

**Table 1. Range of values for the number of proteins per cell based on published studies.**

Reported proteins per cell	Cell volume ( $\mu\text{m}^3$ )	Inferred proteins per volume ( $10^6/\mu\text{m}^3$ )	Mismatch from calculation	BNID, Ref, Method
<i>M. pneumoniae</i> $0.05 \times 10^6$	0.015	3	<2-fold	Kühner et al. [6]. Using cryoEM counting of ribosomes for normalization. Volume calculated based on pear shaped $700 \text{ nm} \times 300 \text{ nm}$ .
<i>L. interrogans</i> <sup>a</sup> $(1.0-1.2) \times 10^6$	0.22	5	<2-fold	Schmidt et al. [7]. Summing table SV. Volume given in Maier et al. [36] citing Beck et al. [37].
<i>E. coli</i> $2.36 \times 10^6$	0.86	2.7	<2-fold	100088, Neidhardt & Umbarger, EcoSal Ch. 3, 1996, 40 min doubling time, 0.95 pg cell total weight and assuming cell density of 1.1 (used for normalization by Lu [30]). Original calculation based on average protein MW = 40 kDa but weighing by abundance gives MW $\approx 30 \text{ kDa}$ that will make value higher by a third.
$2.3 \times 10^6$	0.7	3.3	<2-fold	Arike et al. [18]. Volume not specified
<sup>a</sup> $0.1 \times 10^6$		N/A	N/A	Taniguchi et al. [32], cover about 1/4 of genome. Growth at $30^\circ\text{C}$ (based on fluorescent protein).
<sup>a</sup> $280 \times 10^6$		N/A	N/A	Ishihama et al. [8], they report a massive overestimate in ribosomal protein counts
<i>B. subtilis</i> <sup>a</sup> $2.3 \times 10^6$	1.13	2.0	<2-fold	Maass et al. [33], exponential growth, early stationary, and late stationary, respectively. Only cytosolic proteins with isoelectric point at pH 4-7 quantified.
<sup>a</sup> $1.3 \times 10^6$	0.62	2.1	<2-fold	
<sup>a</sup> $1.8 \times 10^6$	0.85	2.1	<2-fold	
<i>S. aureus</i> <sup>a</sup> $0.35 \times 10^6$	0.33	1.1	$\approx 3$ -fold	Maass et al. [33], exponential growth, early stationary, and late stationary, respectively. Only cytosolic proteins with isoelectric point at pH 4-7 quantified.
<sup>a</sup> $0.27 \times 10^6$	0.23	1.2	$\approx 3$ -fold	
<sup>a</sup> $0.26 \times 10^6$	0.23	1.1	$\approx 3$ -fold	
<i>S. cerevisiae</i> (haploid) $50 \times 10^6$	$\approx 30-40$	1-2	$\approx 2$ -fold	106198, Futcher et al. [34], based on 1977 paper measuring 4 fg of protein per cell (used for normalization by Lu [30])
<sup>a</sup> $47 \times 10^6$				Ghaemmaghani et al. [31], summing up all measured proteins (based on TAP tag).
$53 \times 10^6$ ( $30 \times 10^6-80 \times 10^6$ )				104313, von der Haar [35], the author merged various high throughput measurements.
<i>S. pombe</i> $60.3 \times 10^6$	$\approx 100$	0.6	$\approx 5$ -fold	Marguerat et al. [9]. Mass Spectrometry, exponential growth.
<i>M. musculus</i> (NIH3T3 cells) <sup>a</sup> $3 \times 10^9$	$\approx 2,000$	1.5	<2-fold	Schwanhäusser et al. [10] updated in Nature 2013. SILAC medium. Volume based on BNID 108979.
<i>H. sapiens</i> (U2OS) <sup>a</sup> $(0.95-1.7) \times 10^9$	$\approx 4,000$	0.2-0.4	$\approx 10$ -fold	Beck et al. [11]. Range stems from the 11 most highly abundant proteins for which the authors could not calibrate accurately and originally reported as $>20$ million copies per cell. Assuming 20 million gives the lower value and using the original measured higher values gives the upper bound.
<i>H. sapiens</i> (HeLa) <sup>a</sup> $2.0 \times 10^9$	$\approx 2,000$	1	$\approx 3$ -fold	Nagaraj et al. [12].
<sup>a</sup> $2.3 \times 10^9$	$\approx 2,000$	1	$\approx 3$ -fold	Finka and Goloubinoff [19]. Analyzing data from Geiger et al. [13].

In some cases the number is inferred from supplementary information and was not reported as such. When cell volume was not reported in the study, literature values under similar conditions were used. Mismatch between values inferred from the literature per unit volume and estimates given in this paper (2-4 million proteins per micron cubed) is calculated.

<sup>a</sup> Value for total proteins per cell was not explicitly reported and is based on summing the abundance values as reported in the supplementary material across the proteome.