

Table 4.2 Scores and Alignment Statistics

tRNA	Score	# σ	Matches	mms.	Indels
ala-1a	12.2	-0.2	14	2	0
ala-1b	12.2	-0.1	14	2	0
cys	21.0	6.2	40	10	5
asp-1	10.8	-1.1	22	8	2
glu-1	10.9	-0.8	21	9	1
glu-2	12.8	0.6	22	8	1
phe	13.0	0.6	32	10	5
gly-1	9.4	-1.4	15	4	1
gly-2	9.5	-1.2	35	15	6
gly-3	14.4	1.5	41	14	7
his-1	13.2	1.1	28	12	2
ile-1	13.6	0.9	41	26	2
ile-2	14.0	1.3	35	10	6
lys	10.7	-0.5	23	7	3
leu-1	13.8	0.7	49	28	5
leu-2	11.7	-0.7	33	17	3
leu-5	13.4	0.4	36	14	5
met-f	12.0	-0.03	44	20	7
met-m	11.4	-0.2	21	4	3
asn	15.3	2.4	33	13	3
gln-1	11.8	0.1	23	8	2
gln-2	12.1	0.2	26	11	2
arg-1	13.3	0.7	48	23	7
arg-2	12.8	0.3	26	8	3
ser-1	11.1	-1.3	29	11	4
ser-3	13.8	0.3	42	18	6
thr-ggt	10.1	-1.3	15	1	2
val-1	11.9	-0.2	22	9	1
val-2a	11.3	-0.7	14	3	0
val-2b	11.3	-0.4	14	3	0
trp	11.0	-0.7	22	10	1
tyr-1	11.7	-0.4	31	17	2
tyr-2	10.9	-0.9	42	19	7

σ , the number of standard deviations above the mean value (for comparing the two random sequences of similar lengths); mms., mismatches; indels, insertions/deletions.