Uri Book Table- Appendix to Typical parameter values for the Bacterial *E. coli* cell, the single celled eukaryote *Saccharomyces cerevisiae* (Yeast), and a Mammalian cell (Human Fibroblast)

Cell volume

Bacteria (*E. coli*) ~1.1 (Range 0.44-1.79) μm^3 (BNID 100004)
***Ref**: Kubitschek HE, Friske JA. Determination of bacterial cell volume with the Coulter Counter. J Bacteriol. 1986 Dec168(3):1466-7. Table link-http://tinyurl.com/cphmpq PMID 3536882*
Measurement Method: Coulter counter. Cells of several different sizes were obtained from either stationary- or exponential-phase cultures of E. coli B/rA grown overnight at 37°C in a shaker water bath in nutrient broth or M9-glucose (10 g/liter) medium. Culture volumes were 160 ml for stationary-phase cultures and 50 ml for exponentially growing cultures.
Comments: value is average of 10 measurements in table 1.

Yeast (*Saccharomyces cerevisiae*)
37 μm^3 (BNID 100430)
***Ref**: Tyson CB, Lord PG, Wheals AE. Dependency of size of Saccharomyces cerevisiae cells on growth rate. J Bacteriol. 1979 Apr138(1):92-8. PMID 374379*
Measurement Method: The mean volume of a haploid yeast cell in exponential phase growing in YEP+Glucose at 30°. Taken from cultures with different doubling times in range 75-84.2 min

~70 μm^3 (BNID 100452)
***Ref**: Roskams and Rodgers, LabRef*

Human HeLa cell 4400 – 5000 μm^3 (BNID 103719)
***Ref**: Cohen LS, Studzinski GP. Correlation between cell enlargement and nucleic acid and protein content of HeLa cells in unbalanced growth produced by inhibitors of DNA synthesis. J Cell Physiol. 1967 Jun69(3):331-9 PMID 4230858*
Measurement Method: Cells allowed to enter logarithmic phase. Cell number was obtained with a Coulter counter, while cell sizing was performed with the automatic particle size distribution analyser Model J Electronic Co., Hialeah, Fla.
Comments: Please note-BNID 103725 gives HeLa cell volume range of 760-2730 um^3

Proteins/cell

E. coli 2.35×10^6 Copies/cell (BNID 102990)
***Ref**: Neidhardt F.C. Escherichia coli and Salmonella: Cellular and Molecular Biology. Vol 1. ASM Press 1996. table link- http://tinyurl.com/cr3y57*
Comments: Calculated for an average cell of E. coli B/r in balanced growth at 37 degrees celsius in aerobic glucose minimal medium with a 40 minute mass doubling time. This cell is 44% through its division cycle.

S. cerevisiae 5.3×10^7 (Range 3×10^7 - 8×10^7) Copies/cell (BNID 104313)
***Ref**: von der Haar T. A quantitative estimation of the global translational activity in logarithmically growing yeast cells. BMC Syst Biol. 2008 Oct 162:87 Fig. 2 PMID 18925958*

Comments:The sum of proteins per cell predicted from the curated dataset is about 53 million proteins for a fast-growing haploid yeast cell, with 90% confidence limits of 30–80 million.

Entry to be filled-Human

Size of genome

E. coli ~4×10^6 bp (BNID 100269)
***Ref**: Blattner FR et al, The complete genome sequence of Escherichia coli K-12, Science. 1997 Sep 5277(5331):1453-74. PMID 9278503*
Comments: The 4,639,221-base pair sequence of Escherichia coli K-12 is presented.

S. cerevisiae ~12×10^6 bp (BNID 100459)
***Ref**: http://www.yeastgenome.org/cache/genomeSnapshot.html*
Comments: The Budding yeast genome size is 12,156,676 base pairs as of May 6th 2009

Human 3.08×10^9 bp (BNID 101484)
***Ref**: International Human Genome Sequencing Consortium. Finishing the euchromatic sequence of the human genome. Nature. 2004 Oct 21 431(7011):931-45. PMID 15496913*
Comments: This value is the "Golden path", the best effort draft full genome sequence (3.093×10^9 base pairs as of May 2009). Total genome size estimated at ~3.25e9 bp at Assembly: NCBI 36, Oct 2005 Genebuild: Ensembl, Dec 2006 Database version: 54.36p
http://www.ensembl.org/Homo_sapiens/index.html See also BNID 100396

Number of genes

E. coli 4489 (BNID 100272)
***Ref**: http://biocyc.org/ECOLI/NEW-IMAGE?object=Genes*
Comments: Based on the sum of genes as it appears in ecocyc on May 16 2008

S. cerevisiae 6609 (BNID 100237)
***Ref**: http://www.yeastgenome.org/cache/genomeSnapshot.html*
Comments: Assembly: NCBI 36, Oct 2005 Genebuild: Ensembl, Dec 2006 Database version: 49.36k

Human 21541 (BNID 100399)
***Ref**: http://www.ensembl.org/Homo_sapiens/index.html*
Comments: Assembly: NCBI 36, Oct 2005 Genebuild: Ensembl, Dec 2006 Database version: 49.36k

Size of average:

Regulator binding site

E. coli, S. cerevisiae, Human 6-10 bp (BNID 104511)
***Ref**:Matthew W. Hahn, Jason E. Stajich, and Gregory A. Wray, The effects of selection against spurious transcription factor binding sites, MBE (Molecular Biology and Evolution) Advance Access published April 25, 2003 pp. 3, Link - http://tinyurl.com/lkwrm7*
***Primary Source**: FAIRALL, L. and J. W. R. SCHWABE 2001. DNA binding by transcription factors. Pp. 65-84 in J. Locker, eds. Transcription factors. Academic Press, Inc, San Diego.*
Comments: Transcription is regulated by transcription factors and other parts of the transcriptional machinery in a complicated cellular environment by interacting directly in a sequence-specific manner with short stretches of DNA surrounding the target gene. These binding sites, often found in a well-defined promoter region upstream of the start of transcription, are typically 6-10 base pairs (bp) long (Fairall and Schwabe 2001).

Average promoter

E. coli 60 base pairs (BNID 104339)
***Ref**: Huerta AM, Francino MP, Morett E, Collado-Vides J. Selection for unequal densities of sigma70 promoter-like signals in different regions of large bacterial genomes. PLoS Genet. 2006 Nov 102(11):e185 PMID 17096598*
Comments: The canonical model of the σ70 promoter is defined as a simple pair of hexamers, positioned at −35 and −10 base pairs (bp) from the transcription start (+1), with respective consensus sequences TTGACA and TATAAT, and separated by a spacer of 15 to 21 bp

S. cerevisiae 455 base pairs (BNID 104338)
***Ref**:* Kristiansson E, Thorsen M, Tamás MJ, Nerman O. Evolutionary forces act on promoter length: identification of enriched cis-regulatory elements. Mol Biol Evol. 2009 Jun26(6):1299-307 *PMID 19258451*
Measurement Method: Sequence Data and Analysis, Transcription Factor Binding Site Data and Phylogenetic Filtering, Three Tests for Enrichment of Transcription Factor Binding Sites

Average gene

E. coli 1100 base pairs (BNID 100022)
***Ref**: http://redpoll.pharmacy.ualberta.ca/CCDB/cgi-bin/STAT_NEW.cgi*

S. cerevisiae 1600 base pairs (BNID 101458)
***Ref**: B. Lewin, Genes 5, Table 2-2. Oxford University Press.*
***Primary Source**: 3 Primary Sources: (1)Dujon B, Alexandraki D, André B, Ansorge W, Baladron V, Ballesta JP, Banrevi A, Bolle PA, Bolotin-Fukuhara M, Bossier P, et al. Complete DNA sequence of yeast chromosome XI. Nature. 1994 Jun 2369(6479):pp. 375 (2) Feldmann H, Aigle M, Aljinovic G, André B, Baclet MC, Barthe C, Baur A, Bécam AM, Biteau N, Boles E, et al. Complete DNA sequence of yeast chromosome II. EMBO J. 1994 Dec 1513(24):pp. 5803 (3)Johnston M, Andrews S, Brinkman R, Cooper J, Ding H, Dover J, Du Z, Favello A, Fulton L, Gattung S, et al. Complete nucleotide sequence of Saccharomyces cerevisiae chromosome VIII. Science. 1994 Sep 30265(5181):pp. 2077 PMIDs (1) 8196765*

(2) 7813418 (3) 8091229
Measurement Method: Primary Source (1) gives value of 1,464 bp for chromosme XI (2) gives value of 1,424 for chromosome II (3) gives value of 1,446 for chromosome VIII
Comments: For a depiction of the full distribution see: http://tinyurl.com/oz66dx. For median RNA molecule of 1474 nucleotides see BNID 100202

Human 10000-15000 base pairs (BNID 104316)
***Ref**: Tom Strachan and Andrew P. Read, Human Molecular Genetics , 1999 Garland Science section 7.2 http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=hmg.table.686*
Comments: Gene size average 10–15 kb, but enormous variation. ~0.2kb (Tyrosine tRNA gene) - ~2500kb (dystrophin gene). See fig 7.7 http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=hmg.figgrp.682

Concentration of one protein/cell

E. coli one molecule per cell transformed to units of concentration is ~1 nM (BNID 102068)
***Ref**: Calculated according to cell volume, please see Measurement Method*
Measurement Method: Calculated using Avogadro's constant according to one cell volume=1E-12 cm^3=1E-15 liter (BNID 100004). 1 particle/1E-15liter=X particles/liter>>X=1E15 particles/liter 1E15(particles/liter)/6E23(particles/mole)= 1.666E-9M=~1 nM.

S. cerevisiae one molecule per cell transformed to units of concentration is ~10 pM (BNID 104518)
***Ref**: Calculated according to cell volume, please see Measurement Method*
Measurement Method: Calculated using Avogadro's constant according to cell volume of 50 um^3= 5E-14liter (BNIDs 100430, 100452). 1 particle/5E-14liter=X particles/liter>>X=2E13particles/liter. 2E13(particles/liter)/6E23(particles/mole) = ~3E-11M=~10 pM. Note: 3e-11M and 1e-11M are on same order of magnitude, allowing approximation.
Comments: pM=1e-12 Molar

Human HeLa cell one molecule per cell transformed to units of concentration is ~0.1 pM (BNID 104519)
***Ref**: Calculated according to cell volume, please see Measurement Method*
Measurement Method: Calculated using Avogadro's constant according to one cell volume=5000um^3=5E-12liter (BNID 103719). 1 particle/5E-12liter=X particles/liter>>X=2E11particles/liter 2E11(particles/liter)/6E23(particles/mole) = ~3E-13M=~0.1 pM. Thus 1mM=~10^{10} molecules per cell. Note: 3e-13M and 1e-13M are on same order of magnitude, allowing approximation.

Average concentration of protein/cell ~1 (0.4-1.4) μm (BNID 104520)
***Primary Source**: Ghaemmaghami, S. et al. Global analysis of protein expression in yeast. Nature. 2003. 425(6959) pp.737-41. Table link - http://tinyurl.com/5naz4m PMID 14562106*
Measurement Method: *Calculated manually from 2 sources: (1)Primary Source: Average protein copy number is ~12100 (column C in table). Dividing by Avogadro's number and cell volume (50um^3=5e-14 liter BNIDs 100430,100452). ~12100/6e23mol^-1/5e-14liter ~ 0.4uM. (2) BNID 104245. Column W in Table link-*

http://tinyurl.com/l82da6. A similar calculation using average protein copy number of 41000 gives concentration of 1.4uM

Comments: (To Primary Source) More than 3000 protein levels. This table is the Supplemental Data from the reference. The proteins are ordered by gene name, but could be sorted based on abundance using the function on Excel. It is also possible to search for protein abundance by gene name at the yeastgfp site (BNID 100600). Note-Wagner (2005) gives protein abundance of 2460 copies/cell (BNID 100208). Using this value in a similar calculation as in Measurement method one arrives at concentration of 8.2e-8M=~0.1uM

Human -to fill

Diffusion time of protein across cell

E. coli ~0. 1 sec (BNID 104667)

Ref*:* Calculated manually. Please see measurement method.

Measurement Method: According to equation: t diffusion=~X^2/2D. Taking X, distance to be traveled, as 1um and D, diffusion coefficient, as 100um^2/sec. D calculated from D=KBT/6/pi/η/R where R=2.5nm, typical protein diameter. KB=Boltzmann's constant, η(eta)=viscousity of the medium, taken as 0.001 Pa*sec for water at ~300 Kelvin, T=temperature in degrees Kelvin, pi=~3.14. (1.380 6504(24)×10^−23 Kgm^2 sec^−2K^−1×300K)/(6×3.14×0.001Kgm^−1sec^−1×2.5× 10^−9 m)=8.8 × 10^−11m^2/sec= 88um^2sec=~100um^2/sec

Comments: Diffusion coefficient of 100 um^2/sec refers to water. In cytoplasm D is smaller than 100um^2/sec as there are solutes, in the range of 5-15 um^2/sec (BNIDs 100193, 100198). Taking D as 10 um^2/sec, actual time of diffusion would be (1um)^2/(2×10)um^2/sec=~0.1 sec

S. cerevisiae 1 sec (BNID 104672)

Ref*: Calculated according to yeast cell diameter and average protein diameter. Please see Measurement Method*

Measurement Method: According to equation: t diffusion=~X^2/2D. Taking X, distance to be traveled, as 4.5um (Yeast cell diameter BNID 100451) and D, diffusion coefficient, as 100um^2/sec. D calculated from D=KBT/6/pi/η/R where R=2.5nm, typical protein diameter. KB=Boltzmann's constant, η(eta)=viscousity of the medium, taken as 0.001 Pa*sec for water at ~300 Kelvin, T=temperature in degrees Kelvin, pi=~3.14. (1.380 6504(24)×10^−23Kgm^2 sec^−2K^−1×300K)/(6×3.14×0.001Kgm^−1sec^−1×2.5× 10^−9 m)=8.8 × 10^−11m^2/sec= 88um^2sec=~100um^2/sec

Comments: Diffusion coefficient of 100 um^2/sec refers to water. In cytoplasm D is smaller than 100um^2/sec as there are solutes, in the range of 5-15 um^2/sec (See BNIDs 100193, 100198). Taking D as 10 um^2/sec, actual time of diffusion would be (4.5um)^2/(2×10)um^2/sec=~1 sec

Human (vertebrate) 5 sec for hemoglobin to move across erythrocyte (BNID 104673)

Ref*: Calculated according to erythrocyte diameter. Please see Measurement Method*

Measurement Method: Calculated with equation d^2=2Dt where d=distance to pass, length of erythrocyte, 10um. D of hemoglobin in erythrocyte cytoplasm is lower than in water due to presence of solutes, in the range of 5-15 um^2/sec (BNIDs 100193, 100198). Taking D as 10 um^2/sec, actual time of diffusion would be (10um)^2/(2×10)um^2/sec=~5 sec

Comments: See BNID 104106 for diffusion time in water medium

Diffusion time of small molecule across cell

E. coli 0.001 sec for a small molecule (lactate) to move across cell (BNID 104674)
Ref*: Calculated according to E. coli cell diameter. Please see Measurement Method*
Measurement Method: Calculated with equation d^2=2Dt where d=distance to pass, diameter of E. coli cell (1um BNID 100002). D=diffusion coefficient of lactate in cytoplasm, 210 um^2/sec (BNID 104644). (1um)^2/(2*210)um^2/sec=0.0023 sec=~0.001sec
Comments: Actual value is higher than 0.001 sec, as D of glucose in E. coli cytoplasm is lower than in water due to presence of solutes. See D of lactate in cytoplasm 210um^2/sec, BNID 104644. For diffusion time of glucose across cell in water see BNID 104526

S. cerevisiae 0.05 sec for a small molecule (lactate) to move across cell (BNID 104675)
Ref*: Calculated according to yeast cell diameter. Please see Measurement Method*
Measurement Method: Calculated with equation d^2=2Dt where d=distance to pass 4.5um (Yeast cell diameter BNID 100451). D=diffusion coefficient of lactate in cytoplasm, 210 um^2/sec (BNID 104644). (4.5um)^2/(2*210um^2/sec)=~0.05 sec
Comments: See BNID 104527 for diffusion time of glucose in water across cell 0.02 sec

Human 0.2 sec for a small molecule (lactate) to move across intestinal cell (BNID 104676)
Ref*: Calculated according to intestinal cell diameter. Please see Measurement Method*
Measurement Method: Calculated with equation d^2=2Dt where d=distance to pass, length of intestinal cell, 10um. D=diffusion coefficient of lactate in cytoplasm, 210 um^2/sec, BNID 104644. t=d^2/2D=(10um)^2/(2*210)um^2/sec=~0.2sec
Comments: For theoretical time of diffusion of glucose in water medium intestinal cell see BNID 104088

Time to transcribe a gene

E. coli, S. cerevisiae -to fill

Human (Mammalian culture cell) ~20 min (BNID 104587)
Ref*: Darzacq X. et al, In vivo dynamics of RNA polymerase II transcription, Nature Structural & Molecular Biology - 14, 796 - 806 (2007) PMID 17676063*
Primary Source*: Kimura H, Sugaya K, Cook PR. The transcription cycle of RNA polymerase II in living cells. J Cell Biol. 2002 Dec 9159(5):777-82 PMID 12473686*
Measurement Method: parameter optimization of FRAP and photoactivation data in U2OS 200 copy gene array. LacI gene integrated into Human U2OS osteosarcoma cells. Primary source: Bleaching
Comments: Ref researchers used Human U2OS osteosarcoma cells and arrived at elongation speed of 0.4 +- 0.08 kb/min. This result is in accordance with Primary source (in Chinese Hamster cells) result that RNA polymerase's average residence time in random positions of the nucleus is about 20 min, corresponding to an elongation speed of 0.7 kb min- 1 for an average transcription-unit size of 14 kilobases.

Time to translate a protein

E. coli, *S. cerevisiae*, Human, *To enter*

Typical mRNA lifetime

E. coli 2.7 minutes (half life) (BNID 104324)
***Ref**: Bernstein JA, Lin PH, Cohen SN, Lin-Chao S. Global analysis of Escherichia coli RNA degradosome function using DNA microarrays. Proc Natl Acad Sci U S A. 2004 Mar 2101(9):2758-63 Table link - http://tinyurl.com/kk8dkh PMID 14981237*
Measurement Method: To investigate the degradosome's proposed role as an RNA decay machine, researchers used DNA microarrays to globally assess alterations in the steady-state abundance and decay of 4,289 E. coli mRNAs at single-gene resolution in bacteria carrying mutations in the degradosome constituents RNase E, polynucleotide phosphorylase, RhlB helicase, and enolase.
Comments: Calculated as average of different strains in table. Table gives median mRNA half life and generation times of different strains

S. cerevisiae ~30 min (BNID 100205)
***Ref**: Wagner, A., Energy Constraints on the Evolution of Gene Expression, Mol. Biol. Evol. 22(6):1365–1374. 2005 PMID 15758206*
***Primary Source**: Wang Y, Liu CL, Storey JD, Tibshirani RJ, Herschlag D, Brown PO. Precision and functional specificity in mRNA decay. Proc Natl Acad Sci U S A. 2002 Apr 30 99(9):5860-5 PMID 11972065*
Measurement Method: By using DNA microarrays, we precisely measured the decay of each yeast mRNA, after thermal inactivation of a temperature-sensitive RNA polymerase II: Yeast was grown on YPD at 24 degrees celsius, transferred to a similar medium at 49 degrees and 0, 5, 10, 15, 20, 30, 40, 50, and 60 min after the temperature shift harvested on a nitrocellulose filter followed by liquid nitrogen freezing and total RNA extraction by hot phenol extraction. A nonlinear least squares model was fit to determine the decay rate constant (k) and half-life (t1/2) of each mRNA. The decay rate constant, k, is the value that minimized $\Sigma i = 1,n[y(ti) - exp(-k \cdot ti)]2$, where y(t) is the mRNA abundance at time t and the summation is taken over all observations for the particular mRNA. The half-life is $t1/2 = ln2/k$. The goodness of fit of the decay model for each gene was assessed with the F statistic (ref 20 of primary source), based on the null hypothesis that the data fit a first-order decay model. A bootstrap method was used to calculate confidence intervals for both t1/2 and k (ref 21 of primary source). Median mRNA decay constant is 5.6×10^{-4} sec^{-1} which is equal to mRNA half of about 30 min: $(5.6\times10^{-4}\ sec^{-1})^{-1}$=1785.7 sec=29.8 min

Human 10 hours (half life) (BNID 104747)
***Ref**: Systems Biology: Properties of Reconstructed Networks, Bernhard O. Palsson, Cambridge University Press, pp. 12*
***Primary Source**: Decay Rates of Human mRNAs: Correlation With Functional Characteristics and Sequence Attributes, Genome Res. Yang et al. 13:1863-1872, 2003 PMID 12902380*
Measurement Method: (Primary source): Researchers measured mRNA decay rates in two human cell lines (Hep G2-Hepatocellular carcinoma) and Bud8 primary cells with high-density oligonucleotide arrays that enable the measurement of decay rates simultaneously for thousands of mRNA species. To study the rates of mRNA degradation ("decay") in human cells, they measured changes in mRNA levels following application of the RNA polymerase inhibitor Actinomycin D with Affymetrix U95Av2 high-density

oligonucleotide arrays. They collected RNA from cells after 2–3 h of inhibition and used the Affymetrix Microarray Suite (MAS) 5.0 to analyze the changes from the untreated state. Four experiments (i.e., eight hybridizations) were performed in HepG2 cells, and they conducted an additional experiment in Bud8 primary cells to exclude the possibility of cancer-cell-specific artifacts.
Comments: Combining the decay rate for all the probe sets present in the initial and final conditions, they find that the median half life in both cell types is ~10h. However, 5% of transcripts showed fast decay rates >0.5h^-1 or half life<2h, among which were the transcription factor transcripts. Biosynthesis and other housekeeping transcripts showed slower decay rates.

Number mRNA per cell

E. coli 1380 Copies/cell (BNID 100064)
***Ref**: Neidhardt F.C. Escherichia coli and Salmonella: Cellular and Molecular Biology. Vol 1. ASM Press 1996.*
Measurement Method: Calculated for an average cell of E. coli B/r at 37 degrees celsius in aerobic glucose with a 40 minute mass doubling time. This cell is 44% through its division cycle.

S. cerevisiae ~12200 (Range 6100-18300) Copies/cell (BNID 102988)
***Ref**: von der Haar T. A quantitative estimation of the global translational activity in logarithmically growing yeast cells. BMC Syst Biol. 2008 Oct 162:87 PMID 18925958*
Measurement Method: Analysis of Yeast datasets
Comments: Although the total mass of cellular RNA cannot be calculated in the same way because non-coding mRNA regions for each gene contribute to the molecular weight but are not accurately known, the total number of mRNAs in the dataset can easily be calculated as about 12,200, with 95% confidence limits between 6,100 and 18,300 mRNAs per cell.

Human 3×10^5 Copies/cell (BNID 104330)
***Ref:** Velculescu VE et al. Analysis of human transcriptomes. Nat Genet. 1999 Dec23(4):387-8 PMID 10581018*
Measurement Method: Researchers analysed 3.5-million transcripts from 19 normal and diseased tissue types.

Characteristic cell generation time in ideal lab conditions

E. coli 20 min (BNID 103514)
***Ref:** Sezonov G, Joseleau-Petit D, D'Ari R. Escherichia coli physiology in Luria-Bertani broth. J Bacteriol. 2007 Dec189(23):8746-9 PMID 17905994*
Measurement Method: The widely used wild-type E. coli K-12 strain MG1655 (1), which has been sequenced and annotated (2, 10), was chosen for this study. An overnight culture in Luria-Bertani broth was diluted 5,000-fold in 250 ml fresh medium in a 1-liter Erlenmeyer flask and cultivated in a shaking water bath (180 rpm) at 37°C. The OD600 and number of cells per milliliter were monitored.
Comments: Doubling rate during steady state growth in Luria-Bertani broth. A culture of MG1655 was grown for 24 h in Luria- Bertani broth (final OD600 of 6.49).

S. cerevisiae 100 minutes (BNID 100270)
Ref: *JR Warner,The economics of ribosome biosynthesis in yeast,Trends Biochem Sci. 1999 Nov24(11):437-40 PMID 10542411*
Comments: Can reach ~70 minutes under ideal conditions (see BNID 101747)

Human HeLa cell ~16 hours (BNID 103804)
Ref: *Kumei Y, Nakajima T, Sato A, Kamata N, Enomoto S. Reduction of G1 phase duration and enhancement of c-myc gene expression in HeLa cells at hypergravity. J Cell Sci. 1989 Jun93 (Pt 2):221-6. PMID 2693468*
Measurement Method: Hypergravity cell culture, [3 H] thymidine incorporation, Cell cycle analysis, RNA blot hybridization (Northern analysis) **Comments**: Research checked difference between HeLa cells in hypergravity conditions and control. No significant differences in shape or size were observed by phase-contrast microscopy between the 35g culture and the control (Fig. 2). Predominantly triangular or polygonal cells were observed, with few cells in mitosis.

Ribosomes/cell

E. coli 6,800-72,000 Copies/cell (BNID 101441)
Ref: *Bremer, H., Dennis, P. P. (1996) Modulation of chemical composition and other parameters of the cell by growth rate. Neidhardt, et al. eds. Escherichia coli and Salmonella typhimurium: Cellular and Molecular Biology, 2nd ed. chapter 97, pp. 1559, Table 3*
Comments: lower value is for slow division rate (100 minutes) and higher value is for fast division rate (24 minutes)

S. cerevisiae 187,000 Copies/cell (BNID 100267)
Ref*: von der Haar T. A quantitative estimation of the global translational activity in logarithmically growing yeast cells. BMC Syst Biol. 2008 Oct 162:87 PMID 18925958*
Primary Source*: Warner JR. The economics of ribosome biosynthesis in yeast, Trends Biochem Sci. 1999 Nov24(11):437-40 PMID 10542411*
Measurement Method: (For primary source, value of 200000 ribosomes/cell). Based on comparison of the size of the genome (1.43×10^7 bp) with the RNA in a ribosome (5469 nucleotides), and using ratio of DNA to rRNA
Comments: (For von der Haar ref above) Independent estimates for the cellular ribosome content have been generated by analysing the abundance of ribosomal RNA (rRNA) species in several studies [25-30], with reported values ranging from 150,000 to 350,000 copies of ribosomal RNA per cell for fast-growing haploid yeast strains.

Human- Entry to be filled

Transitions between protein states (active/inactive)

E. coli, S. cerevisiae, Human 100-200 μs (Bacteria Thermotoga maritima) (BNID 104596)
Ref*: Chung HS, Louis JM, Eaton WA. Feature Article: Experimental determination of upper bound for*

transition path times in protein folding from single-molecule photon-by-photon trajectories. Proc Natl Acad Sci U S A. 2009 Jul 10 PMID 19584244
Measurement Method: The cold-shock protein from Thermotoga maritima (CspTm) was labeled with a green-fluorescing and a red-fluorescing dye, serving as FRET donor and acceptor, respectively. FRET upon excitation by a laser beam allows folded and unfolded molecules to be distinguished on the basis of the strong distance dependence of energy transfer between the chromophores.

Timescale for equilibrium binding of small molecule to protein (diffusion limited)

Entries to be filled- *E. coli, S. cerevisiae,* Human

Timescale of transcription factor binding to DNA site

Entries to be filled- *E. coli, S. cerevisiae,* Human

Mutation rate (per base pair per generation)

E. coli 5.4E-10 mutation/bp/replication (BNID 100263)
Ref*:* Drake JW, A constant rate of spontaneous mutation in DNA-based microbes.Proc Natl Acad Sci U S A. 1991 Aug 1588(16):7160-4 Table 1 *PMID 1831267*
Measurement Method: Value is mean of two strains-hisGDCBHAFE (one measurement) and LacI (2 measurements)

S. cerevisiae 2.2E-10 mutation/bp/replication (BNID 100457)
Ref*: Drake JW, Charlesworth B, Charlesworth D, Crow JF. Rates of spontaneous mutation. Genetics. 1998 Apr148(4):1667-86 PMID 9560386*

Human 5E-11 mutation/bp/replication (BNID 100414)
Ref*: Drake JW, Charlesworth B, Charlesworth D, Crow JF. Rates of spontaneous mutation. Genetics. 1998 Apr148(4):1667-86 PMID 9560386*