Table 1: Empirical parameter ranges

Parameter		x	σ_x	e^x		e^{σ_x}	# samples	ref.
Turnover rate	k^{cat}	1.95	3.3	7.0	s^{-1}	27.1	7559	[18]
Substrate constant	k^M	-1.77	3.0	0.17	mM	20.1	44766	[18]
Inhibition constant	k^I	-2.81	4.1	0.06	mM	60.3	4338	[18]
Energy constant	k^G	-0.24	0.18	0.79		1.2	142	[23]
Equilibrium constant	k^{eq}	-	5.4	-		212	1309	[19]
Protein molecules/cell		7.82	1.56	2480		4.7	3868	[20]
Protein concentration	E_i	-10.23	1.56	$3.6 \cdot 10^{-5}$	mM	4.7	3868	[20]
Metab. concentration	c_i	-1.97	1.94	0.14	mM	7.0	49	[24]

Typical ranges of system parameters (top) and state parameters (bottom). Different types of parameters show specific mean values and standard deviations. Energy constants were predicted from the molecule structures, all other data were obtained from experiments. Numbers of protein molecules were measured in the yeast *S. cerevisiae*. The symbols x and σ_x denote mean values and standard deviations of the natural logarithms, in data sets of different sizes ("# samples"). These values can be used to predefine a prior distribution for model parameters. The exponential values $\exp(x)$ and $\exp(\sigma_x)$ denote, respectively, the geometric mean and a typical uncertainty factor of the parameter type.