

TABLE 7. Temperature dependence of parameters related to RNA synthesis

Temp (°C)	Bacterial growth rate* ^a (μ) (doublings/h)	Stable RNA* (R_s) (10^{16} nucl./OD ₄₆₀)	Protein* (P) (10^{17} amino acids/OD ₄₆₀)	RNA polymerase synthesis* (α_p) (%)	Synthesis of stable RNA* (r_s/r_t) (%)	Stable RNA chain growth rate* (c_s) (nucleotide residues/s)	Ribosomal protein synthesis (α_r) (%)	Protein synthesis per ribosome (e_r) (amino acid residuals/s)
20	0.41 (0.43)	5.90	5.60	1.06	56	30	13	3.82
25	0.65 (0.66)	5.90	5.60	1.06	56	45	13	6.07
30	0.91 (0.90)	5.90	5.60	1.06	56	59	13	8.49
35	1.18 (1.16)	5.90	5.60	1.06	56	76	13	11.01
40	1.35 (1.44) ^b	5.90	5.60	1.06	56	103	13	12.60
Equation or reference	Fig. 3d	Fig. 3a	Fig. 3b	Fig. 3f	Fig. 3c	Fig. 3e	$\alpha_r = 1.19(R_s/P) \times 100\%$	$e_r = \frac{(aa/rib) (\ln 2/\tau)}{\alpha_r \cdot 60(\text{s/min})}$; reference 10

TABLE 7—Continued

RNA polymerase synthesizing stable RNA (ψ_s) (%)	Stable RNA synthesis rate (r_s) (10^{13} nucleotides per s per OD ₄₆₀)	mRNA synthesis rate (r_m) (10^{13} nucleotides per s per OD ₄₆₀)	Total RNA synthesis rate (r_t) (10^{13} nucleotides per s per OD ₄₆₀)	Active RNA polymerase (N_p^*) (10^{11} polymerase molecules/OD ₄₆₀)	Total RNA polymerase (N_p) (10^{11} RNA polymerase molecules/OD ₄₆₀)	RNA polymerase activity (β_p) (%)	Guanosine tetraphosphate (ppGpp) (pmol/OD ₄₆₀)
43	0.56	0.44	1.00	4.47	16.20	28	13
43	0.93	0.67	1.56	5.09	16.20	31	18
43	1.25	0.98	2.22	4.98	16.20	31	19
43	1.61	1.27	2.88	5.01	16.20	31	26
43	1.85	1.45	3.29	4.21	16.20	26	48
$\psi_s = \frac{100\%{}^c}{1 + [(r_s/r_t)^{-1} - 1][c_s/c_m]}$	$r_s = [1.2 R_s (\ln 2/\tau)]^d$	$r_m = r_s [(r_s/r_t)^{-1} - 1]$	$r_t = r_s + r_m$	$N_p^* = (r_s/c_s) + (r_m/c_m)$	$N_p = (\alpha_p \times P) / 3,660^e$	$\beta_p = (N_p^*/N_p) \times 100\%$	Fig. 3g

^a Parameters with an asterisk (*) were observed (Fig. 3a through g; using the smoothed curves shown rather than actually observed values); all others (without asterisk) were calculated.

^b Values in parentheses were calculated from c_s and e_r , using the formula $\mu = 0.40 \sqrt{c_s e_r}$ (see the text).

^c c_m = mRNA chain elongation rate, assumed to be 0.6 of stable RNA chain elongation rate; for equation see reference 4.

^d The factor 1.2 corrects for unstable spacers in the stable RNA precursors, i.e., r_s includes synthesis of the spacers.

^e The number 3,660 = amino acid residues per core RNA polymerase molecule.