**Table 1.** The summary of translational parameters calculated in the model.

| organism | | $L$ | $x$ | $b$ | $g$ | $w$ | $I$ | $E$ | $\bar{e}$ | $m$ |
|---|---|---|---|---|---|---|---|---|---|---|
| E.coli | mean | 335 | 3.6 | 47 | 1.3 | 4.0 | 62 | 40 | 119 | 7.5 |
| | median | 298 | 1.7 | 28 | 0.8 | 2.3 | 15 | 35 | 119 | 6.8 |
| | sd | 203 | 5.6 | 60 | 1.3 | 5.0 | 206 | 24 | 9 | 4.0 |
| | min | 15 | 0.1 | 0 | 0 | 0 | 2 | 2 | 87 | 2.0 |
| | max | 1487 | 54.0 | 940 | 6.6 | 41.2 | 5091 | 178 | 177 | 42.3 |
| S.cerevisiae | mean | 513 | 7.8 | 116 | 1.1 | 5.6 | 54 | 116 | 224 | 33.2 |
| | median | 431 | 2.7 | 58 | 0.8 | 3.1 | 28 | 96 | 229 | 27.4 |
| | sd | 365 | 29.0 | 188 | 0.9 | 7.3 | 186 | 84 | 31 | 26.8 |
| | min | 37 | 0.1 | 1 | 0.0 | 0.0 | 2 | 4 | 98 | 4.3 |
| | max | 4911 | 591.3 | 2543 | 6.6 | 142.1 | 6714 | 1074 | 360 | 677 |
| H.sapiens | mean | 676 | 85.9 | 9171 | 2.3 | 11.5 | 7 | 59 | 87 | 6.5 |
| | median | 506 | 42.6 | 5616 | 2.1 | 10.1 | 4 | 44 | 87 | 9.2 |
| | sd | 620 | 171.9 | 9739 | 1.4 | 7.22 | 23 | 54 | 4 | 6.3 |
| | min | 38 | 0.9 | 14 | 0.0 | 0.0 | 1 | 3 | 75 | 3.0 |
| | max | 14508 | 4e3 | 83e3 | 7.5 | 131.6 | 1372 | 1232 | 108 | 34.6 |

Column description: ($L$) transcript length; ($x$) number of gene transcripts; ($b$) number of proteins produced from one transcript; ($g$) ribosome density in number of ribosomes per 100 codons; ($w$) number of ribosomes on a transcript; ($I$) initiation time in s; ($E$) elongation time in s; ($\bar{e}$) mean elongation time of one transcript codon in ms; and ($m$) mean transcript lifetime in min (bacteria, yeast), or in h (humans). For all parameters, except $b$ and $m$, the rows 1–15 were calculated for 1738, 4470, and 7494 genes for bacteria, yeast, and humans, respectively. For parameter $b$ and $m$, the rows were calculated for 1574, 3425, and 6205 genes, respectively.