**Table S2. Specific stochastic protein turnover models**

“Non-fitted” model (Fig. S6):

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Constraints | | Rate values | | | | | |
| Protein | Mean mRNA level  [sup. ref. 6, see Text S1] | Mean protein level  [13] | kon (hrs-1) | koff (hrs-1) | ksm (min-1) | m (hrs-1) | ksp (min-1) | p (hrs-1) |
| Flip | 17 | 2000 | 0.388 | 10.05 | 2.6186 | 0.3466 | 2.7182 | 1.39 |
| Mcl-1 | 17 | 20000 | 0.388 | 10.05 | 2.6186 | 0.3466 | 27.182 | 1.39 |

“Fitted” model (Figs. 3,4,6,7):

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Constraints | | Rate values | | | | | |
| Protein | Mean mRNA level  [sup. ref. 6, see Text S1] | Mean protein level  [13] | kon (hrs-1) | koff (hrs-1) | ksm (min-1) | m (hrs-1) | ksp (min-1) | p (hrs-1) |
| Flip | 17 | 2000 | 0.0417 | 0.0625 | 0.4910 | 0.6931 | 3.3978 | 1.73 |
| Mcl-1 | 17 | 20000 | 0.0417 | 0.0625 | 0.4910 | 0.6931 | 33.9780 | 1.73 |