

Table 1. Summary of information relevant to eIF gene expression.

Factor	Prot./cell	mRNA/cell ^a	Codon adapt. index ^b	Codon bias ^b	5'UTR length	Pred. sec. struct. of 5' UTR (kcal/mol) ^c	Other 5' UTR features
eIF1	250 000	12.5	0.239	0.243	20 (Yoon and Donahue, 1992)	- 1.5	
eIF1A	50 000	7.1	0.404	0.357	Not publ.	- 17.8 (80 nt)	uORFs?
eIF2 α	180 000	3.7	0.371	0.347	Not publ.	- 7.1 (80 nt)	
eIF2 β	180 000	5.8	0.285	0.313	64 (Donahue <i>et al.</i> , 1988)	- 6.3	
eIF2B α	30 000	2.4	0.140	0.029	Not publ.	- 7.5 (80 nt)	
eIF3g	100 000	8.3	0.249	0.298	Not publ.	- 13.7 (80 nt)	
eIF4A	800 000	21.4/17.0	0.753/0.751	0.772/ 0.772	Not publ.	- 1.8/-9.1	
eIF4B	155 000	5.2	0.351	0.443	Not publ.	- 8.5 (80 nt)	
eIF4E	340 000	15.6	0.387	0.380	84 (Altmann <i>et al.</i> , 1987)	- 15.1	
eIF4G1	17 500	3.4	0.251	0.324	295 (Goyer <i>et al.</i> , 1993)	- 56.9	6 uORFs
eIF4G2	ND	0.7	0.177	0.142	-300 (Goyer <i>et al.</i> , 1993)	- 68.4	uORFs
p20	350 000	7.3	0.356	0.377	Not publ.	- 8.1 (80 nt)	

a. From Holstege *et al.* (1998).

b. From SGD (<http://genome-www.stanford.edu/Saccharomyces/>).

c. Predicted using RNAfold (Mathews *et al.*, 1999).

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