Table 1
Parameters pertaining to the synthesis rates of ribosomes and RNA polymerase in exponentially growing *E. coli* B/r as a function of growth rate at 37 °C.

At τ (min) and μ (doublings/h):										
Parameter	Symbol	Units	$\tau \rightarrow 100$	60	40	30	24	20	Observed parameter(s)	Footnote
			$\mu \rightarrow 0.6$	1.0	1.5	2.0	2.5	3.0		
RNAP synthesizing stable RNA	Ψ_s	%	24	36	56	69	79	86	r_s/r_t, c_s, c_m	[a]
RNAP synthesizing rRNA	Ψ_r	%	21	31	48	59	68	74	Ψ_s, f_t	[b]
rRNA chain elong.	c_r	Nucl./s	85	85	85	85	85	85	Indirect	[c]
RNAP activity	β_p	%	15.5	16.8	17.6	21.9	28.2	36.2	r_s, r_m, c_s, c_m, N_p	[d]
RNAP/total protein	α_p	%	0.90	1.10	1.30	1.45	1.55	1.60	α_p	[e]
Peptide chain elong.	c_p	aa resid./s	13	18	21	22	22	22	Indirect	[f]
Ribosome activity	β_r	%	85	85	85	85	85	85	Indirect	[g]
Ribos. prot/tot. prot.	α_r	%	7.7	9.2	11.6	15.0	18.8	22.7	α_r	[h]
Ribosomes/cell	N_r	10^3 Ribos./cell	8.0	14.9	25.9	43.9	61.4	72.9	R_C, f_s, f_t	[i]
RNAP molec./cell	N_p	10^3 RNAP/cell	1.8	3.5	5.7	8.4	10.0	10.2	α_p, P_C	[j]
RNAP/ribosome	N_p/N_r	Factor	0.23	0.24	0.22	0.19	0.16	0.14	N_p, N_r	[k]
RNAP prot/rib.prot.	α_p/α_r	Factor	0.12	0.12	0.11	0.10	0.08	0.07	α_p, α_r	[l]
Factor (Equation (1a))	a	See text	0.030	0.049	0.078	0.121	0.177	0.248	Ψ_r, c_r, β_p	[m]
Factor (Equation (2a))	b	See text	0.0016	0.0027	0.0038	0.0044	0.0047	0.0048	α_p, c_p, β_r	[n]
Calc. growth rate	μ	Doublings/h	0.6	1.0	1.5	2.0	2.5	3.0	a, b	[o]
Change in a	f_a	Factor	1.0	1.6	2.6	4.0	5.9	8.3	a, a_1	[p]
Change in b	f_b	Factor	1.0	1.7	2.4	2.8	2.9	3.0	b, b_1	[q]
Change in μ	f_μ	Factor	1.0	1.7	2.5	3.3	4.2	5.0	μ, μ_1	[r]

[a] Fraction of active RNA polymerase synthesizing stable RNA (from Table 3 in [3], originally calculated: $\Psi_s = 1/[1 + [1/(r_s/r_t) - 1]\ (c_s/c_m)]$, using values for r_s/r_t, c_s and c_m shown in the same Table).

[b] Fraction of active RNA polymerase synthesizing rRNA, $\Psi_r = (1 - f_t)\,\Psi_s$, where f_t is the fraction of stable RNA that is tRNA = 0.14 (Table 1 in [3]).

[c] Stable RNA (or rRNA) chain elongation rate (from Table 3 in [3]; originally determined from the accumulation *rm*-terminal 5S-rRNA or tRNA after stopping transcription initiation with rifampicin).

[d] Fraction of total RNA polymerase that is actively transcribing (from Table 3 in [3]; originally calculated using the relationship: $\beta_p = (r_s/c_s + r_m/c_m)/N_p$, using values for r_s, r_m, c_s, c_m, and N_p in the same Table).

[e] Fraction of total protein that is core RNA polymerase (from Table 3 in [3]; determined from the β and β′ subunit content measured after sodium dodecyl sulfate-gel electrophoresis).

[f] Peptide chain elongation rate (from Table 3 in [3]; calculated from the amount of protein per cell, P_C, and the number of active ribosomes per cell, $\beta_r\ N_r$, using the relationship $c_p = (\ln 2/\tau)\text{-}P_C/(\beta_r\text{-}N_r)$, as explained in the same table).

[g] Fraction of total ribosomes active in polypeptide synthesis (from Table 3 in [3], originally measured as fraction of ribosomes in polysomes, with a correction for active 70S ribosomes, as explained in the same table).

[h] Fraction of total protein that is ribosomal protein (from Table 3 in [3], originally determined as the fraction of labeled protein in 30S and 50S ribosomal particles).

[i] Number of ribosomes per cell (from Table 3 in [3], determined from the amount of total RNA per cell, R_C, the fraction of total RNA that is stable RNA, $f_s = 0.98$, the fraction of stable RNA that is tRNA, $f_t = 0.14$ and the number of RNA nucleotides per 70S ribosome, nucl./rib = 4566: $N_r = R_C\ f_s\ (1 - f_t)/$(nucl./rib).

[j] Number of core RNA polymerase per cell [from Table 3 in [3], calculated from the amount of protein per cell, P_C, the fraction of total protein that is RNA polymerase, α_p (this table, footnote [e]), and the number of amino acid residues per core RNA polymerase, aa/pol = 3707: $N_p = P_C\ \alpha_p/$(aa/pol)].

[k] Number of RNA polymerase molecules per ribosome, N_p/N_r, using the values for N_p and N_r in this table (footnotes [i] and [j]).

[l] RNA polymerase protein per ribosomal protein, α_p/α_r, using the values for α_p and α_r in this table (footnotes [e] and [h]).

[m] Factor a in Equation (1a): $a = (\Psi_r\ c_r\ \beta_p)/$(nuc/rib), using the values for Ψ_r, c_r and β_p in this table (footnotes [b], [c], and [d]) and the number of nucleotides per 70 ribosome, (nuc/rib) = 4566.

[n] Factor b in Equation (2a): $b = (\alpha_p\ c_p\ \beta_r)/$(aa/pol), using the values for α_p, c_p and β_r in this table (footnotes [e], [f], and [g]) and the number of amino acid residues per core RNA polymerase, (aa/pol) = 3707.

[o] Calculated growth rate (doublings/h), using Equation (7): $\mu = (60/\ln 2)\sqrt{ab}$ with the values for a and b in this table (footnotes [m and n]).

[p] Change in a, $f_a = a(\mu > 0.6)/a\ (\mu = 0.6)$.

[q] Change in b, $f_b = b(\mu > 0.6)/b\ (\mu = 0.6)$.

[r] Change in μ, f_μ=$(\mu > 0.6)/0.6$.