

Table S8. Protein abundances

Protein	Experiment [15,16] (per haploid cell)	Simulation before parameter optimization	Simulation after parameter optimization
Whi5	1440	1683 ± 10	1712 ± 14
Net1	1590	1521 ± 9	2246 ± 18
Cdc15	238	245 ± 1	275 ± 2
Tem1	573	490 ± 3	551 ± 4
Cln3	108	81 ± 2	76 ± 1
Cln2	1589	1473 ± 33	2800 ± 65
Clb5	438	964 ± 15	1239 ± 25
Clb2	639	389 ± 16	516 ± 25
CKI	768	532 ± 16	668 ± 31

Abundances of some of the key cell cycle proteins: experimental vs. model values. Abundance data is collected in the simulations as described in [8] on page 59. Simulation statistics (mean ± standard deviation) are computed from 15 realizations. In each realization, twenty pedigrees are generated independently. Each pedigree of cells is initiated by a single daughter (D) or mother (M) cell. In some cases, experimental abundance data from diploid cells are halved for approximating the abundances in haploid cells.

8. Laomettachit T (2011) Mathematical modeling approaches for dynamical analysis of protein regulatory networks with applications to the budding yeast cell cycle and the circadian rhythm in cyanobacteria. Ph.D. thesis, Virginia Institute of Technology. ETDs website. Available: <http://scholar.lib.vt.edu/theses/available/etd-11072011-021528/>.