate
Wild-type	Sm <sup>S</sup>	-	0.80	74.0
Wild-type	Sm <sup>S</sup>	-	0.75 <sup>a</sup>	74.0
SmP	Sm <sup>P</sup>	-	0.34	7.8
SmP	Sm <sup>P</sup>	+	0.46	60.7
<i>rpsL221</i>	Sm <sup>R</sup>	-	0.68	59.9
<i>rpsL221</i>	Sm <sup>R</sup>	+	0.69	70.7
<i>rpsL222</i>	Sm <sup>R</sup>	-	0.45 <sup>a</sup>	11.7
<i>rpsL222</i>	Sm <sup>R</sup>	+	0.46 <sup>a</sup>	14.2
<i>rpsL224</i>	Sm <sup>R</sup>	-	0.58 <sup>a</sup>	32.2
<i>rpsL224</i>	Sm <sup>R</sup>	+	0.64 <sup>a</sup>	134.6
<i>rspL226</i>	Sm <sup>R</sup>	-	0.68 <sup>a</sup>	65.5
<i>rspL226</i>	Sm <sup>R</sup>	+	0.70 <sup>a</sup>	82.8
<i>rpsL282</i>	Sm <sup>R</sup>	-	0.53	12.2
<i>rpsL282</i>	Sm <sup>R</sup>	+	0.52	13.8
<i>rpsD12</i>	Sm <sup>S</sup>	-	0.44	386.5
<i>rpsD14</i>	Sm <sup>S</sup>	-	0.55	885.5
<i>rpsD16</i>	Sm <sup>S</sup>	-	0.41	624.8
<i>rpsE1023</i>	Sm <sup>S</sup>	-	0.74	423.5

Sm<sup>S</sup> and Sm<sup>R</sup> stand for streptomycin-sensitive and streptomycin-resistant character, respectively, and Sm<sup>P</sup> streptomycin-pseudodependent. (+/- Sm) represents assays with or without a supplement of 100 µg/ml streptomycin.

<sup>a</sup> Indicates that the processivity numbers were obtained using the assay of Jørgensen & Kurland (1990).