

Table S3: The translational parameters calculated for 14 genes coding proteins of the 20S yeast proteasome. Row descriptions: (gene) systematic name of the gene; (subunit) name of the corresponding proteasomal subunit; (L) length of the coding sequence in codons; (x) number of transcripts per cell; (B) number of synthesised protein molecules per cell; (g) ribosome density in ribosomes per 100 codons; (w) absolute number of ribosomes per transcript; (P) translation initiation frequency (the inverse of I); (Pz) the relative rate of binding of free ribosomes to the 5' end of a transcript; (Ps) the relative, normalised rate of a successful accomplishment of translation initiation once the ribosome-mRNA complex is formed; (T) total time of translation of one protein molecule from a given transcript in clock notation (min:sec); (I) total time required for translation initiation in clock notation (min:sec); (mean_E) mean time required for translation elongation of a transcript in clock notation (min:sec); (mean_E) mean time required for elongation of one codon of a transcript in sec; (h) estimated half-life of a transcript in clock notation (h:min:sec); and (m) estimated mean life-time of a transcript in clock notation (h:min:sec).

| gene subunit | YGL011C alpha-1 | YML092C alpha-2 | YGR135W alpha-3 | YOL038W alpha-4 | YGR253C alpha-5 | YMR314W alpha-6 | YOR362C alpha-7 |
|-----------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| L | 253 | 251 | 259 | 255 | 261 | 235 | 289 |
| x | 5.12 | 8.95 | 20.43 | 16.19 | 16.20 | 14.03 | 13.06 |
| B | 3488 | 5481 | 972 | 624 | 318 | 1038 | 3076 |
| g | 2.77 | 1.64 | 0.77 | 0.76 | 1.40 | 1.03 | 0.8 |
| w | 7.01 | 4.11 | 1.99 | 1.94 | 3.67 | 2.42 | 2.34 |
| P | 1.3e-04 | 7.2e-05 | 3.7e-05 | 2.9e-05 | 6.4e-05 | 4.6e-05 | 4.1e-05 |
| Pz | 1.4e-04 | 2.5e-04 | 5.7e-04 | 4.5e-04 | 4.5e-04 | 3.9e-04 | 3.6e-04 |
| Ps | 1.4e-02 | 4.4e-03 | 9.9e-04 | 9.9e-04 | 2.2e-03 | 1.8e-03 | 1.7e-03 |
| T | 0:59 | 1:11 | 1:21 | 1:40 | 1:13 | 1:14 | 1:23 |
| I | 0:07 | 0:14 | 0:27 | 0:34 | 0:16 | 0:22 | 0:25 |
| E | 0:52 | 0:57 | 0:54 | 1:06 | 0:57 | 0:52 | 0:58 |
| mean_E | 0.206 | 0.227 | 0.208 | 0.259 | 0.219 | 0.223 | 0.199 |
| h | 0:58:27 | 1:37:57 | 0:14:52 | 0:15:10 | 0:03:32 | 0:18:32 | 1:06:56 |
| m | 1:24:20 | 2:21:19 | 0:21:26 | 0:21:53 | 0:05:06 | 0:26:44 | 1:36:34 |
| gene subunit | YJL001W beta-1 | YOR157C beta-2 | YER094C beta-3 | YER012W beta-4 | YPR103W beta-5 | YBL041W beta-6 | YFR050C beta-7 |
| L | 216 | 262 | 206 | 199 | 288 | 242 | 267 |
| x | 16.64 | 3.99 | 22.61 | 4.09 | 14.08 | 7.15 | 9.41 |
| B | 11185 | 2581 | 2468 | 2674 | 2670 | 1657 | 3549 |
| g | 0.86 | 4.32 | 0.61 | 3.02 | 0.83 | 2.21 | 1.42 |
| w | 1.86 | 11.31 | 1.26 | 6.01 | 2.39 | 5.35 | 3.80 |
| P | 3.9e-05 | 1.8e-04 | 2.7e-05 | 1.4e-04 | 4.3e-05 | 1.0e-04 | 6.7e-05 |
| Pz | 4.6e-04 | 1.1e-04 | 6.3e-04 | 1.1e-04 | 3.9e-04 | 2.0e-04 | 2.6e-04 |
| Ps | 1.3e-03 | 2.6e-02 | 6.6e-04 | 1.9e-02 | 1.7e-03 | 7.9e-03 | 3.9e-03 |
| T | 1:12 | 1:05 | 1:22 | 0:49 | 1:19 | 1:01 | 1:11 |
| I | 0:25 | 0:05 | 0:36 | 0:07 | 0:23 | 0:10 | 0:15 |
| E | 0:47 | 1:00 | 0:46 | 0:42 | 0:56 | 0:51 | 0:56 |
| mean_E | 0.218 | 0.228 | 0.223 | 0.209 | 0.194 | 0.213 | 0.212 |
| h | 3:16:42 | 0:39:32 | 0:45:47 | 0:52:24 | 0:51:19 | 0:25:48 | 1:04:52 |
| m | 4:43:48 | 0:57:03 | 1:06:03 | 1:15:36 | 1:14:02 | 0:37:33 | 1:33:34 |