Table 2 GTP hydrolysis, dipeptide formation and translocation times for wild-type, SmP and SmD ribosomes

Ribosome		τ _{GTP} (ms)	τ _{dip} † (ms)	τ _{trans} ‡ (ms)	$ au_{ m dip} + au_{ m trans} \ (ms)$	Calculated k_{cat} (s ⁻¹)
Wild-type	-Sm	10	30	22	52	19.2
	+Sm	9.1	58	109	167	6.0
SmP	-Sm	24	56	27.5	83.5	12.0
	+Sm	7·1	64	35.5	99.5	10.0
SmD	-Sm	158	190	19	209	4.8
	+Sm	50	83	24	107	9.3

[†] See Figure 1, legend. ‡ From Bilgin et al. (1988) (-Sm); from N. Bilgin (unpublished) (+Sm). § $k_{\rm cat}$ is calculated as: $k_{\rm cat} = 1/(\tau_{\rm dip} + \tau_{\rm trans})$. Compare with measured $k_{\rm cat}$ values in Table 3.