

Table 2. *E. coli* tRNAs and the codon recognition pattern

tRNA	Anticodon (5'-3')	Codon recognition (5'-3')	Spot number on 2D gel	No. of molecules per cell	Fraction of tRNA out of total tRNA (%)
Ala1B	UGC	GCU, GCA, GCG	46	3250(±223)	5.04
Ala2	GGC	GCC	28, 29	617(±64)	0.95
Arg2	ACG	CGU, CGC, CGA	21, 22	4752(±440)	7.37
Arg3	CCG	CGG	37	639(±63)	0.99
Arg4	UCU	AGA	17	867(±160)	1.34
Arg5	CCU	AGG	16	420(±69)	0.65
Asn	GUU	AAC, AAU	42	1193(±127)	1.85
Asp1	GUC	GAC, GAU	12	2396(±346)	3.72
Cys	GCA	UGC, UGU	25	1587(±126)	2.46
Gln1	UUG	CAA	31	764(±66)	1.18
Gln2	CUG	CAG	32	881(±94)	1.36
Glu2	UUC	GAA, GAG	47	4717(±411)	7.32
Gly1 ^a	CCC	GGG	24		
Gly2	UCC	GGA, GGG	24	2137(±320)	3.31
Gly3	GCC	GGC, GGU	34, 35	4359(±378)	6.76
His	GUG	CAC, CAU	26	639(±95)	0.99
Ile1	GAU	AUC, AUU	13	3474(±94)	5.39
Ile2 ^a	CAU	AUA	13		
Leu1	CAG	CUG	7	4470(±346)	6.94
Leu2	GAG	CUC, CUU	5	943(±97)	1.46
Leu3	UAG	CUA, CUG	23	666(±94)	1.03
Leu4	CAA	UUG	10, 11	1913(±190)	2.97
Leu5	UAA	UUA, UUG	2	1031(±117)	1.60
Lys	UUU	AAA, AAG	44	1924(±185)	2.97
Met f1	CAU	AUG	38	1211(±191)	1.88
Met f2	CAU	AUG	40	715(±107)	1.11
Met m	CAU	AUG	41	706(±96)	1.09
Phe	GAA	UUC, UUU	33	1037(±162)	1.60
Pro1	CGG	CCG	43	900(±150)	1.38
Pro2	GGG	CCC, CCU	27	720(±125)	1.11
Pro3	UGG	CCA, CCU, CCG	45	581(±95)	0.90
Sec	UCA	UGA	15	219(±73)	0.34
Ser1	UGA	UCA, UCU, UCG	4	1296(±94)	2.01
Ser2	CGA	UCG	3	344(±62)	0.53
Ser3	GCU	AGC, AGU	1	1408(±126)	2.18
Ser5	GGA	UCC, UCU	9	764(±127)	1.18
Thr1	GGU	ACC, ACU	14	104(±34)	0.16
Thr2	CGU	ACG	18	541(±94)	0.84
Thr3	GGU	ACC, ACU	19	1095(±62)	1.70
Thr4	UGU	ACA, ACU, ACC	8	916(±64)	1.42
Trp	CCA	UGG	39	943(±162)	1.46
Tyr1	GUA	UAC, UAU	49	769(±95)	1.19
Tyr2	GUA	UAC, UAU	48	1261(±126)	1.95
Val1	UAG	GUA, GUG, GUU	36	3840(±218)	5.96
Val2A	GAC	GUC, GUU	30	630(±98)	0.97
Val2B	GAC	GUC, GUU	20	635(±95)	0.98
4.5 S RNA			6	416(±63)	0.64

The assignment of individual tRNA identities to the electrophoretic components in the two-dimensional gel (Figure 1B) is represented by spot numbers. The number of tRNA molecules per cell and the fraction of tRNA out of total tRNA population in *E. coli* grown at 0.4 doubling per hour are shown here, as described in the text. ± stands for the standard deviations calculated from six independent measurements for each individual tRNA isoacceptor. The data on tRNA-codon recognition patterns were obtained from Komine *et al.* (1990), Björk (1995), Ikemura & Ozeki (1983), Ikemura (1985), Garcia *et al.* (1986) and Saxena & Walker (1992).

^a The tRNA isoacceptors Gly1 and Gly2 are treated collectively as is the data for Ile1 and Ile2.