

# A mutation at the universally conserved position 529 in *Escherichia coli* 16S rRNA creates a functional but highly error prone ribosome

U.V. SANTER,<sup>1</sup> J. CEKLENIK,<sup>1</sup> S. KANSIL,<sup>1</sup> M. SANTER,<sup>1</sup> M. O'CONNOR,<sup>2</sup> and A.E. DAHLBERG<sup>2</sup>

<sup>1</sup> Department of Biology, Haverford College, Haverford, Pennsylvania 19041, USA

<sup>2</sup> Section of Biochemistry, Brown University, Providence, Rhode Island 02912, USA

## ABSTRACT

A base substitution of G to U was constructed at position 529 in *Escherichia coli* 16S rRNA. The U529 mutant ribosomes were functional and present on polysomes but were highly error prone and caused a progressive loss of cell viability. They displayed elevated levels of readthrough of stop codons and frameshifting, and an increase in thermal sensitivity of  $\beta$ -galactosidase, suggestive of missense errors. These results demonstrate that the universally conserved G529 is involved in tRNA selection at the A site during protein synthesis.

**Keywords:** A site; rRNA mutant; 30S subunit; translational fidelity

## INTRODUCTION

Many of the nucleotides in the 530 loop region of *Escherichia coli* 16S rRNA are universally conserved (Gutell et al., 1985; Noller, 1993). There is considerable evidence that this region is involved in functional interactions with elongation factor EF-Tu-tRNA and with mRNA (Moazed & Noller, 1990; Dontsova et al., 1992) and that it ensures the accuracy of translation (O'Connor et al., 1992). Positions 529, 530, and 531 are protected from chemical modification by tRNA placed in the A site on 30S ribosomes, whereas base 532 is protected by P site bound tRNA (Moazed & Noller, 1990; Noller, 1993) and has been crosslinked to mRNA (Dontsova et al., 1992) (see Fig. 1). Base changes at position 530 are lethal (Powers & Noller, 1990), and only low levels of the mutant ribosomes are found in the polysome fraction in vivo. In vitro studies showed an impaired interaction between mutant ribosomes and the EF-Tu-tRNA-GTP ternary complexes (Powers & Noller, 1993). Parallel studies with in vitro reconstituted U530 ribosomes demonstrated that although the mutant ribosomes were competent in polyphenylalanine synthesis in a polyU-directed translation system, they were unable to elongate on a natural mRNA (M. Santer et al., 1993). Mutations elsewhere on the 530 loop region caused less severe effects. These included

base changes at position 517, which increased readthrough of nonsense codons and frameshifting (O'Connor et al., 1992); mutations at 523 (Gauthier et al., 1988) and 525 (Melancon et al., 1988), which conferred streptomycin resistance; and mutations at 527 and 528, which affected growth only when mutant rRNA was expressed at high levels (U.V. Santer et al., 1993).

The profound negative effect of mutations at position 530 on ribosome function and cell growth led us to investigate mutations at the adjacent base G529. In this paper we demonstrate that the G to U transversion at position 529 is a lethal mutation. The mutant ribosomes are functional in vivo and are found in polysomes and in 70S and 30S ribosomes at levels comparable to wild-type ribosomes. However, the mutant ribosomes are very error prone and display high levels of misreading. In addition, the mutant ribosomes have a reduced capacity to translate low abundance mRNAs. These results underline the importance of this region of 16S rRNA in the selection and binding of tRNA to the ribosome and in ensuring the accuracy of protein synthesis.

## RESULTS

### Construction and characterization of the lethal mutant U529

A G to U mutation at position 529 in 16S rRNA was introduced into plasmid pNO2680 $\Delta$ H, which had the *rrnB* operon under control of the PL promoter. Expression

Reprint requests to: Albert E. Dahlberg, Section of Biochemistry, Box G-J4, Brown University, Providence, Rhode Island 02912, USA; e-mail: me599010@brownvm.brown.edu.



**TABLE 1.** Cell counts after expression of wild-type and mutant 16S rRNA.<sup>a</sup>

Plasmid	Growth conditions	$A_{600\text{nm}}$ at plating	Viable cells per mL	Viable cells per $A_{600\text{nm}}$ plated
pNO2680 $\Delta$ H (WT)	30 °C	0.1	$6 \times 10^7$	$6 \times 10^8$
pNO2680 $\Delta$ H (WT)	42 °C, 320 min	1.2	$5 \times 10^8$	$4.2 \times 10^8$
pNOU529	30 °C	0.1	$6 \times 10^7$	$6 \times 10^8$
pNOU529	42 °C, 320 min	0.64	$3 \times 10^5$	$4.7 \times 10^5$

<sup>a</sup> DH1 with pc1857, carrying mutant or wild-type plasmid, was grown at 30 °C to an O.D. of 0.1 on LB broth supplemented with ampicillin (200  $\mu\text{g}/\text{mL}$ ) and neomycin (50  $\mu\text{g}/\text{mL}$ ). An aliquot was removed for a viable cell count at 0 min and the culture shifted to 42 °C. After 320 min, a second aliquot was removed and viable cells (colony forming units) were determined by serial dilution, plating on unsupplemented LB agar and growing at 30 °C for 48 h.

The levels of  $\beta$ -galactosidase synthesized from the wild-type lac plasmid (pSG25) were identical in cells with wild-type and mutant U529 ribosomes (Table 2). However, upon heating at 56 °C for 20 min, the  $\beta$ -galactosidase synthesized in cells containing mutant ribosomes was only 82% as active as the wild type (Table 3). Susceptibility of the enzyme to thermal denaturation suggested the possibility that the U529 ribosomes misread sense codons, inserting incorrect amino acids throughout the  $\beta$ -galactosidase chain, as well as causing frameshifting and readthrough events. Mutants of EF-Tu that cause increased misreading have analogous and quantitatively similar effects on the thermal lability of proteins (Hughes, 1991).

**TABLE 2.** Effects of the U529 mutation on stop codon readthrough and frameshifting.<sup>a</sup>

lacZ mutant	$\beta$ -Galactosidase activity <sup>b</sup>		Ratio of mutant/WT
	In pNO2680 $\Delta$ H (WT)	In pNOU529	
<b>Nonsense mutants</b>			
pSG3/4 UGA	121.6 $\pm$ 8.4	417.1 $\pm$ 20.5	3.4
pSG34-11 UGA	39.0 $\pm$ 1.9	127.1 $\pm$ 10.0	3.3
pSG12-6 UAG	18.4 $\pm$ 0.8	44.9 $\pm$ 2.6	2.4
pSG163 UAG	36.0 $\pm$ 1.4	98.8 $\pm$ 2.9	2.7
pSG627 UAA	4.9 $\pm$ 0.3	16.2 $\pm$ 1.2	3.3
pSG853 UAA	12.0 $\pm$ 0.1	54.8 $\pm$ 4.0	4.6
<b>Frameshift mutants</b>			
pSGlac7 (+1)	45.8 $\pm$ 3.8	277.8 $\pm$ 16.1	6.1
pSG12DP (-1)	110.7 $\pm$ 3.5	376.2 $\pm$ 16.8	3.4
pSG375 (+1)	1.6 $\pm$ 0.2	9.2 $\pm$ 0.9	4.8
pSGCCCU (+1)	19.0 $\pm$ 1.4	59.5 $\pm$ 3.9	3.1
<b>Wild-type lacZ</b>			
pSG25 ( $P_{\text{tac}}$ )	6,487.5 $\pm$ 645	7,593.0 $\pm$ 742.3	1.17
p90.91 ( $P_{\text{lac}}$ WT)	750.9 $\pm$ 28.4	441.5 $\pm$ 32.9	0.59
F'128	1,655.9 $\pm$ 54.9	910.2 $\pm$ 59.5	0.55

<sup>a</sup> Each culture was grown at 42 °C for 150 min (to induce transcription of mutant rRNA) before being assayed. The strains used are described in the Materials and methods section.

<sup>b</sup> Miller (1972) units. Each number is the mean activity of three to six independent cultures  $\pm$  one standard error.

### Differences in the level of synthesis of $\beta$ -galactosidase by mutant and wild-type ribosomes: A reflection of the abundance of mRNA

In *E. coli* MC140, the constitutive level of wild-type  $\beta$ -galactosidase was unaffected by the U529 mutation when the lacZ mRNA was abundant (i.e., transcribed from the strong promoter in pSG 25; see Table 2). However, a decrease in  $\beta$ -galactosidase was observed when the lacZ gene was present on a single copy episome (F'128) or transcribed from a weaker promoter (p90.91). When the mRNA was transcribed from the chromosomal wild-type lacZ gene in *E. coli* DH1 (Table 4), a pronounced reduction in the level of  $\beta$ -galactosidase was correlated with induction of mutant ribosome synthesis. When the chromosomal lacZ gene in *E. coli* DH1/pc1857 was induced with IPTG immediately upon transfer to 42 °C and assayed for enzyme 15 min later, cells containing the U529 plasmid had essentially the same level of enzyme as cells containing the wild-type plasmid. Cells assayed for enzyme 60 min later expressed one-half the activity of cells assayed at 15 min. If induction of enzyme with IPTG was delayed to 30 min after growth at 42 °C, the level of  $\beta$ -galactosidase activity fell by 100-fold. Thus, the level of  $\beta$ -galactosidase expressed from the chromosomal lacZ gene declined dramatically as mutant ribosomes accumulated.

**TABLE 3.** Heat lability of  $\beta$ -galactosidase: a measure of missense errors by the U529 mutant ribosomes.<sup>a</sup>

Plasmid	% of initial activity	Ratio of activity relative to WT
pNO2680 $\Delta$ H (WT)	80.8 $\pm$ 5.0	1.00
pNOU529	66.5 $\pm$ 1.9	0.82

<sup>a</sup> Measurements of percentage of initial activity were made after 20 min at 56 °C. All values are the mean of three independent measurements  $\pm$  one standard error. Cell extracts were prepared as described in the Materials and methods section.

**TABLE 4.**  $\beta$ -Galactosidase activity in DH1 cells with U529 plasmid.<sup>a</sup>

Experiment	Length of induction of rRNA synthesis (at 42 °C) prior to adding IPTG (min)	Time of $\beta$ -gal assay after IPTG addition (min)	$\beta$ -Galactosidase activity <sup>b</sup>		
			pNOU529	pNO2680 $\Delta$ H (WT)	Ratio of mutant/WT
I	0	15	100	90	1.1
		60	1,160	2,400	0.5
II	30	15	80	500	0.16
		70	60	1,100	0.05
		100	80	7,600	0.01

<sup>a</sup> DH1 pc 1857 cells with a chromosomal *lacZ* gene, containing WT or U529 pNO2680 $\Delta$ H plasmid, were shifted from 30 °C to 42 °C at time 0 at an O.D. of 0.2 (Exp. I) or 0.05 (Exp. II). IPTG was added simultaneously (Exp. I) or after 30 min (Exp. II).  $\beta$ -Galactosidase was assayed at various times after IPTG addition, as indicated.

<sup>b</sup> Miller (1972) units.

## DISCUSSION

We have produced a mutation in a functional region of 16S rRNA that is essential for maintaining translational fidelity (Moazed & Noller, 1990; Powers & Noller, 1990, 1993; Dontsova et al., 1992; O'Connor et al., 1992). The mutation, U529, has a drastic effect on cell growth, causing a greater than sixfold increase in doubling time within 90 min and ultimately leading to cell death. It is interesting that the 30S subunits containing mutant rRNA were found in polysomes in approximate proportion to their percentage in the total cellular pool. This is in contrast to a mutation at the adjacent position, 530, which is excluded from polysomes (Powers & Noller, 1990). Since the mutant U529 30S ribosomes are found in the polysomes, one can examine the effects of this mutation in vivo by regulating expression from a plasmid under the control of a repressible promoter. As the 529 mutant ribosomes accumulate in the cell, the growth rate decreases and the number of polysomes in the cell decreases, even in the presence of wild-type 30S subunits. This may reflect a progressive, generalized accumulation of inaccurately translated proteins. In fact, the demonstration of thermally sensitive  $\beta$ -galactosidase (from a high copy mRNA) suggests the presence of missense errors in all nascent cellular proteins. The synthesis of defective proteins, such as seen previously with mutants C to G at 726 (Prescott & Dahlberg, 1990) and G to C at 517 (O'Connor et al., 1992) in 16S rRNA or induced by low levels of streptomycin (Rosenberger, 1982), can have a profound effect on cell viability and could account for the observed lethality of the U529 mutation.

The U529 mutant ribosomes affected the level of translation of wild-type  $\beta$ -galactosidase. A 2–100-fold reduction in the steady state level of  $\beta$ -galactosidase was found when *lacZ* mRNA was present in amounts consistent with a single copy gene (Table 4). A similar reduction was also noted with weak promoters (p90.9/ $P_{lac}$  WT) or with the single copy gene F'128  $P_{lac}$  WT (Table 2). Under ordinary conditions, transcription and

translation are tightly coupled in *E. coli*, and ribosomal protein mutants have been found to influence premature termination of transcription (Jørgensen & Kurland, 1990). Consequently, the defects in the U529 mutant ribosomes may not be limited to translational events but might also affect transcriptional processes. This could account for the fact that the units of  $\beta$ -galactosidase did not increase with time when *lacZ* mRNA synthesis was induced in cells with U529 ribosomes (Experiment II, Table 4). When the *lacZ* mRNA was abundant (pSG25,  $P_{tac}$ ), however, both mutant and wild-type strains produced equivalent amounts of  $\beta$ -galactosidase. If we generalize the differential effect of the mutant ribosomes on the translation of low abundance mRNA to the many mRNA species present at low levels in the cell, then clearly the mutant rRNA is expected to have disastrous consequences on cell physiology.

The severity of the effect of the 529 mutation on translational accuracy is clearly demonstrated by its effect on readthrough and frameshifting (Table 2). The lethal effect of the 530 mutation may be due to an inability to carry out proper elongation. A mutation at 531 (U to G) has no demonstrable effect on growth or protein synthesis (U.V. Santer et al., 1993). All three bases—529, 530, and 531—are part of the A site as judged by footprinting experiments (Moazed & Noller, 1990), but mutations at these three positions affect A site function in quantitatively different ways. The differential effects might reflect perturbations of different parts of the complex pathway leading to the proper placement of the aminoacyl-tRNA in the A site (Thompson, 1988; Ehrenberg et al., 1990; Weijland & Parmeggiani, 1994).

## MATERIALS AND METHODS

The following strains of *E. coli* were used in these studies: *E. coli* DH1, HB101, and MC140 (O'Connor et al., 1992; M. Santer et al., 1993). Strains were transformed with plasmid pc1857, which encodes the temperature-sensitive  $\lambda$  repressor and the neomycin resistance marker. A derivative of plasmid

pNO2680 (Tapprich et al., 1990) lacking one *Hind* III restriction site in the pBR322-derived portion of the plasmid was prepared and is referred to as pNO2680 $\Delta$ H. This plasmid contains the *rrnB* operon under control of the  $\lambda$  P<sub>L</sub> promoter (O'Connor et al., 1992).

The lac mutants used in this study to monitor readthrough and frameshifting carried the *lacZ* gene, transcribed from the tac promoter in the absence of any lac repressor, on a tetracycline-resistant plasmid derived from pACYC184 (O'Connor & Dahlberg, 1993). Strain MC140 (F<sup>-</sup>*thi*<sup>-</sup> $\Delta$ (lac-pro) recA<sup>-</sup>), carrying the lambda temperature-sensitive repressor on a neomycin-resistant plasmid (pLG857) (O'Connor et al., 1992), was used as the host for all the *lacZ* mutants and plasmids carrying the *rrnB* operon under the control of the lambda P<sub>L</sub> promoter (Gourse et al., 1985).

### Site-specific mutagenesis

A 568-bp *Hind* III fragment from positions 80 to 648 of 16S rRNA was inserted into M13 mp19. Oligonucleotide-directed, site-specific mutagenesis at base 529 was carried out using standard procedures (Kunkel et al., 1987). Screening for mutants was facilitated by the fact that a base change at position 529 abolished a *Sac* II site. The *Hind* III fragment containing a G to U base change at position 529 was isolated from the RF of M13mp19 and cloned into plasmid pNO2680 $\Delta$ H to give pNOU529. All base changes were verified by restriction enzyme analysis and DNA sequencing (Sanger et al., 1977) of the M13 insert and the reconstructed plasmid.

### Growth experiments

Growth experiments were carried out with *E. coli* DH1 containing pNO2680 $\Delta$ H or pNOU529, and plasmid pCL857. Cells were grown on LB agar with the appropriate antibiotic at 30 °C, suspended in broth, and grown at 30 °C in LB medium containing ampicillin and neomycin (200 mg/L and 50 mg/L) or only ampicillin. Unless otherwise indicated, the flasks were transferred to 42 °C when the cells reached A<sub>600nm</sub> of 0.1. To establish whether cells were viable after growth at 42 °C, they were initially grown to an optical density of about 0.1 at 30 °C, transferred to 42 °C, and after 320 min, aliquots of each culture were serially diluted, plated on unsupplemented LB agar, and grown at 30 °C for 48 h.

### Measurement of $\beta$ -galactosidase and analysis of proteins

Cells were grown at 30 °C until A<sub>600nm</sub> reached 0.15–0.2. An aliquot of cells was diluted fourfold into the appropriate medium prewarmed to 42 °C. *E. coli* DH1 cells were induced with IPTG (final concentration, 1 mM) immediately or 30 min later after transfer to 42 °C. At various times after addition of IPTG,  $\beta$ -galactosidase was assayed (Miller, 1972). To determine the degree of readthrough of nonsense codons and frameshifting,  $\beta$ -galactosidase assays were carried out on *E. coli* MC140 cultures grown overnight at 30 °C in LB medium supplemented with appropriate antibiotics (neomycin [50 mg/L], tetracycline [25 mg/L], and ampicillin [200 mg/L]). The cultures were diluted 1/50 and incubated with vigorous shaking at 42 °C for 2.5 h and then assayed as described (O'Connor et al., 1992).

### Heat lability of $\beta$ -galactosidase

Plasmid-encoded rRNA synthesis in MC140, pLG857, and pSG25 containing either pNO2680 $\Delta$ H (wt) or pNOU529 was induced by growth at 42 °C for 3 h. Cell extracts were prepared by passage through a French press as described by Hughes (1991). Gel electrophoresis of  $\beta$ -galactosidase, purified by affinity immunochromatography (ProtoSorb, Promega, Madison, Wisconsin, USA), showed a single band of the enzyme and no evidence of enhanced proteolytic degradation in the mutant cells.

### Isolation of rRNA from ribosome fractions and determination of levels of plasmid-encoded rRNA

*E. coli* cells containing mutant and wild-type plasmids were harvested at various times after being shifted to 42 °C. Total ribosomal RNA and ribosomal fractions were prepared. Polyosomes and 70S and 30S ribosome fractions were separated by sucrose density gradient fractionation, and rRNA was isolated. The relative amounts of wild-type and mutant (plasmid-encoded) rRNA were determined by the primer extension method of Sigmund et al. (1988) using an oligonucleotide complementary to bases 547–532.

### ACKNOWLEDGMENTS

We thank James Dahlberg for critical reading of the manuscript, Joanna Frank for technical assistance with the manuscript, and George Q. Pennable for numerous discussions. This research was supported in part by grant DMB9104717 from the U.S. National Science Foundation to U.V.S. and M.S., and grant GM19756 from the U.S. National Institutes of Health to A.E.D.

Received December 5, 1994; returned for revision January 10, 1995; revised manuscript received February 2, 1995

### REFERENCES

- Dontsova O, Kopylov A, Brimacombe R. 1992. Location of mRNA in the ribosomal 30S initiation complex; site-directed cross-linking of mRNA analogues carrying several photo-reactive labels simultaneously on either side of the AUG start codon. *EMBO J* 10: 2613–2620.
- Ehrenberg M, Rogas AM, Weiser S, Kurland CG. 1990. How many EF-Tu molecules participate in aminoacyl-tRNA binding and peptide bond formation in *Escherichia coli* translation? *J Mol Biol* 211:739–749.
- Gauthier P, Turmel M, Lemieux C. 1988. Mapping of chloroplast mutations conferring resistance to antibiotics in *Chlamydomonas*: Evidence for a novel site of streptomycin resistance in the small subunit rRNA. *Mol Gen Genet* 214:192–197.
- Gourse R, Takebe Y, Sharrock RA, Nomura M. 1985. Feedback regulation of rRNA and tRNA synthesis and accumulation of free ribosomes after conditional expression of rRNA genes. *Proc Natl Acad Sci USA* 82:1069–1073.
- Gutell R, Larsen N, Woese CR. 1994. Lessons from an evolving rRNA: 16S and 23S rRNA structures from a comparative perspective. *Microbiol Rev* 58:10–26.
- Gutell RR, Weiser B, Woese CR, Noller HF. 1985. Comparative anatomy of 16-S-like ribosomal RNA. *Progr Nucleic Acids Res Mol Biol* 32:155–216.
- Hughes D. 1991. Error-prone EF-Tu reduces in vivo enzyme activity and cellular growth rate. *Mol Microbiol* 5:623–630.
- Jemiolo DK, Taurence JS, Giese S. 1991. Mutations in 16S rRNA in

- Escherichia coli* at methyl-modified sites: G966, C967, G1207. *Nucleic Acids Res* 19:4259-4265.
- Jørgensen F, Kurland CG. 1990. Processivity errors of gene expression in *Escherichia coli*. *J Mol Biol* 215:511-521.
- Kunkel TA, Roberts JD, Zakoar RA. 1987. Rapid and efficient site-specific mutagenesis without phenotypic selection. *Methods Enzymol* 154:367-382.
- Melancon P, Lemieux C, Brakier-Gingras L. 1988. A mutation in the 530 loop of *Escherichia coli* 16S ribosomal RNA causes resistance to streptomycin. *Nucleic Acids Res* 16:9631-9639.
- Miller JH. 1972. Assay of  $\beta$ -galactosidase. In: *Experiments in molecular genetics*. Plainview, New York: Cold Spring Harbor Laboratory Press. pp 352-355.
- Moazed D, Noller HF. 1990. Binding of tRNA to the ribosomal A and P sites protects two distinct sets of nucleotides in 16S rRNA. *J Mol Biol* 211:135-145.
- Noller HF. 1993. On the origin of the ribosome: Coevolution of subdomains of tRNA and rRNA. In: Gesteland R, Atkins JF, eds. *The RNA world*. Plainview, New York: Cold Spring Harbor Laboratory Press. pp 137-156.
- O'Connor M, Dahlberg AE. 1993. Mutations at U2555, a tRNA-protected base in 23S rRNA, affect translational fidelity. *Proc Natl Acad Sci USA* 90:9214-9218.
- O'Connor M, Göringer HU, Dahlberg AE. 1992. A ribosomal ambiguity mutation in the 530 loop of *E. coli* 16S rRNA. *Nucleic Acids Res* 20:4221-4227.
- Powers T, Noller HF. 1990. Dominant lethal mutations in a conserved loop in 16S rRNA. *Proc Natl Acad Sci USA* 87:1042-1046.
- Powers T, Noller HF. 1993. Evidence for functional interaction between elongation factor Tu and 16S ribosomal RNA. *Proc Natl Acad Sci USA* 90:1364-1368.
- Prescott C, Dahlberg AE. 1990. A single base change at 726 in 16S rRNA radically alters the pattern of protein synthesized in vivo. *EMBO J* 9:289-294.
- Rosenberger RF. 1982. Streptomycin-induced protein error propagation appears to lead to cell death in *Escherichia coli*. *IRCS Med Sci* 10:874-875.
- Sanger F, Nicklen S, Coulson AR. 1977. DNA sequencing with chain-terminating inhibitors. *Proc Natl Acad Sci USA* 74:5463-5467.
- Santer M, Santer U, Nürse K, Bakin A, Cunningham P, Zain M, O'Connell D, Ofengand J. 1993. Functional effects of a G to U base change at position 530 in a highly conserved loop of *Escherichia coli* 16S RNA. *Biochemistry* 32:5539-5547.
- Santer UV, Cekleniak JA, Santer M. 1993. The 530 loop of 16S ribosomal RNA: Each base change confers its own phenotype. *Mol Biol Cell* 4:420a.
- Sigmund CD, Ettayebi M, Borden A, Morgan EA. 1988. Antibiotic resistance mutations in ribosomal RNA genes of *Escherichia coli*. In: Noller HF, Moldave K, eds. *Methods Enzymol* 164:673-690.
- Tappich WE, Göringer HU, De Stasio E, Dahlberg AE. 1990. Site-directed mutagenesis of *E. coli* rRNA. In: Spedding G, ed. *Ribosomes and protein synthesis: A practical approach*. London: IRL Press. pp 253-271.
- Thompson RC. 1988. EF-Tu provides an internal kinetic standard for translational accuracy. *Trends Biochem Sci* 13:91-93.
- Weijland A, Parmeggiani A. 1994. Why do two EF-Tu molecules act in the elongation cycle of protein biosynthesis? *Trends Biochem Sci* 19:188-193.