

Supplementary Information: Decomposition of  
time-dependent fluorescence signals reveals  
codon-specific kinetics of protein synthesis

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## Kinetic rates

Table S1: Kinetic rates as used in the Markov model description of the translation process [1].

Rates	k-notation	37°C	Units
$\kappa_{\text{on}}$	$k_1$	$175 \pm 25$	$\mu\text{M}^{-1} \text{s}^{-1}$
$\omega_{\text{off}}$	$k_{-1}$	$700 \pm 270$	$\text{s}^{-1}$
$\omega_{\text{rec}}$	$k_2$	$1500 \pm 450$	$\text{s}^{-1}$
$\omega_{21}$	$k_{-2,\text{co}}$	$2 \pm 0.6$	$\text{s}^{-1}$
$\omega_{23}$	$k_{3,\text{co}}$	$1500 \pm 450$	$\text{s}^{-1}$
$\omega_{\text{con}}$	$k_4$	450	$\text{s}^{-1}$
$\omega_{40}$	$k_{7,\text{co}}$	1	$\text{s}^{-1}$

Table S2: Fitted *in-vitro* rates of ribosomal transitions. The standard deviation of the fitting parameters was calculated by analyzing the goodness-of-fit parameter  $\chi^2$ .

Rates	37°C	Units
$\omega_{\text{trans}}$	$53 \pm 4$	$\text{s}^{-1}$
$\omega_{45_1}$	$109 \pm 3$	$\text{s}^{-1}$
$\omega_{45_2}$	$11 \pm 0.5$	$\text{s}^{-1}$
$\omega_{45_3}$	$43 \pm 4$	$\text{s}^{-1}$
$\omega_{45_4}$	$2 \pm 0.1$	$\text{s}^{-1}$
$\omega_{45_5}$	$20 \pm 1$	$\text{s}^{-1}$
$\omega_{\text{end}}$	0.3	$\text{s}^{-1}$

# Intrinsic Fluorescence Intensities

Table S3: IFIs obtained from fluorescence signatures of *phe1* to *phe5* mRNA translation

#	no EF-G	<i>phe1</i>	<i>phe2</i>	<i>phe3</i>	<i>phe4</i>	<i>phe5</i>
(IFI <sub>1</sub> )	(1)	(1)	(1)	(1)	(1)	(1)
IFI <sub>1</sub> <sup>pep</sup>	1.124	1.146	1.081	1.168	1.183	1.157
IFI <sub>1</sub> <sup>trans</sup>		1.069				
IFI <sub>2</sub>			1.019	1.015	0.977	0.980
IFI <sub>2</sub> <sup>pep</sup>			1.149			
IFI <sub>3</sub>				1.320	1.390	1.383
IFI <sub>3</sub> <sup>pep</sup>				1.088		
IFI <sub>4</sub>					1.068	(1.068)
IFI <sub>4</sub> <sup>pep</sup>					1.182	
IFI <sub>5</sub>						0.988
IFI <sub>5</sub> <sup>pep</sup>						1.261

Table S4: IFIs obtained from fluorescence signatures of *phe4* mRNA translation under different ternary complex concentrations

#	0.15 $\mu$ M	0.3 $\mu$ M	2 $\mu$ M	10 $\mu$ M
(IFI <sub>1</sub> )	(1)	(1)	(1)	(1)
IFI <sub>1</sub> <sup>pep</sup>	1.235	1.224	1.179	1.174
IFI <sub>2</sub>	1.024	1.003	0.975	0.983
IFI <sub>3</sub>	1.299	1.342	1.408	1.383
IFI <sub>4</sub>	1.073	1.061	1.071	1.117
IFI <sub>4</sub> <sup>pep</sup>	1.172	1.176	1.186	1.189

Table S5: Averaged IFIs obtained from fluorescence signatures of *phe1* to *phe5* mRNA translation ( $\pm$  SD)

#	Fluorescence value	SD	SD [%]	Relative change [%]
(IFI <sub>1</sub> )	(1)	-	-	-
IFI <sub>1</sub> <sup>pep</sup>	1.143	0.031	2.7	14.3
IFI <sub>1</sub> <sup>trans</sup>	1.069	-	-	6.9
IFI <sub>2</sub>	0.998	0.017	1.7	0.2
IFI <sub>2</sub> <sup>pep</sup>	1.149	-	-	14.9
IFI <sub>3</sub>	1.364	0.027	2.0	36.4
IFI <sub>3</sub> <sup>pep</sup>	1.088	-	-	8.8
IFI <sub>4</sub>	1.068	-	-	6.8
IFI <sub>4</sub> <sup>pep</sup>	1.182	-	-	18.2
IFI <sub>5</sub>	0.988	-	-	1.2
IFI <sub>5</sub> <sup>pep</sup>	1.261	-	-	26.1

Table S6: Averaged IFIs obtained from fluorescence signatures of *phe4* mRNA translation under different ternary complex concentrations ( $\pm$  SD)

#	Fluorescence value	SD	SD [%]	Relative change [%]
(IFI <sub>1</sub> )	(1)	-	-	-
IFI <sub>1</sub> <sup>pep</sup>	1.203	0.028	2.2	20.3
IFI <sub>2</sub>	0.996	0.019	1.9	0.4
IFI <sub>3</sub>	1.358	0.041	3.1	35.8
IFI <sub>4</sub>	1.080	0.022	2.0	8.0
IFI <sub>4</sub> <sup>pep</sup>	1.181	0.007	0.6	18.1

## Additional figures: Markov Process Representations

no EF-G

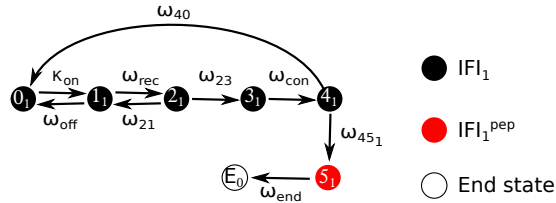


Figure S1: Representation of *phe* mRNA translation elongation as a Markov process without EF-G.

*phe1*

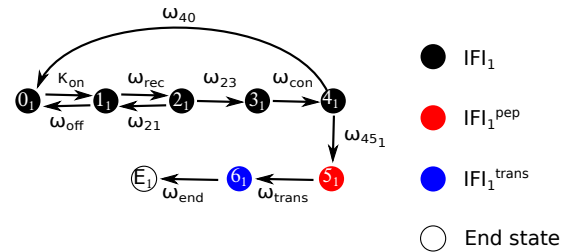


Figure S2: Representation of *phe1* mRNA translation elongation as a Markov process.

*phe2*

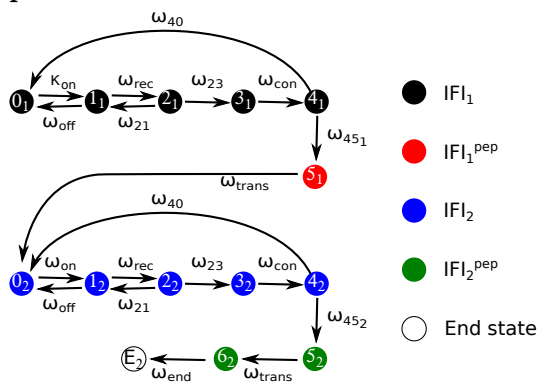


Figure S3: Representation of *phe2* mRNA translation elongation as a Markov process.

*phe3*

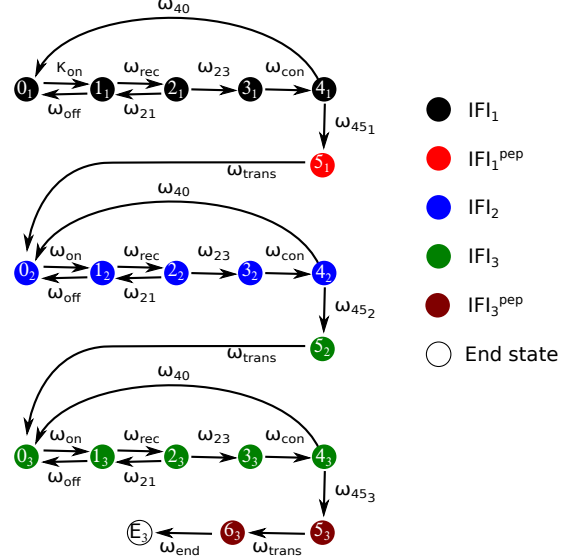


Figure S4: Representation of *phe3* mRNA translation elongation as a Markov process.

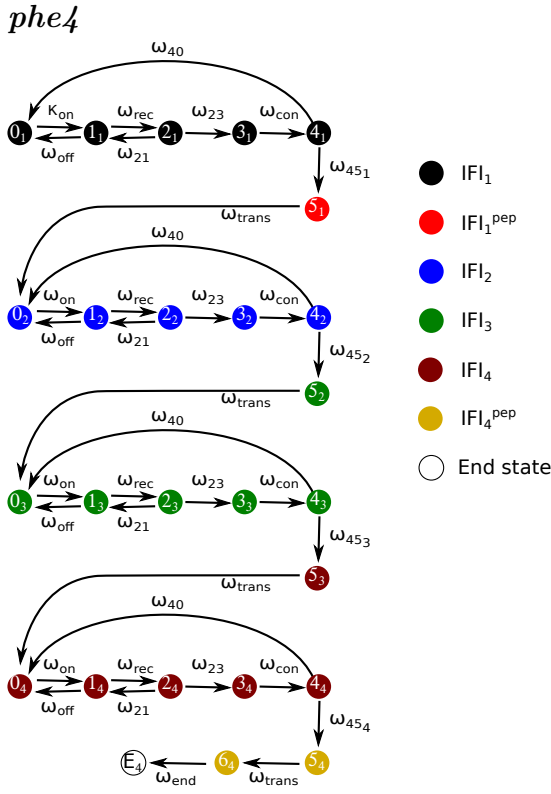


Figure S5: Representation of *phe4* mRNA translation elongation as a Markov process.

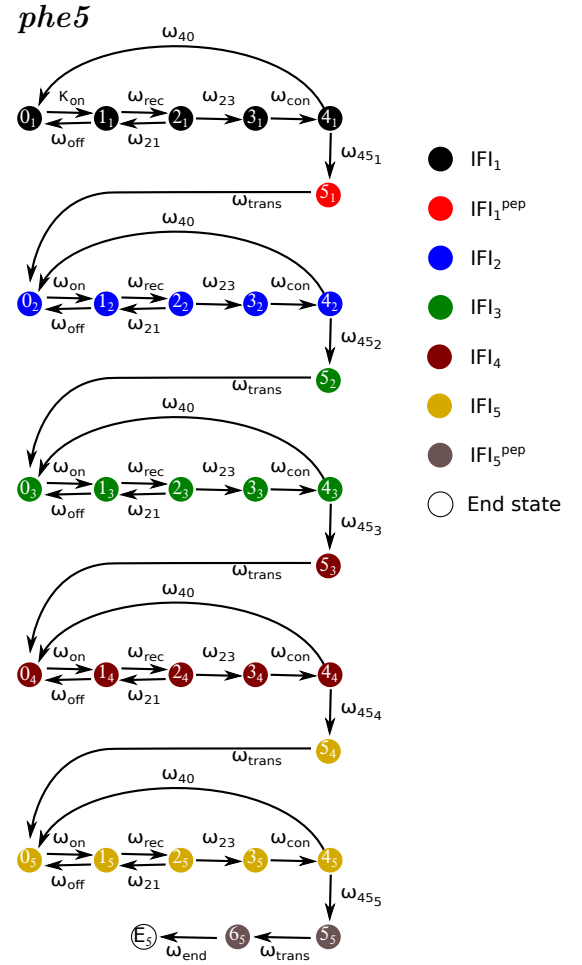


Figure S6: Representation of *phe5* mRNA translation elongation as a Markov process.

The figures S1-S6 represent Markov process descriptions of the *in-vitro* translation elongation cycle for truncated poly(U) mRNAs in the presence of only cognate ternary complexes. Each state of the Markov process corresponds to one sub-step of the elongation cycle. The fluorescent initiation complex consisting of a ribosome with BOF-Met-tRNA<sup>Met</sup> in the P site and the first UUU codon in the A site starts in state 0<sub>1</sub>. Initial selection (0<sub>1</sub>-4<sub>1</sub>) is followed by A-site accommodation of the first Phe-tRNA<sup>Phe</sup>. After peptide bond formation (5<sub>1</sub>), the ribosome translocates to the second Phe codon (state 0<sub>2</sub>). The ribosomes repeat the elongation cycle until they reach the end of the truncated mRNA, thus ending up in an end state (E<sub>n</sub>) without mRNA in their A sites. Dots with the same color indicate states that are assigned the same intrinsic fluorescence intensity (IFI).

## References

- [1] S. Rudorf, M. Thommen, M.V. Rodnina, and R. Lipowsky. Deducing the kinetics of protein synthesis in vivo from the transition rates measured in vitro. *PLoS Computational Biology*, 10(10), 2014.