

Supporting Information: S7 Table

Protein Synthesis in E. coli: Dependence of Codon-specific Elongation on tRNA Concentration and Codon Usage

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Table S7. *In-vivo* codon usages p_c in percent for all sense codons c in *E. coli*. For the specific growth rate of 2.5 h^{-1} , the codon usages were determined from relative mRNA abundances of 4215 different genes [1]. In all other cases, data from [2] were used and rescaled to exclude stop codons.

	Specific growth rate [h^{-1}]					Specific growth rate [h^{-1}]			
	0.7	1.07	1.6	2.5		0.7	1.07	1.6	2.5
AAA	4.67	4.94	5.24	5.50	GAA	5.43	5.54	5.72	4.46
AAC	2.84	2.88	2.93	2.72	GAC	2.98	3.11	3.26	2.63
AAG	1.28	1.38	1.50	1.96	GAG	1.69	1.71	1.75	1.74
AAU	0.89	0.78	0.65	0.96	GAU	2.36	2.25	2.13	2.35
ACA	0.33	0.30	0.27	0.42	GCA	2.23	2.25	2.33	2.50
ACC	2.69	2.73	2.77	2.09	GCC	1.86	1.69	1.48	1.51
ACG	0.70	0.62	0.52	1.01	GCG	2.97	2.86	2.75	2.37
ACU	1.52	1.69	1.85	1.97	GCU	3.05	3.26	3.51	3.74
AGA	0.10	0.08	0.07	0.54	GGA	0.25	0.22	0.18	0.63
AGC	1.15	1.08	1.00	1.38	GGC	3.58	3.58	3.58	2.97
AGG	0.01	0.01	0.00	0.34	GGG	0.43	0.36	0.28	0.92
AGU	0.36	0.30	0.24	0.61	GGU	3.94	4.07	4.26	3.62
AUA	0.09	0.08	0.06	0.20	GUA	1.72	1.88	2.01	2.06
AUC	3.80	3.94	4.17	3.18	GUC	1.06	0.98	0.89	1.08
AUG	2.25	2.25	2.25	2.08	GUG	2.05	1.90	1.79	1.79
AUU	2.06	1.94	1.79	1.80	GUU	3.33	3.58	3.85	3.19
CAA	0.97	0.90	0.81	1.14	UAC	1.65	1.68	1.70	1.15
CAC	1.40	1.40	1.42	1.20	UAU	1.00	0.90	0.79	0.65
CAG	2.90	2.85	2.79	2.81	UCA	0.36	0.31	0.26	0.41
CAU	0.88	0.82	0.73	0.76	UCC	1.16	1.22	1.24	1.21
CCA	0.65	0.64	0.61	0.68	UCG	0.54	0.46	0.38	0.50
CCC	0.28	0.21	0.14	0.43	UCU	1.36	1.42	1.50	1.77
CCG	2.94	2.91	2.92	2.31	UGC	0.51	0.48	0.44	0.68
CCU	0.49	0.48	0.47	0.72	UGG	0.93	0.87	0.81	0.81
CGA	0.12	0.10	0.08	0.35	UGU	0.40	0.37	0.33	0.49
CGC	2.25	2.25	2.19	2.02	UUA	0.55	0.47	0.36	0.75
CGG	0.15	0.12	0.09	0.53	UUC	2.27	2.26	2.29	2.13
CGU	3.37	3.68	3.99	3.16	UUG	0.63	0.58	0.50	0.62
CUA	0.19	0.15	0.11	0.13	UUU	1.16	1.04	0.88	1.19
CUC	0.59	0.56	0.51	0.84					
CUG	6.10	6.17	6.21	5.28					
CUU	0.53	0.47	0.40	0.94					

References

1. Zhang G, Fedyunin I, Kirchner S, Xiao C, Valleriani A, et al. (2012) FANSe: an accurate algorithm for quantitative mapping of large scale sequencing reads. *Nucleic Acids Research* 40.
2. Dong H, Nilsson L, Kurland CG (1996) Co-variation of tRNA abundance and codon usage in *Escherichia coli* at different growth rates. *Journal of Molecular Biology* 260: 649-663.