Table 1
Quantitative data for *Escherichia coli* protein synthesis

Cell growth rate[a] (dbl/h)	1	1.5	2	2.4	2.9	[Ref.]
Cell volume[b] (10^9 nm^3)	1.1	1.4	1.7	2.1	2.5	[25,26]
Genomes/cell	1.6	2.2	2.8	3.4	4.8	[11]
70 S/genome[c]	4500	7100	9400	11 200	13 700	[11–13]
tRNA/genome[d]	63 000	84 000	106 000	120 000	135 000	[11,12]
Synthetases/genome[e]	9400	12 000	13 700	15 100	16 000	[27]
aa Residues/genome (10^8)	3.4	4.0	4.0	4.0	4.0	[11]
tRNA/70 S	13.8	11.9	11.3	10.7	9.9	
Synthetases/70 S	2.1	1.7	1.5	1.3	1.2	
EFTu/70 S[f]	15.8	12.6	10.4	?	?	[28]
70 S-to-70 S distance[g] (nm)	54	45	40	38	34	
Elongation rate[h] (aa × 70 S^{-1} × s^{-1})	14.5	16.3	16.4	16.5	16.3	[11]
tRNA cycle[i] (s)	0.96	0.73	0.69	0.65	0.60	

Calculated quantities are: [a]growth rate at 37°C; [b]from cell diameter [25] and length [26]; [c] from the total quantity of RNA [11] and the ratio rRNA/RNA [12] assuming 77% of total rRNA exists in active (polypeptide elongating) ribosomes [13] and 1.8 × 10^6 as mol. wt of 79 S rRNA; [d]since only 2–4% of RNA is mRNA [11] and tRNA mol. wt is 25 000 we assume tRNA/RNA = 1 – rRNA/RNA; [e]we double the quantity obtained for 10 of these enzymes as recommended in [27]; [f]we adjust published values [28] since only 77% of rRNA is in active ribosomes; EFG, EFTs and 70 S are in equimolar quantities at all growth rates [29]; [g]the side of a cube containing one ribosome assuming uniform distribution in the cell of all ribosomes; [h]the average number of residues incorporated into polypeptides × s^{-1} × ribosome^{-1}: (cell growth rate) × log 2 × (residues/genome) × (70 S/genome)$^{-1}$ × (3600 s/h)$^{-1}$ as in [11]; [i]the mean time for a tRNA to complete a cycle: (tRNA/70 S) × (elongation rate)$^{-1}$