TABLE 1. Codon misreading in vivo in *E. coli*

Codon and error type	Amino acid		Error	Frequency of error	Comments	References
	Normal	Substituted				
Basal-level errors						
AAC	Asn	Lys	Third-position C as purine	4×10^{-4}		231
AAU	Asn	Lys	Third-position U as purine	2×10^{-3}		231
CGU	Arg	Cys	First-position C as U	1×10^{-3}	One codon in *rplL*	28, 29
CGU/C	Arg	Cys	First-position C as U	5×10^{-5}	Average at 11 codons in *hag*	74
GGC	Gly	Ser	First-position G as A	1×10^{-3}		297
UGG	Trp	Cys	Third-position G as pyrimidine	3×10^{-3}		28, 29
UUU/C	Phe	Cys	Second-position U as G			170
Errors in stressed cells[a]						
AAA/G	Lys	Asn	Third-position pyrimidine as purine	8×10^{-3}	Substitution inferred	228
AGA	Arg	Lys	Second-position G as A	0.05–0.12	Substitution confirmed but misacylation not eliminated	271
AUA	Ile	Met	Third-position A as G	3×10^{-2}	Li and Parker, unpublished	
AUU	Ile	Met	Third-position U as G	3×10^{-2}	Li and Parker, unpublished	
CAC/U	His	Gln	Third-position pyrimidine as purine	>0.1	Substitution inferred	219, 232
UUU	Phe	Leu	Third-position U as purine	0.0–0.6	Very context dependent, misread position inferred (Precup, Ulrich, and Parker, unpublished)	233
UUC	Phe	Leu	Third-position C as purine	0.0–0.6	Very context dependent, misread position inferred (Precup, Ulrich, and Parker, unpublished)	233

[a] These errors are detected in stressed cells only. Stresses include limitation for an amino acid and, in the case of AGA, high-level production of a particular protein.

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