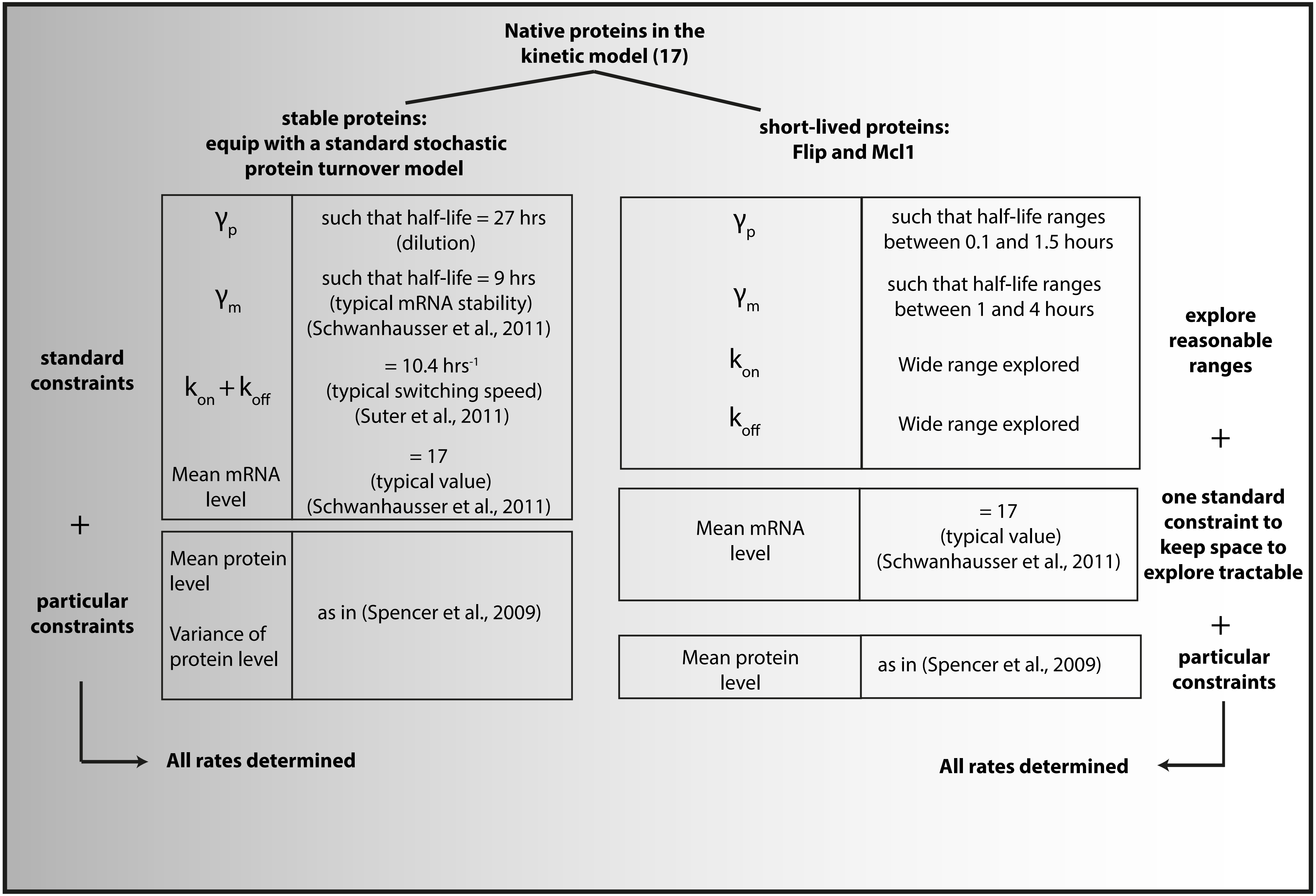

Native proteins in the kinetic model (17)

stable proteins: equip with a standard stochastic protein turnover model

standard constraints

γ_p	such that half-life = 27 hrs (dilution)
γ_m	such that half-life = 9 hrs (typical mRNA stability) (Schwanhausser et al., 2011)
$k_{on} + k_{off}$	= 10.4 hrs^{-1} (typical switching speed) (Suter et al., 2011)
Mean mRNA level	= 17 (typical value) (Schwanhausser et al., 2011)

+

particular constraints

Mean protein level Variance of protein level	as in (Spencer et al., 2009)

All rates determined

short-lived proteins: Flip and Mcl1

explore reasonable ranges

γ_p	such that half-life ranges between 0.1 and 1.5 hours
γ_m	such that half-life ranges between 1 and 4 hours
k_{on}	Wide range explored
k_{off}	Wide range explored

+

one standard constraint to keep space to explore tractable

Mean mRNA level	= 17 (typical value) (Schwanhausser et al., 2011)

+

particular constraints

Mean protein level	as in (Spencer et al., 2009)

All rates determined