Table 1.5 Relative synonymous codon usage (*RSCU*) in bacteria (*E. coli*), yeast (*S. cerevisiae*), fruit fly (*D. melanogaster*), and human.

Amino Acid	Codon	Bacteria		Yeast		Fruit fly		Human	
		High[a]	Low[b]	High	Low	High	Low	G+C[c]	A+T[d]
Leu	UUA	0.06	1.24	0.49	1.49	0.03	0.62	0.05	0.99
	UUG	0.07	0.87	**5.34**	**1.48**	0.69	1.05	0.31	1.01
	CUU	0.13	0.72	0.02	0.73	0.25	0.80	0.20	1.26
	CUC	0.17	0.65	0.00	0.51	0.72	0.90	1.42	0.80
	CUA	0.04	0.31	0.15	0.95	0.06	0.60	0.15	0.57
	CUG	**5.54**	**2.20**	0.02	0.84	**4.25**	**2.04**	**3.88**	**1.38**
Val	GUU	**2.41**	**1.09**	**2.07**	**1.13**	0.56	0.74	0.09	1.32
	GUC	0.08	0.99	1.91	0.76	1.59	0.93	1.03	0.69
	GUA	1.12	1.63	0.00	1.18	0.06	0.53	0.11	0.80
	GUG	0.40	1.29	0.02	0.93	**1.79**	**1.80**	**2.78**	**1.19**
Ile	AUU	0.48	1.38	1.26	1.29	0.74	1.27	0.45	1.60
	AUC	**2.51**	**1.12**	**1.74**	**0.66**	**2.26**	**0.95**	**2.43**	**0.76**
	AUA	0.01	0.50	0.00	1.05	0.00	0.78	0.12	0.64
Phe	UUU	0.34	1.33	0.19	1.38	0.12	0.86	0.27	1.20
	UUC	**1.66**	**0.67**	**1.81**	**0.62**	**1.88**	**1.14**	**1.73**	**0.80**

Source: Modified from Sharp et al. (1988).
Note: Codons with the highest usage in the *High* genes and their corresponding usages in the *Low* genes are shown in boldface.
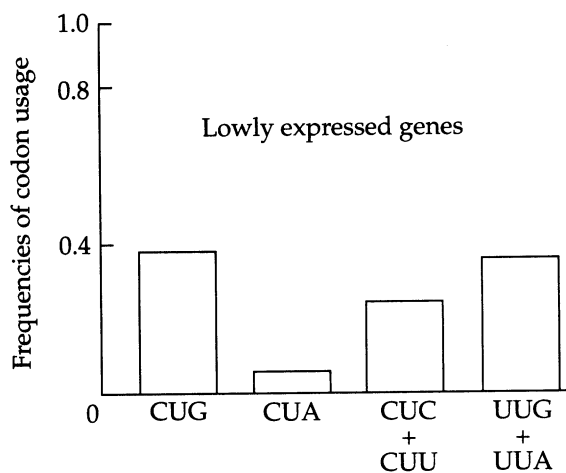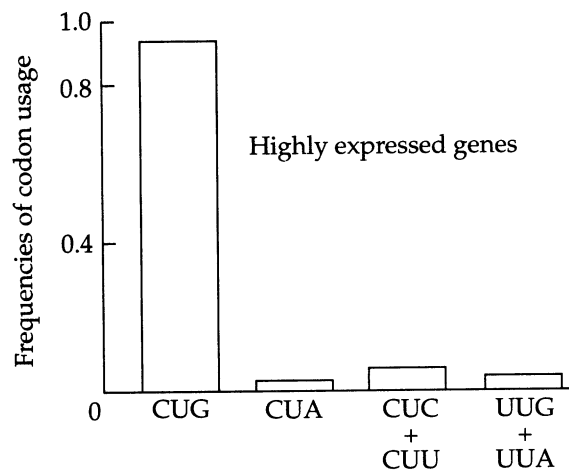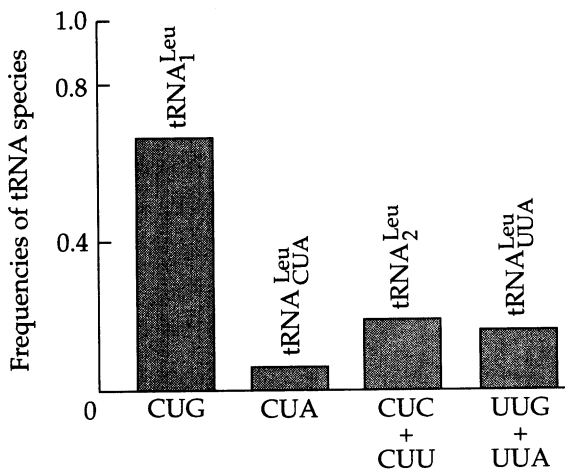
[a]*High* denotes genes with high levels of gene expression.
[b]*Low* denotes genes with low levels of gene expression.
[c]In humans, "G + C" refers to genes in GC-rich regions.
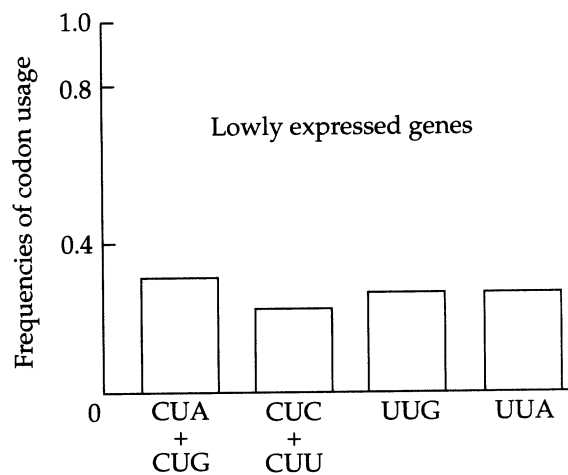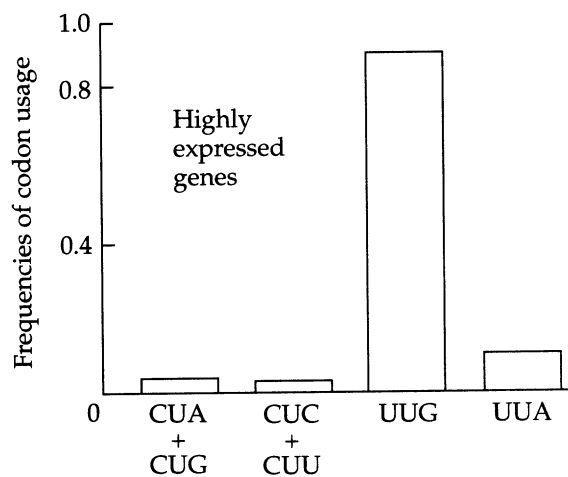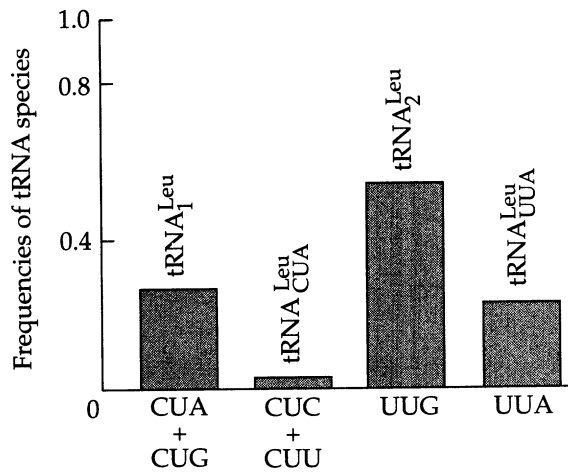[d]In humans, "A + T" refers to genes in AT-rich regions.

FIGURE 4.13 Diagram illustrating the relationship between the relative frequency of codon usage for leucine (open bars) and the relative abundance of the corresponding cognate tRNA species (gray bars) in (a) *Escherichia coli* and (b) the yeast *Saccharomyces cerevisiae*. The plus signs between codons indicate that the two condons are recognized by a single tRNA species (e.g., both CUC and CUU in *E. coli* are recognized by tRNA$_2^{Leu}$).