

Supplementary Table 4: Cell volumes and total proteins per cell used to derive equations 5 and 6. Values were derived from [109] and the references indicated in the table.

Group	Species	$N_{tot,r}$ (10^3)	V (μm^3)	$N_{tot,p}$ (10^6)	References
Bacteria	<i>Bacillus subtilis</i>		1.4	1.8	[199]
Bacteria	<i>Leptospira interrogans</i>		0.22	1.1	[200]
Bacteria	<i>Mycoplasma pneumoniae</i>		0.032	0.066	[201]
Bacteria	<i>Staphylococcus aureus</i>		0.288	0.29	[199]
Bacteria	<i>Escherichia coli</i>	10	0.983	2.47	[202–205]
Fungi	<i>Saccharomyces cerevisiae</i>	60	69	46.66	
				48.11	[205–210]
Fungi	<i>Schizosaccharomyces pombe</i>	41	120	60.3	
				161.2	[210, 211]
Metazoa	Mouse fibroblast NIH3T3	173	2040	3133	[212, 213]
Metazoa	Human HeLa cells		2750	2000	
				2982	[210, 214, 215]

109. Milo R. 2013. What is the total number of protein molecules per cell volume? A call to rethink some published values. *Bioessays* **35**(12):1050–1055.
199. Maass S, Sievers S, Zühlke D, Kuzinski J, Sappa PK, Muntel J, Hessling B, Bernhardt J, Sietmann R, Völker U, Hecker M, Becher D. 2011. Efficient, global-scale quantification of absolute protein amounts by integration of targeted mass

spectrometry and two-dimensional gel-based proteomics. *Anal Chem* **83**(7):2677–2684.

200. Schmidt A, Beck M, Malmström J, Lam H, Claassen M, Campbell D, Aebersold R. 2011. Absolute quantification of microbial proteomes at different states by directed mass spectrometry. *Mol Syst Biol* **7**:510.
201. Maier T, Schmidt A, Güell M, Kühner S, Gavin AC, Aebersold R, Serrano L. 2011. Quantification of mRNA and protein and integration with protein turnover in a bacterium. *Mol Syst Biol* **7**:511.
202. Neidhardt FC, Umberger HE. Chemical composition of *Escherichia coli*. In: Neidhardt FC, Curtiss III R, Ingraham JL, Lin ECC, Low KB, Magasanik B, Reznikoff WS, Riley M, Schaechter M, Umberger HE, editors. *Escherichia coli* and *Salmonella*: cellular and molecular biology. 2nd ed. Washington, D.C.: ASM Press; 1996. pp.13–16
203. Wiśniewski JR, Rakus D. 2014. Quantitative analysis of the *Escherichia coli* proteome. *Data in Brief* **1**:7–11.
204. Taniguchi Y, Choi PJ, Li GW, Chen H, Babu M, Hearn J, Emili A, Xie XS. 2010. Quantifying *E. coli* proteome and transcriptome with single-molecule sensitivity in single cells. *Science* **329**(5991):533–538.
205. Lu P, Vogel C, Wang R, Yao X, Marcotte EM. 2007. Absolute protein expression profiling estimates the relative contributions of transcriptional and translational regulation. *Nat Biotechnol* **25**(1):117–124.
206. Ghaemmaghami S, Huh WK, Bower K, Howson RW, Belle A, Dephoure N, O’Shea EK, Weissman JS. 2003. Global analysis of protein expression in yeast. *Nature* **425**(6959):737–741.
207. Miura F, Kawaguchi N, Yoshida M, Uematsu C, Kito K, Sakaki Y, Ito T. 2008. Absolute quantification of the budding yeast transcriptome by means of competitive PCR between genomic and complementary DNAs. *BMC Genomics* **9**:574.
208. Zenklusen D, Larson DR, Singer RH. 2008. Single-RNA counting reveals alternative modes of gene expression in yeast. *Nat Struct Mol Biol* **15**(12):1263–1271.
209. Holstege FC, Jennings EG, Wyrick JJ, Lee TI, Hengartner CJ, Green MR, Golub TR, Lander ES, Young RA. 1998. Dissecting the regulatory circuitry of a eukaryotic genome. *Cell* **95**(5):717–728.
210. Kulak NA, Pichler G, Paron I, Nagaraj N, Mann M. 2014. Minimal, encapsulated proteomic-sample processing applied to copy-number estimation in eukaryotic cells. *Nat Methods* **11**(3):319–324.
211. Marguerat S, Schmidt A, Codlin S, Chen W, Aebersold R, Bähler J. 2012. Quantitative analysis of fission yeast transcriptomes and proteomes in proliferating and quiescent cells. *Cell* **151**(3):671–683.

212. Lang F, Ritter M, Wöll E, Weiss H, Häussinger D, Hoflacher J, Maly K, Grunicke H. 1992. Altered cell volume regulation in ras oncogene expressing NIH fibroblasts. *Pflügers Arch* **420**(5-6):424–427.
213. Schwanhäusser B, Busse D, Li N, Dittmar G, Schuchhardt J, Wolf J, Chen W, Selbach M. 2011. Global quantification of mammalian gene expression control. *Nature* **473**(7347):337–342.
214. Nagaraj N, Wisniewski JR, Geiger T, Cox J, Kircher M, Kelso J, Pääbo S, Mann M. 2011. Deep proteome and transcriptome mapping of a human cancer cell line. *Mol Syst Biol* **7**:548.
215. Moran U, Phillips R, Milo R. 2010. SnapShot: key numbers in biology. *Cell* **141**(7):1262–1262.e1.