

## Effective procedure to develop alternative annotations of bacterial tRNA genes by means of deductive inference on the basis of characteristic tandems of tRNA genes

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### Abstract

In a series of analysis of genomic DNA sequences, we have established an induction-deduction method to dig up hidden tRNA and rRNA genes from bacterial genome DNA sequences by means of a concept of a characteristic tRNA-gene tandem we have developed, and are accumulating information on positions of putative tRNA and rRNA genes to be proposed as alternative annotations to the DDBJ/GenBank/EMBL Database. We have searched the DNA sequences near the existing tRNA genes as golcondas for tRNA genes, and found more than fifty genes, e.g. tRNA-Ser and tRNA-Met in [AB013377], and 5S rRNAs in [AE014192], [AE017000], and others. A part of miserable states of the Database was partly introduced, and it is discussed how such status will be dissolved. In addition, we proposed some ideas to maintain and improve the DDBJ/GenBank/EMBL database.

### 1. Introduction(\*)

It is known that Archaeobacteria has several consensus gene clusters, e.g., " $\Sigma A \Delta \Phi$ " (note: our notation for [16S rRNA][tRNA-Ala][23S rRNA][5S rRNA]; See Appendix 1) in many species of *eutyarchaeota* and " $\Sigma \Delta \dots \Phi$ " in some species of *crenarchaeota*<sup>1)</sup>. Phylogenetical relationship among *Bacillus subtilis*<sup>2)</sup> and some Mycoplasma species (*Acholeoplasma laidlawii*,<sup>3)</sup> *Mycoplasma mycoides*<sup>4)</sup>, *Mycoplasma capricolum*<sup>5)</sup> and *Spiroplasma melliferum*<sup>6)</sup>) was discussed using several consensus clusters such as AtgeMeatIcat-Stga. We made an optimistic hypothesis that the cluster AMIS is characteristic of Gram-positive bacteria (including Mycoplasmas), and would be found neither in Gram-negative bacteria nor Archaeobacteria, and then made it clear that, in many cases, the AMIS consisted of Atge of a clus-

ter RacgPtggAtgc and another cluster MeatIcatStga<sup>7)</sup>. Since, at that time, we began to consider importance of the order of genes in a cluster, we temporarily used a term genic sequence of tRNA genes to avoid confusion with a DNA nucleotide sequence, and now we adopt a term tandem (See Appendix 1 on Notations.) We have edited an ongoing tandem index. Entries that were registered in our earliest time are exemplified as follows.: (M: Mycoplasmas, P: Gram-positive bacteria, N: Gram-negative bacteria, and A: Archae bacteria)  
M : Y(UAC)Q(CAA), and K(AAA)L(UUA),  
M & P : M(AUG)M/I(AUG)S(UCA), E(GAA)D-(GAC), and K(AAA)L(CUA),  
P : H(CAC)Q(CAA), and K(AAA)L(CUG),  
N : RH, LP, PHP, NL, G(GGA)T(ACC), M(AUG-)M(AUG), and  $\Sigma E(GAA) \Delta$ ,

A :T(ACA)P(CCA), D(DAC)K(AAA), and  $\Phi$  C(UGC),

M, P, N, & A(i.e. ubiquitous) : I(AUC)A(GCA)

Studying tandems annotated in the DDBJ/GenBank/EMBL Database, near the tandem D(ATC)F(GGC) of [U15182] of a Gram-positive bacterium *Mycobacterium leprae*, we accidentally found a new putative tandem EtcDgtc, and then detected deductively Fgaa (See [U15182] in Table 4). In order to know whether this induction-deduction method is useful, we tried to detect tRNA and/or rRNA genes. The present paper enumerates a collection of putative tRNA and sometimes also rRNA genes that we detected. They may be used as alternatives of the Annotations in the Database. Moreover, we insist necessity of any cooperation system for maintenance and improvement of quality of sets of original data and annotations in this complicated discipline.

## 2. Method

We use more than one procedure. A main one is a set of inductive and deductive inferences where we select arbitrarily a tRNA gene (as a part of a tandem) or a tandem as a clue to detect any hidden gene(s). The clue is treated as an imperfect tandem, and compared with other tandems to be perfect ones in the alignment manner and the like. Considering that a logical difference between them suggests a missing link, we search the DNA sequence containing subsequence of the clue for DNA subsequences of any hidden genes to be obtained as the logical difference between the (imperfect) clue and one of the (perfect) templates.

## 3. Result

We collected about 3200 tRNA-gene tandems from the DDBJ/GenBank/EMBL, Release 58. Table 1 displays a small part of them. Then we picked up about eight hundred names of relevant bacteria (data not shown). Table 2 shows our own classification system and a genus index consisting

of names and class codes of the genera. Table 3 exemplifies all of the tandems beginning with "H" for His. Table 4 lists the putative tRNA and rRNA genes we found which are underlined. Because the Annotations are always updated and improved, a part of our sauce data cited from the Database may be changed.

## 4. Consideration

We could show more examples, but stopped because we think these cases are enough to prove the power and usefulness of our induction-deduction method.

### 4.1 Detection of putative genes

#### 4.1.1 tRNA genes (Direct)

A few of the results are explained as follows.

We discovered accidentally a putative tandem EtcDgtc in [U15182] of the Gram-positive bacterium (*Mycobacterium leprae* B6-2-1-1-3-2-1) when we attempted to construct cloverleaf structures of the annotated tandem D(ATC)F(GGC). Then we made [ED] a clue, and searched our tandem index for any template tandems, which are VED ([X15246] *Lactobacillus* B6-1-2-1) and KEDF ([X00889] *Bacillus* B6-1-1-1-1). We found Fgtt downstream of the clue.

A clue [RG] [AB031213] (*Bacillus halodurans*). A template is RPG of [AP001508] (the same) and we found Ptgg at the corresponding position, the middle of the clue.

A clue [G] (a single gene) [AB031215] (*Bacillus halodurans*). The clue is compared with GRG [AP001516] (*Bacillus halodurans*), and R was found downstream of the first G.

A clue [AYHQGR] [AB013377] (*Bacillus halodurans*). The clue was aligned with ASMYHQGRG of [AP001516] (*Bacillus halodurans*), and we found a tandem SM between A and Y, and Q just on the second H, respectively. The subsequence downstream of R is too short for the second G to be found.

A clue [Q(CAA)V YQK] [AY224382] (*Bacillus cereus* B6-1-1-1-1). The clue was aligned with

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Table 1 A list of the tandems (Part)

@ A name of a bacterium(Genus and species,(strain))

Classification in the database

a tandem:tRNA genes(, rRNAs and CDS) and space length (bp) between them

[Accession Number] Complete/Fragment

@ *Acholeplasma laidlawii*

Bacteria; Firmicutes; Mollicutes; Acholeplasmatales; Acholeplasmataceae; *Acholeplasma*

16S	139	Igat	22	Atgc	70	23S [D13259] Frag.								
S???	2	Ettc [X61065] Frag.												
Hgtg	23	Qttg	28	Ltag [X61067] Frag.										
23S	63	5S	28	Vtac	8	Ttgt	6	Kttt	14	Ltaa	22	Atgc	4	5
		Mcat	4	Mcat	22	Stga	40	Mcat	24	Dgtc	7	Fgaa [X61068] Frag.		

@ *Agrobacterium tumefaciens* str. C58

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; *Agrobacterium*

16S	321	Igat	55	Atgc	471	~Atu0056	2978	5S	235	Mcat	152	recQ [AE008980] Frag.		
~Vtac	445	Dgtc	38	Dgtc [AE009088] Frag.										
~Atu1993	306	Ygta	22	Gtcc	266	Atu1990 [AE009151*] Frag.								
~purC	585	16S	321	Igat	55	Atgc	15	~Atu2544 [AE009201*] Frag.						
Igat	55	Atgc	471	~Atu3940	2978	5S	235	Mcat	46	Atu3945 [AE009325] Frag.				
~Atu4179	103	16S	308	Igat	55	Atgc	403	~Atu4183	2932	5S	236	Mcat	-	2.5
		~Atu4188 [AE009348] Frag.												

@ *Bacillus amyloliquefaciens*

Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*

16S	98	Igat	18	Atgc	83	23S [AF478079] Frag.							
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@ *Bacillus anthracis* str. Ames

Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group

purA	139	Kttt	13	Ettc	20	Dgtc	41	Fgaa	403	yycF	548601	BA5126	131	
	16S	178	23S	101	5S	4	Vtac	4	Ttgt	9	Hgtg	22	L t	
ag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg	15	Atgc	20	Mcat	4	
		Mcat	17	Stga	27	Mcat	1	Dgtc	12	Fgaa	14	Ttgt	10	K t
tt	13	Gtcc	10	Igat	7	Nggt	7	Sgct	6	Ettc	657	ldh-2	360	
546	BA4712	-15	Gtcc	1	Rtct	407	BA4711	3538237	~BA0720	138	~Ettc	1	~ N	
ggt	8	~Igat	10	~Wcca	6	~Ttgt	9	~Fgaa	8	~Dgtc	4	~Mcat	2	0
		~Stga	54	~Stga	20	~Atgc	16	~Ptgg	10	~Racg	3	~Ltaa	16	~ G
gcc	29	~Ltag	14	~Kttt	4	~Qttg	11	~Vtac	5	~5S	101	~23S	178	
	~16S	722	BA0719	198628	BA0540	207	~Lcaa	10	~Cgea	14	~Ggcc	5	~Qt	

tg	63	~Hgtg	19	~Wcca	7	~Ygta	10	~Ttgt	18	~Fgaa	9	~Dgtc	3
	~Mcat	24	~Vtac	5	~Ettc	17	~Sgga	2	~Nggt	8	~5S	100	~23
S	171	~16S	-5	~BA0539	236341	~purE	698	~5S	50	~23S	178	~16S	504
	BA0287	2748	bacA-1	450	~5S	50	~23S	178	~16S	-5	~BA0281	7355	B
A0273	137	~5S	49	~23S	178	~16S	322	~BA0272	13177	~BA0258	174	~Dgtc	3
	~Mcat	12	~5S	49	~23S	178	~16S	103	~Gtcc	1	~Ptgg	4	~Ra
cg	95	~Lgag	17	~Kttt	5	~Qttg	88	~Dgtc	46	~Vtac	4	~Ettc	8
	~Sgct	3	~Nggt	114	~BA0257	90939	~rocF	1470	~Atgc	10	~Ggcc	5	~Kt
tt	5	~Qttg	65	~Ygta	17	~Vtac	5	~Ettc	24	~Tggt	4	~Nggt	9
	~5S	86	~23S	178	~16S	-5	~BA0152	57544	~ctsR	206	~5S	49	~23
S	178	~16S	400	~lysS	13236	~spoIIE	352	~Ettc	13	~Mcat	160	~BA0060	292
99	~BA0025	190	~5S	48	~23S	94	~Atgc	8	~Igat	150	~16S	245	~bo
fA	11682	~guaB	1149	~5S	48	~23S	94	~Atgc	8	~Igat	150	~16S	268
	~gyrA	[AE016879*]	Comp.										
gyrA	268	16S	150	Igat	8	Atgc	94	23S	48	5S	1149	guaB	116
82	bofA	245	16S	150	Igat	8	Atgc	94	23S	48	5S	190	B
A0025	29299	BA0060	160	Mcat	13	Ettc	352	spoIIE	13236	lysS	400	16S	178
	23S	49	5S	206	ctsR	57544	BA0152	-5	16S	178	23S	86	5S
	9	Nggt	4	Tggt	24	Ettc	5	Vtac	17	Ygta	65	Qttg	5
	Kttt	5	Ggcc	10	Atgc	1470	rocF	90939	BA0257	114	Nggt	3	Sg
ct	8	Ettc	4	Vtac	46	Dgtc	88	Qttg	5	Kttt	17	Lgag	9 5
	Racg	4	Ptgg	1	Gtcc	103	16S	178	23S	49	5S	12	M
cat	3	Dgtc	174	BA0258	13177	BA0272	322	16S	178	23S	49	5S	137
	~BA0273	7355	BA0281	-5	16S	178	23S	50	5S	450	~bacA-1	2748	~ B
A0287	504	16S	178	23S	50	5S	698	purE	236341	BA0539	-5	16S	171
	23S	100	5S	8	Nggt	2	Sgga	17	Ettc	5	Vtac	24	M
cat	3	Dgtc	9	Fgaa	18	Ttgt	10	Ygta	7	Wcca	19	Hgtg	6 3
	Qttg	5	Ggcc	14	Cgca	10	Lcaa	207	~BA0540	198628	~BA0719	722	1 6
S	178	23S	101	5S	5	Vtac	11	Qttg	4	Kttt	14	Ltag	2 9
	Ggcc	16	Ltaa	3	Racg	10	Ptgg	16	Atgc	20	Stga	54	S t
ga	20	Mcat	4	Dgtc	8	Fgaa	9	Ttgt	6	Wcca	10	Igat	8
	Nggt	1	Ettc	138	BA0720	3538237	~BA4711	407	~Rtet	1	~Gtcc	-15	~ B
A4712	360546	~ldh-2	657	~Ettc	6	~Sgct	7	~Nggt	7	~Igat	10	~Gtcc	1 3
	~Kttt	10	~Ttgt	14	~Fgaa	12	~Dgtc	1	~Mcat	27	~Stga	17	~ M
cat	4	~Mcat	20	~Atgc	15	~Ptgg	10	~Racg	3	~Ltaa	16	~Ggcc	2 9
	~Ltag	22	~Hgtg	9	~Ttgt	4	~Vtac	4	~5S	101	~23S	178	~16
S	131	~BA5126	548601	~yycF	403	~Fgaa	41	~Dgtc	20	~Ettc	13	~Kttt	139
	~purA	[AE016879]	Comp.										
gyrA	268	16S	150	Igat	8	Atgc	94	23S	48	5S	1149	guaB	116
82	bofA	245	16S	150	Igat	8	Atgc	94	23S	48	5S	190	?C
DS	29299	?CDS	160	Mcat	13	Ettc	352	spoIIE	13236	lysS	400	16S	178
	23S	49	5S	206	ctsR	57544	?CDS	-5	16S	178	23S	86	5S



Table 2 The genera classification system and a genus index

## (a) Our classification system

**Class code and name**

A Archaea	B6-1-1-2 Paenibacillaceae	B12-1-3-3 Brucellaceae
A1 Euryarchaeota	B6-1-1-3Listeriaceae	B12-1-3-4 Methylobacteriaceae
A1-1 Archaeoglobi	B6-1-1-4Staphylococcus	B12-1-3-5 Phyllobacteriaceae
A1-1-1Archaeoglobales	B6-1-2 Lactobacillales	B12-1-3-6 Bartonellaceae
A1-1-1Archaeoglobaceae	B6-1-2-1 vCarnobacteriaceae	B12-1-4 Sphingomonadales
	B6-1-2-2Enterococcaceae	B12-1-4-1 Sphingomonadaceae
A1-2 Halobacteria	B6-1-2-3 Lactobacillaceae	B12-1-5Caulobacteriales
A1-2-1Halobacteriales	B6-1-2-4 Streptococcaceae	B12-1-5-1 Caulobacteraceae
A1-2-1-1Halobacteriaceae	B6-1-2-5 Weissella	B12-1-6 Rickettsiales
	B6-1-3 Mollicutes	B12-1-6-1 Rickettsiaceae
A1-3 Methanobacteria	B6-1-3-1 Acholeplasmatales	
A1-3-1Methanobacteriales	B6-1-3-1-1 Acholeplasmataceae	B12-2 Betaproteobacteria
A1-3-1-1Methanobacteriaceae	B3-1-3-2 Anaeroplasmatales	B12-2-1 Neisseriales
A1-3-1-2Methanothermaceae	B6-1-3-2-1Anaeroplasmataceae	B12-2-1-1Neisseriaceae
		B12-2-2 Burkholderiales
A1-4 Methanococci	B6-1-3-3Entomoplasmatales	B12-2-2-1Alcaligenaceae
A1-4-1Methanococcales	B6-1-3-3-1 Spiroplasmataceae	B12-2-2-2Burkholderiaceae
A1-4-1-1 Methanocaldococcaceae	B6-1-3-4 Mycoplasmataceae	B12-2-2-3Thiomonas
A1-4-1-2Methanococcaceae	B6-1-3-4-1Mycoplasmataceae	B12-2-2-4
	B6-1-4 Clostridia	B12-2-3 Nitrosomonadales
A1-5 Methanomicrobia	B6-1-4-1 Clostridiales	B12-2-3-1Nitrosomonadaceae
A1-5-1Methanosarcinales	B6-1-4-1-1 Acidaminococcaceae	
A1-5-1-1-Methanosarcinaceae	B6-1-4-1-2 Clostridiaceae	B12-3 Gammaproteobacteria
	B6-1-4-1-3 Ethanologenbacterium	B12-3-1 Acidithiobacillales
A1-6 Methanopyri	B6-1-4-1-4 Peptostreptococcaceae	B12-3-1-1 Acidithiobacillaceae
A1-6-1Methanopyrales	B6-1-4-2 Thermoanaerobacteriales	B12-3-2 Aeromonadales
A1-6-1-1Methanopyraceae	B6-1-4-2-1 Thermoanaerobacteriaceae	B12-3-2-1 Aeromonadaceae
	B6-2 High GC G-P	B12-3-3 Alteromonadales
A1-7 Thermococci	B6-2-1 Actinobacteria	B12-3-3-1 Alteromonadaceae
A1-7-1Thermococcales	B6-2-1-1Actinobacteridae	B12-3-4 Enterobacteriales
A1-7-1-1Thermococcaceae	B6-2-1-1-1 Actinomycetales	B12-3-4-1 Enterobacteriaceae
	B6-2-1-1-1-1Propionibacterineae	B12-3-5 Oceanospirillales
A1-8 Thermoplasma	B6-2-1-1-1-1-1Nocardiodiaceae	B12-3-5-1 Alcanivoraxaceae
A1-8-1Thermoplasmatales	B6-2-1-1-2Streptomycineae	B12-3-5-2 Halomonadaceae
A1-8-1-1Thermoplasmataceae	B6-2-1-1-2-1 Streptomycetaceae	B12-3-6 Pasteurellales
	B6-2-1-1-3 Corynebacterineae	B12-3-6-1 Pasteurellaceae
A2 Crenarchaeota	B6-2-1-1-3-1Corynebacteriaceae	B12-3-7 Pseudomonadales
A2-1 Thermoprotei	B6-2-1-1-3-2 Mycobacteriaceae	B12-3-7-1 Moraxellaceae
A2-1-1Sulfobacterales	B6-2-1-1-4 Micrococcineae	B12-3-8 Pseudomonadales
A2-1-1-1Sulfobacteraeae	B6-2-1-1-4-1 Cellulomonadaceae	B12-3-8-1Pseudomonadaceae
	B6-2-2W1-1-4-2 Micrococcaceae	B12-3-9 Thiotrichales
A2-1-2Thermoproteales	B6-2-1-1-2 Bifidobacteriales	B12-3-9-1 Piscirickettsiaceae
A2-1-2-1Thermofiliaceae	B6-2-1-1-2-1 Bifidobacteriaceae	B12-3-10 Vibrionales
		B12-3-10-1 Vibrionaceae
A2-1-2-2Thermoproteaceae		B12-3-11 Xanthomonadales
	B7 Fusobacteria	B12-3-11-1Xanthomonadaceae
B Bacteria	B7-1 Fusobacteriales	B12-3-12 Cardiobacteriales
B1 Nitrospirae	B7-1-1Fusobacteriaceae	B12-3-12-1 Cardiobacteriaceae
B1-1Nitrospirales		B12-3-13 Legionellales
B1-1-1Nitrospiraceae	B8 Bacteroidetes	B12-3-13-1 Coxiellaceae
	B8-1 Bacteroides (class)	B12-3-13-2 Pasteurellaceae
B2 Aquificae	B8-1-1 Bacteroidales	
B2-1Aquificales	B8-1-1-1Bacteroidaceae	B12-4 Deltaproteobacteria
B2-1-1 Aquificaceae	B8-1-1-2Porphyromonadaceae	B12-4-1 Desulfuovibrionales
	B8-1-1-3 Prevotellaceae	B12-4-2 Desulfuromonadales
B3 Thermotoga	B8-2 Sphingobacteria	B12-4-3 Myxococcales
B3-1Thermotogales	B8-2-1 Sphingobacteriales	B12-4-3-1 Sorangineae
B3-1-1Thermotogaceae	B8-2-1-1 Crenotrichaceae	B12-4-3-1-1 Polyangiaceae
	B8-2-1-2 Saprospiraceae	
B4 Deinococcus-Thermus		B12-5Epsilonproteobacteria
B4-1 Deinococci	B9 Chlorobi	B12-5-1 Campylobacteriales
B4-1-1Deinococcales	B9-1 Chlorobia	B12-5-1-1Campylobacteraceae
B4-1-1-1Deinococcaceae	B9-1-1 Chlorobiales	B12-5-1-2 Helicobacteraceae
B4-1-2Thermales	B9-1-1-1Chlorobiaceae	
B4-1-2-1 Thermaceae		
B5 Cyanobacteria	B10 Spirochaetes	
B5-1 Chroococcales	B10-1 Spirochaetales	
B5-1-1 Chroococcales	B10-1-1 Leptospiraceae	
B5-1-2Chroococcales	B10-1-2 Spirochaetaceae	
B5-1-3 Chroococcales		B11 Chlamydiae & Planctomycetes
B5-2 Nostocales	B11-1 Planctomycetes	B11-1 Planctomycetacia
B5-2-1 Microchaetaceae	B11-1-1 Planctomycetacia	B11-1-1-1 Planctomycetales
B5-2-2Nostocaceae	B11-2 Chlamydiae	B11-2-1 Chlamydiales
B5-2-3 Rivulariaceae	B11-2-1-1Chlamydiaceae	B11-2-2 Parachlamydiaceae
B5-2-4 Scytonemataceae		
B5-3 Oscillatoriales	B12 Proteobacteria	B12-1 Alphaproteobacteria
B5-4 Prochlorophytes	B12-1-1 Rhodospirillales	B12-1-1-1 Acetobacteraceae
B5-5 Stigonematales	B12-1-1-1 Rhodospirillaceae	B12-1-1-2 Rhodobacteriales
	B12-1-2 Rhodobacteraceae	B12-1-2-1 Rhodobacteraceae
B6 Firmicutes	B12-1-3 Rhizobiales	B12-1-3-1 Rhizobiaceae
B6-1 Low GC G-P	B12-1-3-1 Rhizobiaceae	B12-1-3-2 Bradyrhizobiaceae
B6-1-1 Bacillales		
B6-1-1-1 Bacillaceae		

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(b) a genera index		Mycoplasma	B6-1-3-4-1-1
Acetobacter	B12-1-1-1-1	Neisseria	B12-2-1-1-3
Acholeplasma	B6-1-3-1-1-1	Nitrosomonas	B12-2-3-1-1
Acidithiobacillus	B12-3-1-1-1	Nocardioioides	B6-2-1-1-1-1-1-1
Acinetobacter	B12-3-7-1-1	Nostoc	B5-2-2-2
Actinobacillus	B12-3-13-2-1	Novosphingobium	B12-1-4-1-1
Aeromonas	B12-3-2-1-1	Oceanobacillus	B6-1-1-1-3
Afiopia	B12-1-3-2-1	Ochrobactrum	B12-1-3-3-1
Agrobacterium	B12-1-3-1-1	Oscillatoria	B5-3-4
Alcanivorax	B12-3-5-1-1	Paenibacillus	B6-1-1-1-2-2
Aquifex	B2-1-1-1	Parachlamydia	B11-2-2-1
Anabena	B5-2-2-1	Paracoccus	B12-1-2-1-2
Anaeroplasma	B6-1-3-2-1-1	Pectobacterium	B12-3-4-1-5
Archaeoglobus	A1-1-1-1	Pelagibacter(candidatus)	B12-1-6-1-3
Antarctobacter	B12-1-2-1-1	Photobacterium	B12-3-10-1-2
Arsenophonus	B12-3-4-1-1	Photorhabdus	B12-3-4-1-6
Arthrospira	B5-3-1	Phytoplasma	B6-1-3-1-1-2
Azospirillum	B12-1-1-2-1	Pirellula	B11-1-1-1-1
Bacillus	B6-1-1-1-1	Piscirickettsia	B12-3-9-1-1
Bacteroides	B8-1-1-1-1	Polyanguim	B12-4-3-1-1-1
Bartonella	B12-1-3-6-1	Porphyromonas	B8-1-1-2-1
Bifidobacterium	B6-2-1-1-2-1-1	Prevotella	B8-1-1-3-1
Blastobacter	B12-1-3-2-2	Prochlorococcus	B5-4-1
Blochmannia(Candidatus)	B12-3-4-1-11	Pseudaminobacter	B12-1-3-5-2
Bordetella	B12-2-2-1-1	Pseudomonas	B12-3-8-1-1
Borrelia	B10-1-2-1	Pyrobaculum	A2-1-2-2-1
Bradyrhizobium	B12-1-3-2-3	Pyrococcus	A1-7-1-1-1
Brevibacillus	B6-1-1-1-2-1	Ralstonia	B12-2-2-2-2
Brocadia (Candidatus)	B11-1-1-1-2	Renibacterium	B6-2-1-1-4-2-2
Brucella	B12-1-3-3-2	Rhizobium	B12-1-3-1-2
Buchnera	B12-3-4-1-2	Rhodobacter	B12-1-2-1-3
Burkholderia	B12-2-2-2-1	Rhodopseudomonas	B12-1-3-2-4
Calothrix	B5-2-3-1	Rhodothermus	B8-2-1-1-1
Campylobacter	B12-5-1-1-1	Rickettsia	B12-1-6-1-1
Caulobacter	B12-1-5-1-1	Roseobacter	B12-1-2-1-4
Carnobacterium	B6-1-2-1-1	Roseovarius	B12-1-2-1-5
Chlamydia	B11-2-1-1-1	Ruegeria	B12-1-2-1-6
Chlamydomydia	B11-2-1-1-2	Salinibacter	B8-2-1-1-2
Chlorobium	B9-1-1-1-1	Salinivibrio	B12-3-10-1-3
Chlorogloeopsis	B5-5-1	Salmonella	B12-3-4-1-7
Chromobacterium	B12-2-1-1-1	Saprospira	B8-2-1-2-1
Clostridium	B6-1-4-1-2-1	Scytonema	B5-2-4-1
Coleodesmium	B5-2-1-1	Selenomonas	B6-1-4-1-1-1
Coxiella	B12-3-13-1-1	Shewanella	B12-3-3-1-1
Corynebacterium	B6-2-1-1-3-1-1	Shigella	B12-3-4-1-8
Cyanobium	B5-1-1-1	Sinorhizobium	B12-1-3-1-3
Deinococcus	B4-1-1-1-1	Sodalis	B12-3-4-1-9
Desulfovibrio	B12-4-1-1	Sphingomonas	B12-1-4-1-2
Dichelobacter	B12-3-12-1-1	Spiroplasma	B6-1-3-3-1-1
Enterococcus	B6-1-2-2-1	Staphylococcus	B6-1-1-4-1
Erwinia	B12-3-4-1-3	Streptococcus	B6-1-2-4-2
Escherichia	B12-3-4-1-4	Streptomyces	B6-2-1-1-2-1-1
Ethanoligenbacterium	B6-1-4-1-3-1	Sulfobolus	A2-1-1-1-1
Finegoldia	B6-1-4-1-4-1	Synechococcus	B5-1-2-1
Fischerella	B5-5-2	Synechocystis	B5-1-3-1
Fusobacterium	B7-1-1-1	Thermoanaerobacter	B6-1-4-2-1-1
Geitlerinema	B5-3-2	Thermococcus	A1-7-1-1-2
Geobacter	B12-4-2-1	Thermofilum	A2-1-2-1-1
Gloeotrichia	B5-2-3-2	Thermoplasma	A1-8-1-1-1
Gluconacetobacter	B12-1-1-1-2	Thermotoga	B3-1-1-1
Gluconobacter	B12-1-1-1-3	Thermus	B4-1-2-1-1
Haemophilus	B12-3-6-1-1	Thiomonas	B12-2-2-3-1
Haloarcula	A1-2-1-1-1	Tolypothrix	B5-2-1-2
Halobacterium	A1-2-1-1-2	Treponema	B10-1-2-2
Halococcus	A1-2-1-1-3	Trichodesmium	B5-3-6
Helicobacter	B12-5-1-2-1	Tropheryma	B6-2-1-1-4-1-1
Kueneria (Candidatus)	B11-1-1-1-3	Ureaplasma	B6-1-3-4-1-2
Lactobacillus	B6-1-2-3-1	Vibrio	B12-3-10-1-4
Lactococcus	B6-1-2-4-1	Wautersia	B12-2-2-2-3
Leptospira	B10-1-1-1	Weissella	B6-1-2-5-1
Leptospirillum	B1-1-1-1	Wolbachia	B12-1-6-1-2
Liberibacter (candidatus)	B12-1-3-1-4	Xanthomonas	B12-3-11-1-1
Limnithrix	B5-3-5	Xylella	B12-3-11-1-2
Listeria	B6-1-1-1-3-1	Xylophilus	B12-2-2-4-1
Listonella	B12-3-10-1-1	Yersinia	B12-3-4-1-10
Marinibacillus	B6-1-1-1-2	Zymobacter	B12-3-5-2-1
Mesorhizobium	B12-1-3-5-1	Zymomonas	B12-1-4-1-3
Methanobacterium	A1-3-1-1-2		
Methanocaldococcus	A1-4-1-1-1		
Methanococcus	A1-4-1-2-1		
Methanopyrus	A1-6-1-1-1		
Methanosarcina	A1-5-1-1-1		
Methanothermobacter	A1-3-1-1-1		
Methanothermus	A1-3-1-2-1		
Methylobacterium	B12-1-3-4-1		
Microchaetaceae	B5-2-1-3		
Micrococcus	B6-2-1-1-4-2-1		
Microcoleus	B5-3-3		
Microvirgula	B12-2-1-1-2		
Mycobacterium	B6-2-1-1-3-2-1		

Table 3. (I) A list of tRNA gene tandems (The H section for His)

Heading		Class code		bacterial name		Acc. No				
---	---	15	Hatg	23	-gseA	---	B11-2-1-1-2	Chlamydomonadales CWL029	[AE001602*]	
34	taub	68469	CFj01	94	@Hatg	---	B11-2-1-1-2	Chlamydomonadales J138	[AP002545*]	
34	taub	68558	CFn01	94	@Hatg	---	B11-2-1-1-2	Chlamydomonadales J138	[AE001363*]	
21	Ettc	39	Ltag	14	@Hgtg	299	16S	Methanocaldococcus jannaschii	[U067517]	
106	Ptgg	31	Rctt	27	@Hgtg	---	B9-1-1-1-1	Chlorobium tepidum TLS	[AE012843]	
106	Ptgg	31	Rctt	27	@Hgtg	---	B9-1-1-1-1	Chlorobium tepidum TLS	[AE006470]	
---	---	---	BB060	9	@Hgtg	264	Ggcc	Borrelia burgdorferi B31	[AE001162]	
4	Dgtc	4	Fgaa	26	@Hgtg	22	Gtcc	Listeria innocua	[AL592022*]	
4	Dgtc	4	Fgaa	26	@Hgtg	22	Gtcc	Listeria innocua	[AL596170*]	
4	Dgtc	4	Fgaa	28	@Hgtg	23	Gtcc	Listeria monocytogenes	[AL591980*]	
4	Dgtc	4	Fgaa	28	@Hgtg	23	Gtcc	Listeria monocytogenes EGD-e	[NC_003210*]	
4	Dgtc	4	Fgaa	28	@Hgtg	24	Gtcc	Listeria monocytogenes str. 4b F2365	[AE017327*]	
11	Dgtc	12	Fgaa	16	@Hgtg	10	Gtcc	Bacillus subtilis	[K00637]	
11	Dgtc	12	Fgaa	16	@Hgtg	10	Gtcc	Bacillus subtilis	[AL009126*]	
11	Dgtc	12	Fgaa	16	@Hgtg	10	Gtcc	Bacillus subtilis	[AF008220]	
11	Dgtc	12	Fgaa	17	@Hgtg	10	Gtcc	Bacillus subtilis subsp. subtilis str. 168	[Z99119*]	
13	Dgtc	12	Fgaa	17	@Hgtg	10	Gtcc	Bacillus subtilis	[K01390]	
14	Dgtc	10	Fgaa	13	@Hgtg	17	Gtcc	Staphylococcus epidermidis ATCC 12228	[AE016749*]	
21	Dgtc	16	Fgaa	13	@Hgtg	15	Gtcc	Staphylococcus aureus subsp. aureus MW2	[AP004828*]	
14	Dgtc	10	Fgaa	13	@Hgtg	17	Gtcc	Staphylococcus epidermidis ATCC 12228	[AE015929*]	
21	Dgtc	16	Fgaa	13	@Hgtg	15	Gtcc	Staphylococcus aureus subsp. aureus N315	[AP003135*]	
21	Dgtc	16	Fgaa	13	@Hgtg	15	Gtcc	Staphylococcus aureus subsp. aureus N315	[BA000018*]	
21	Dgtc	19	Fgaa	13	@Hgtg	18	Gtcc	Staphylococcus aureus subsp. aureus Mu50	[AP003363*]	
21	Dgtc	19	Fgaa	13	@Hgtg	18	Gtcc	Staphylococcus aureus subsp. aureus Mu50	[BA000017*]	
18	Rctt	27	Hgtg	45	@Hgtg	26	Hgtg	Chromobacterium violaceum ATCC 12472	[AE016916*]	
18	Rctt	27	Hgtg	45	@Hgtg	26	Hgtg	Chromobacterium violaceum ATCC 12472	[AE016825*]	
225	Ptgg	18	Rctt	27	@Hgtg	45	Hgtg	Chromobacterium violaceum ATCC 12472	[AE016916*]	
225	Ptgg	18	Rctt	27	@Hgtg	45	Hgtg	Chromobacterium violaceum ATCC 12472	[AE016825*]	
176	Ptgg	63	Rctt	39	@Hgtg	110	Kctt	Xylella fastidiosa Temecula	[AE012561]	
162	Ptgg	43	Rctt	31	@Hgtg	83	Kctt	Xanthomonas campestris pv. campestris str. ATCC 33913	[AE012195]	
162	Ptgg	43	Rctt	31	@Hgtg	83	Kctt	Xanthomonas campestris str. ATCC 33913	[AE008922]	
176	Ptgg	63	Rctt	39	@Hgtg	110	Kctt	Xylella fastidiosa Temecula	[AE009442]	
176	Ptgg	61	Rctt	39	@Hgtg	110	Kctt	Xylella fastidiosa 9a5c	[AE004082]	
176	Ptgg	61	Rctt	39	@Hgtg	110	Kctt	Xylella fastidiosa	[AE0003849]	
107	Ptgg	7	Gtcc	10	@Hgtg	3	Kctt	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	[AE010498*]	
107	Ptgg	7	Gtcc	10	@Hgtg	3	Kctt	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	[AE009951*]	
53792	ansP3	148	Rccg	83	@Hgtg	16	Lcag	Yersinia pestis biovar Mediaevalis str. 91001	[AE017042]	
53792	ansP3	148	Rccg	83	@Hgtg	16	Lcag	Yersinia pestis biovar Mediaevalis str. 91001	[AE017139]	
---	---	---	Rccg	49	@Hgtg	20	Lcag	Aeromonas hydrophila	[X12977]	
---	---	---	Rccg	57	@Hgtg	20	Lcag	Escherichia coli	[K01994]	
---	?	CDS	102	Rccg	53	@Hgtg	20	Lcag	Salmonella typhimurium	[M95047]



## Effective procedure to develop alternative annotations of bacterial tRNA genes by means of deductive inference on the basis of characteristic tandems of tRNA genes

---	yifK	102	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	---	---	---	---	---	B12-3-4-1-4	Escherichia coli K12	[AE000455]	
45462	yifK	283	Rccg	76	@Hgtg	15	Lcag	42	Ptgg	987	ISPl	###	orn	199	Ggcc ->	B12-3-4-1-6	Photorhabdus luminescens subsp. laumondii TTO1	[BX470251*]
45462	yifK	283	Rccg	76	@Hgtg	15	Lcag	42	Ptgg	987	ISPl	###	orn	199	Ggcc ->	B12-3-4-1-6	Photorhabdus luminescens subsp. laumondii TTO1	[BX571874*]
---	ECs47	102	Rccg	58	@Hgtg	20	Lcag	43	Ptgg	22	Lcag	44	Ptgg	146	ECs47 ->	B12-3-4-1-4	Escherichia coli O157:H7	[AF002567]
32881	ECs47	102	Rccg	58	@Hgtg	20	Lcag	43	Ptgg	22	Lcag	44	Ptgg	146	ECs47 ->	B12-3-4-1-4	Escherichia coli O157:H7	[BA000007]
70027	STY36	102	Rccg	54	@Hgtg	20	Lcag	42	Ptgg	581	-STY3	###	STY3!	380	16S ->	B12-3-4-1-7	Salmonella enterica subsp. enterica serovar Typhi	[AL513382*]
55124	YPO38	148	Rccg	83	@Hgtg	16	Lcag	75	Ptgg	866	YPO3	---	---	---	---	B12-3-4-1-10	Yersinia pestis CO92	[AJ414159*]
---	yifK	102	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	146	asLB	---	---	---	---	B12-3-4-1-4	Escherichia coli O157:H7 EDL933	[AE005611]
---	yifK	233	Rccg	58	@Hgtg	20	Lcag	42	Ptgg	116	asLB	---	---	---	---	B12-3-4-1-8	Shigella flexneri 2a str. 301	[AR015394]
32046	yifK	102	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	146	asLB	---	---	---	---	B12-3-4-1-4	Escherichia coli CFT073	[AR016769]
---	yifK	102	Rccg	58	@Hgtg	20	Lcag	42	Ptgg	146	asLB	###	hemG	377	16S ->	B12-3-4-1-8	Shigella flexneri 2a str. 2457T	[AE016990*]
32000	yifK	233	Rccg	58	@Hgtg	20	Lcag	42	Ptgg	116	asLB	###	hemG	377	16S ->	B12-3-4-1-8	Shigella flexneri 2a str. 301	[AE005674]
32000	yifK	102	Rccg	58	@Hgtg	20	Lcag	42	Ptgg	146	asLB	###	hemG	377	16S ->	B12-3-4-1-8	Shigella flexneri 2a str. 2457T	[AE014073*]
32046	yifK	102	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	146	asLB	###	hemG	377	16S ->	B12-3-4-1-4	Escherichia coli CFT073	[AE014075]
33128	yifK	102	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	146	asLB	###	hemG	380	16S ->	B12-3-4-1-4	Escherichia coli O157:H7	[AR005174]
33151	yifK	102	Rccg	57	@Hgtg	20	Lcag	42	Ptgg	146	asLB	###	hemG	377	16S ->	B12-3-4-1-4	Escherichia coli	[U000096]
7202	rho	296	Rccg	71	@Hgtg	30	Lcag	12	Ptgg	101	-hemD	###	-purH	428	16S ->	B12-3-4-1-11	Candidatus Blochmannia floridanus	[BX248583*]
7202	rho	296	Rccg	71	@Hgtg	30	Lcag	12	Ptgg	101	-hemD	###	-purH	428	16S ->	B12-3-4-1-11	Candidatus Blochmannia floridanus	[BX248586*]
---	yifK	102	Rccg	57	@Hgtg	23	Lcag	45	Ptgg	584	-hemy	---	---	---	---	B12-3-4-1-7	Salmonella typhimurium LT2	[AE008883]
70027	yifK	102	Rccg	54	@Hgtg	20	Lcag	42	Ptgg	581	-hemy	---	---	---	---	B12-3-4-1-7	Salmonella enterica subsp. enterica serovar Typhi	[AL627279*]
70029	yifK	102	Rccg	54	@Hgtg	20	Lcag	42	Ptgg	581	-hemy	###	hemG	387	16S ->	B12-3-4-1-7	Salmonella enterica subsp. enterica serovar Typhi Ty2	[AE016845*]
70029	yifK	102	Rccg	54	@Hgtg	20	Lcag	42	Ptgg	581	-hemy	###	hemG	387	16S ->	B12-3-4-1-7	Salmonella enterica subsp. enterica serovar Typhi Ty2	[AE014613*]
33026	yifK	102	Rccg	57	@Hgtg	23	Lcag	45	Ptgg	584	-hemy	###	hemG	377	16S ->	B12-3-4-1-7	Salmonella typhimurium LT2	[AE006466]
55124	YPO38	148	Rccg	83	@Hgtg	16	Lcag	75	Ptgg	866	tmp	###	hemG	501	16S ->	B12-3-4-1-10	Yersinia pestis	[AL590842*]
---	Y0375	148	Rccg	86	@Hgtg	19	Lcag	-35	~Y0376	---	---	---	---	---	---	B12-3-4-1-10	Yersinia pestis KIM	[AR013638]
55125	Y0375	148	Rccg	86	@Hgtg	19	Lcag	-35	~Y0376	###	hemG	475	16S	59	Igat ->	B12-3-4-1-10	Yersinia pestis KIM	[AE009952]
96981	-fold-	293	Rtct	51	@Hgtg	56	Ltag	571	?CDS	---	---	---	---	---	---	B12-3-8-1-1	Pseudomonas syringae pv. tomato str. DC3000	[AE016869*]
39	?CDS	1E+05	?CDS	28	@Hgtg	50	Ltag	37	?CDS	###	~?CDS	52	-Rtct	35	-Gtcc ->	B4-1-2-1-1	Thermus thermophilus HB27	[AE017221]
39	?CDS	1E+05	?CDS	28	@Hgtg	50	Ltag	37	?CDS	###	~?CDS	52	-Rtct	35	-Gtcc ->	B4-1-2-1-1	Thermus thermophilus HB27	[AE017301]
---	---	---	-DR092:	176	@Hgtg	52	Ltag	141	DR092	---	---	---	---	---	---	B4-1-1-1-1	Deinococcus radiodurans R1	[AE001945*]
-398	DR126	3E+05	-DR092:	176	@Hgtg	52	Ltag	141	DR092	###	~DR06	197	Ptgg	20	Gtcc ->	B4-1-1-1-1	Deinococcus radiodurans	[AE000513*]
361	Vtac	4	Ttgt	9	@Hgtg	22	Ltag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg ->	B6-1-1-1-1	Bacillus cereus ATCC 14579	[AE017013*]
361	Vtac	4	Ttgt	9	@Hgtg	22	Ltag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg ->	B6-1-1-1-1	Bacillus cereus ATCC 14579	[AE016877*]
4	Vtac	4	Ttgt	9	@Hgtg	22	Ltag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg ->	B6-1-1-1-1	Bacillus cereus	[AY224388]
4	Vtac	4	Ttgt	9	@Hgtg	22	Ltag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg ->	B6-1-1-1-1	Bacillus anthracis str. Ames	[AE016879*]
4	Vtac	4	Ttgt	9	@Hgtg	22	Ltag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg ->	B6-1-1-1-1	Bacillus anthracis str. Ames	[AR017039*]
4	Vtac	4	Ttgt	9	@Hgtg	22	Ltag	29	Ggcc	16	Ltaa	3	Racg	10	Ptgg ->	B6-1-1-1-1	Bacillus anthracis str. Ames 0581	[AE017334*]
---	-fold	278	Rtct	51	@Hgtg	54	Ltag	66	Hgtg	697	~?CDS	---	---	---	---	B12-3-8-1-1	Pseudomonas aeruginosa PAO1	[AE004605]
1E+06	-fold	278	Rtct	51	@Hgtg	54	Ltag	66	Hgtg	697	-PAL7	###	PR28	-124	-Ggcc ->	B12-3-8-1-1	Pseudomonas aeruginosa	[AE004091]
96981	-fold-	293	Rtct	51	@Hgtg	56	Ltag	571	PSPT0	###	~PSPT	1722	16S	103	Igat ->	B12-3-8-1-1	Pseudomonas syringae pv. tomato str. DC3000	[AE016853*]
47	Ptgg	5	Rtct	25	@Hgtg	62	Ltag	115	tig	1885	loN-	139	Dgtc	11	Vtac ->	B12-4-2-1	Geobacter sulfurreducens PCA	[AR017180*]
47	Ptgg	5	Rtct	25	@Hgtg	62	Ltag	115	tig	1885	loN-	139	Dgtc	11	Vtac ->	B12-4-2-1	Geobacter sulfurreducens PCA	[AE017213*]
719	Nggt	1	Mcat	13	@Hgtg	26	Mcat	13	Stga	152	Fgaa	169	OB19	---	---	B6-1-1-1-3	Oceanobacillus iheyensis HTE831	[AF004599*]

719	Nggt	1	Mcat	13	@Hgtg	26	Mcat	13	Stga	152	Fgaa	169	OB19:####	-OB09(-> B6-1-1-1-3	Oceanobacillus iheyensis	[BA000028*]		
---	---	---	Ptgg	8	@Hgtg	53	Ptgg	---	---	---	---	---	---	---	Photobacterium phosphoreum	[X12975]		
34	Hgtg	76	Ptgg	49	@Hgtg	64	Ptgg	---	---	---	---	---	---	---	Vibrio harveyi	[M29762]		
53	Ptgg	174	Ptgg	8	@Hgtg	149	Ptgg	---	---	---	---	---	---	---	Photobacterium phosphoreum	[X12976]		
---	---	---	Rccg	29	@Hgtg	24	Ptgg	180	16S	131	Ettc	274	23S	247	5S	Haemophilus influenzae Rd KW20	[U32697*]	
1283	Mcat	2418	Rccg	29	@Hgtg	24	Ptgg	180	16S	131	Ettc	274	23S	247	5S	Haemophilus influenzae Rd	[L42023*]	
57958	wecg	157	Rccg	30	@Hgtg	29	Ptgg	202	16S	80	Ettc	198	23S	242	5S	Haemophilus ducreyi 35000HP	[AE017156*]	
57958	wecg	157	Rccg	30	@Hgtg	29	Ptgg	202	16S	80	Ettc	198	23S	242	5S	Haemophilus ducreyi 35000HP	[AE017143*]	
41	Hgtg	29	Ptgg	77	@Hgtg	27	Ptgg	1282	?CDS	###	?CDS	167	Ettc	4	Kttt	Vibrio vulnificus CMCP6	[AE016800]	
34	Hgtg	66	Ptgg	9	@Hgtg	51	Ptgg	723	AGAD	---	---	---	---	---	---	Photobacterium profundum	[CR378663]	
---	---	---	Rccg	34	@Hgtg	76	Ptgg	49	Hgtg	64	Ptgg	---	---	---	---	Vibrio harveyi	[M29762]	
14144	-?CDS	254	Rccg	41	@Hgtg	29	Ptgg	77	Hgtg	27	Ptgg	1282	?CDS	###	?CDS	Vibrio vulnificus CMCP6	[AE016800]	
14517	-NMB16	294	Rccg	34	@Hgtg	66	Ptgg	9	Hgtg	51	Ptgg	723	AGAD	---	---	Photobacterium profundum	[CR378663]	
---	-VC016	289	Rccg	35	@Hgtg	61	Ptgg	70	Hgtg	61	Ptgg	435	-VC01	----	----	Vibrio cholerae O1 biovar eltor str. NI6961	[AF004107]	
9186	-VC016	289	Rccg	35	@Hgtg	61	Ptgg	70	Hgtg	61	Ptgg	435	-VC01	###	VC03:-->	Vibrio cholerae	[AE003852]	
9312	-VP004	337	Rccg	32	@Hgtg	72	Ptgg	49	Hgtg	24	Ptgg	66	-VP00	----	----	Vibrio parahaemolyticus	[AF005073]	
9312	-VP004	337	Rccg	32	@Hgtg	72	Ptgg	49	Hgtg	24	Ptgg	66	-VP00	###	VP05(->	Vibrio parahaemolyticus RIMD 2210633	[BA000031]	
9269	-VV004	254	Rccg	38	@Hgtg	26	Ptgg	74	Hgtg	24	Ptgg	942	-VV00	###	-VV01(->	Vibrio vulnificus YJ016	[AF005330]	
9269	-VV004	254	Rccg	38	@Hgtg	26	Ptgg	74	Hgtg	24	Ptgg	942	-VV00	###	-VV01(->	Vibrio vulnificus YJ016	[BA000037]	
14144	-VV110	254	Rccg	41	@Hgtg	29	Ptgg	77	Hgtg	27	Ptgg	1282	VV11	###	VV11:-->	Vibrio vulnificus CMCP6	[AE016795]	
---	-?CDS	206	Rccg	52	@Hgtg	15	Ptgg	53	Ptgg	184	-?CDS	----	----	----	----	Shewanella oneidensis MR-1	[AE015865*]	
176	Ptgg	176	Ptgg	8	@Hgtg	53	Ptgg	174	Ptgg	8	Hgtg	149	Ptgg	----	----	Photobacterium phosphoreum	[X12976]	
2B+05	-S0432	206	Rccg	52	@Hgtg	15	Ptgg	53	Ptgg	184	-S043:###	seca	716	16S	->	Shewanella oneidensis MR-1	[AF014299*]	
35	Hgtg	61	Ptgg	70	@Hgtg	61	Ptgg	435	-VC016	----	----	----	----	----	----	Vibrio cholerae O1 biovar eltor str. NI6961	[AF004107]	
35	Hgtg	61	Ptgg	70	@Hgtg	61	Ptgg	435	-VC016	###	VC03: -25	16S	63	Igat	->	Vibrio cholerae	[AE003852]	
32	Hgtg	72	Ptgg	49	@Hgtg	24	Ptgg	66	-VP004	----	----	----	----	----	----	Vibrio parahaemolyticus	[AF005073]	
32	Hgtg	72	Ptgg	49	@Hgtg	24	Ptgg	66	-VP004	###	VP05	85	16S	177	Aggc	->	Vibrio parahaemolyticus RIMD 2210633	[BA000031]
38	Hgtg	26	Ptgg	74	@Hgtg	24	Ptgg	942	-VV004	###	-VV01	537	16S	68	Ettc	->	Vibrio vulnificus YJ016	[AF005330]
38	Hgtg	26	Ptgg	74	@Hgtg	24	Ptgg	942	-VV004	###	-VV01	537	16S	68	Ettc	->	Vibrio vulnificus YJ016	[BA000037]
41	Hgtg	29	Ptgg	77	@Hgtg	27	Ptgg	1282	VV110	###	VV11: 167	Ettc	4	Kttt	->	Vibrio vulnificus CMCP6	[AE016795]	
---	rho	100	Rccg	39	@Hgtg	33	Ptgg	1773	-cyay	----	----	----	----	----	----	Buchnera aphidicola str. Sg (Schizaphis graminum)	[AE014131*]	
---	rho	282	Rccg	40	@Hgtg	35	Ptgg	91	-cyay	###	aroE	204	Ettc	159	23S	->	Buchnera aphidicola str. Bp (Baizongia pistaciae)	[AE014017*]
---	rho	100	Rccg	39	@Hgtg	33	Ptgg	1773	-cyay	###	dut	734	-Meat	133	Nggt	->	Buchnera aphidicola str. Sg (Schizaphis graminum)	[AE013218*]
---	rho	282	Rccg	40	@Hgtg	35	Ptgg	91	-cyay	###	-pyrE	118	-Meat	193	Nggt	->	Buchnera aphidicola (Baizongia pistaciae)	[AF016826*]
---	rho	188	Rccg	29	@Hgtg	36	Ptgg	757	-hemC	###	aroE	152	Ettc	161	23S	->	Buchnera aphidicola str. APS (Acyrthosiphon pisum)	[AP001119*]
---	rho	188	Rccg	29	@Hgtg	36	Ptgg	757	-hemC	###	-pyrE	95	-Meat	134	Nggt	->	Buchnera sp. APS	[AF000398*]
4	Ygta	8	Wcca	2	@Hgtg	11	Qttg	5	Cgca	9	Gtcc	14	Gtcc	11	Gtcc	->	Staphylococcus epidermidis ATCC 12228	[AE015929*]
4	Ygta	8	Wcca	2	@Hgtg	11	Qttg	5	Cgca	9	Gtcc	14	Gtcc	11	Gtcc	->	Staphylococcus epidermidis ATCC 12228	[AE016749*]
5	Ygta	15	Wcca	2	@Hgtg	11	Qttg	5	Cgca	7	Gtcc	103	Gtcc	38	Lcaa	->	Staphylococcus aureus subsp. aureus N315	[AF003135*]
5	Ygta	15	Wcca	2	@Hgtg	11	Qttg	5	Cgca	7	Gtcc	103	Gtcc	38	Lcaa	->	Staphylococcus aureus subsp. aureus MW2	[AF004828*]
5	Ygta	15	Wcca	2	@Hgtg	11	Qttg	5	Cgca	7	Gtcc	103	Gtcc	38	Lcaa	->	Staphylococcus aureus subsp. aureus N315	[BA000018*]
8	Ygta	15	Wcca	5	@Hgtg	11	Qttg	5	Cgca	10	Gtcc	106	Gtcc	41	Lcaa	->	Staphylococcus aureus subsp. aureus Mu50	[AF003363*]
8	Ygta	15	Wcca	5	@Hgtg	11	Qttg	5	Cgca	10	Gtcc	106	Gtcc	41	Lcaa	->	Staphylococcus aureus subsp. aureus Mu50	[BA000017*]

Effective procedure to develop alternative annotations of bacterial tRNA genes by means of deductive inference on the basis of characteristic tandems of tRNA genes

5	Ygta	4	Wcca	36	@Hgtg	14	Qttg	25	Cgca	13	Lcaa	576	~?CDS	---	----	B6-1-2-2-1	Enterococcus faecalis V583	[AE016950]	
4	Ygta	7	Wcca	14	@Hgtg	4	Qttg	20	Cgca	31	Lcaa	115	?CDS	2136	?CDS	->	B6-1-2-3-1	Lactobacillus johnsonii NCC 533	[AE017198*]
4	Ygta	7	Wcca	14	@Hgtg	4	Qttg	20	Cgca	31	Lcaa	115	?CDS	2136	?CDS	->	B6-1-2-3-1	Lactobacillus johnsonii NCC 533	[AE017205*]
5	Ygta	4	Wcca	36	@Hgtg	14	Qttg	25	Cgca	13	Lcaa	576	~EF10:####	EF13:->	----	B6-1-2-2-1	Enterococcus faecalis V583	[AF016830]	
5	Ygta	7	Wcca	59	@Hgtg	9	Qttg	27	Cgca	37	Lcaa	89	labJ	---	----	B6-1-2-3-1	Lactobacillus sakei	[AF401668]	
5	Ygta	8	Wcca	5	@Hgtg	7	Qttg	22	Cgca	55	Lcaa	150	~lp_1:####	lp_1:->	B6-1-2-3-1	Lactobacillus plantarum WCFS1	[AL935263]		
5	Ygta	8	Wcca	5	@Hgtg	7	Qttg	22	Cgca	55	Lcaa	150	~lp_1:####	uvrA:->	B6-1-2-3-1	Lactobacillus plantarum WCFS1	[AL935255]		
10	Ygta	7	Wcca	19	@Hgtg	63	Qttg	5	Ggcc	14	Cgca	10	Lcaa	---	----	B6-1-1-1-1	Bacillus cereus	[AY224386]	
20	Ygta	7	Wcca	15	@Hgtg	29	Qttg	5	Ggcc	19	Cgca	45	Lcaa	348	?CDS	---B6-1-1-3-1	Listeria monocytogenes str. 4b F2365	[AF017330*]	
10	Ygta	7	Wcca	19	@Hgtg	63	Qttg	5	Ggcc	14	Cgca	10	Lcaa	206	~?CDS	---B6-1-1-1-1	Bacillus cereus ATCC 14579	[AF016999]	
10	Ygta	7	Wcca	19	@Hgtg	63	Qttg	5	Ggcc	14	Cgca	10	Lcaa	207	~?CDS	---B6-1-1-1-1	Bacillus anthracis str. Ames	[AE017025]	
10	Ygta	7	Wcca	19	@Hgtg	63	Qttg	5	Ggcc	14	Cgca	10	Lcaa	207	~?CDS	->	B6-1-1-1-1	Bacillus anthracis str. Ames 0581	[AE017334]
10	Ygta	7	Wcca	19	@Hgtg	63	Qttg	5	Ggcc	14	Cgca	10	Lcaa	487	?CDS	->	B6-1-1-1-1	Bacillus cereus ATCC 10987	[AE017266]
10	Ygta	7	Wcca	19	@Hgtg	63	Qttg	5	Ggcc	14	Cgca	10	Lcaa	207	~BA05:->	B6-1-1-1-1	Bacillus anthracis str. Ames	[AF016879]	
10	Ygta	7	Wcca	19	@Hgtg	63	Qttg	5	Ggcc	14	Cgca	10	Lcaa	206	~BC05:->	B6-1-1-1-1	Bacillus cereus ATCC 14579	[AF016877]	
15	Ygta	15	Wcca	5	@Hgtg	24	Qttg	2	Ggcc	8	Cgca	4	Lcaa	186	OB09(---	B6-1-1-1-3	Oceanobacillus iheyensis HFB831	[AF004596]	
15	Ygta	15	Wcca	5	@Hgtg	24	Qttg	2	Ggcc	8	Cgca	4	Lcaa	186	OB09(->	B6-1-1-1-3	Oceanobacillus iheyensis	[BA000028]	
22	Ygta	7	Wcca	14	@Hgtg	31	Qttg	5	Ggcc	19	Cgca	45	Lcaa	187	lin2:->	B6-1-1-3-1	Listeria innocua	[AL596172*]	
22	Ygta	7	Wcca	14	@Hgtg	31	Qttg	5	Ggcc	19	Cgca	45	Lcaa	187	lin2:->	B6-1-1-3-1	Listeria innocua	[AL592022*]	
20	Ygta	7	Wcca	15	@Hgtg	29	Qttg	5	Ggcc	19	Cgca	45	Lcaa	351	lmo2:---	B6-1-1-3-1	Listeria monocytogenes	[AL591983*]	
20	Ygta	7	Wcca	15	@Hgtg	29	Qttg	5	Ggcc	19	Cgca	45	Lcaa	351	lmo2:->	B6-1-1-3-1	Listeria monocytogenes EGD-e	[NC_003210*]	
19	Ygta	5	Wcca	24	@Hgtg	9	Qttg	46	Ggcc	5	Cgca	4	Ltaa	265	Lcaa	->	B6-1-1-1-1	Bacillus subtilis subsp. subtilis str. 168	[Z99108]
22	Ygta	5	Wcca	24	@Hgtg	9	Qttg	49	Ggcc	5	Cgca	7	Ltaa	265	Lcaa	---	B6-1-1-1-1	Bacillus subtilis	[K01389]
22	Ygta	5	Wcca	24	@Hgtg	9	Qttg	49	Ggcc	5	Cgca	7	Ltaa	265	Lcaa	->	B6-1-1-1-1	Bacillus subtilis	[AL009126]
22	Ygta	5	Wcca	24	@Hgtg	9	Qttg	49	Ggcc	5	Cgca	7	Ltaa	265	Lcaa	->	B6-1-1-1-1	Bacillus subtilis	[Z82044]
54	Ygta	11	Wcca	18	@Hgtg	13	Qttg	4	Ggcc	7	Cgca	26	Ltaa	15	Racg	->	B6-1-1-1-1	Bacillus halodurans C-125	[AP001510]
154	Atgc	363	Ygta	12	@Hgtg	15	Qttg	4	Ggcc	1	Racg	---	----	----	----	B6-1-1-1-1	Bacillus halodurans	[AB013377]	
171	Meat	5	Ygta	12	@Hgtg	15	Qttg	4	Ggcc	1	Racg	185	Gtcc	41	~BH28:->	B6-1-1-1-1	Bacillus halodurans C-125	[AF001516*]	
54	Ygta	11	Wcca	18	@Hgtg	13	Qttg	4	Ggcc	464	~TnpA	---	----	----	----	B6-1-1-1-1	Bacillus halodurans	[AB031215]	
7	Gtcc	82	Rtct	7	@Hgtg	6	Qttg	9	Kttt	22	Kttt	13	Ltag	29	Ggcc	->	B6-1-4-1-2-1	Clostridium perfringens str. 13	[AP003193*]
7	Gtcc	82	Rtct	7	@Hgtg	6	Qttg	9	Kttt	22	Kttt	13	Ltag	29	Ggcc	->	B6-1-4-1-2-1	Clostridium perfringens	[BA000016*]
---	Gtcc	4	Rtct	11	@Hgtg	3	Qttg	4	Kttt	38	Lcag	5	Ggcc	25	Kctt	->	B6-1-4-1-1-1	Thermoanaerobacter tengcongensis	[AE013030*]
198	Gtcc	4	Rtct	11	@Hgtg	3	Qttg	4	Kttt	38	Lcag	5	Ggcc	25	Kctt	->	B6-1-4-2-1-1	Thermoanaerobacter tengcongensis	[AE008691*]
10	Gtcc	9	Kctt	17	@Hgtg	7	Qttg	25	Kttt	6	Ltag	18	Ggcc	8	Gtcc	->	B6-1-4-1-2-1	Clostridium acetobutylicum	[AE001437*]
10	Gtcc	9	Kctt	17	@Hgtg	7	Qttg	25	Kttt	6	Ltag	18	Ggcc	8	Gtcc	->	B6-1-4-1-2-1	Clostridium acetobutylicum	[AF007764*]
4	Rtct	4	Kctt	11	@Hgtg	9	Qttg	3	Kttt	23	Ltag	19	Ggcc	11	Gtcc	->	B6-1-4-1-2-1	Clostridium tetani E88	[AF015944*]
4	Rtct	4	Kctt	11	@Hgtg	9	Qttg	3	Kttt	23	Ltag	19	Ggcc	11	Gtcc	->	B6-1-4-1-2-1	Clostridium tetani E88	[AE015927*]
6	Gtcc	38	Rtct	7	@Hgtg	8	Qttg	10	Kttt	13	Ltag	26	Ggcc	6	Gtcc	->	B6-1-4-1-2-1	Clostridium perfringens str. 13	[AP003193*]
6	Gtcc	38	Rtct	7	@Hgtg	8	Qttg	10	Kttt	13	Ltag	26	Ggcc	6	Gtcc	->	B6-1-4-1-2-1	Clostridium perfringens	[BA000016*]
9	Gtcc	9	Rtct	16	@Hgtg	7	Qttg	25	Kttt	6	Ltag	18	Ggcc	8	Gtcc	->	B6-1-4-1-2-1	Clostridium acetobutylicum	[AF007764*]
9	Gtcc	9	Rtct	16	@Hgtg	7	Qttg	25	Kttt	6	Ltag	18	Ggcc	8	Gtcc	->	B6-1-4-1-2-1	Clostridium acetobutylicum	[AF001437*]
2	Fgaa	98	Wcca	18	@Hgtg	6	Qttg	-1	Lcaa	---	----	----	----	----	----	B6-1-2-4-2	Streptococcus agalactiae	[AF302130]	
11	Ygta	34	Wcca	18	@Hgtg	6	Qttg	0	Lcaa	---	----	----	----	----	----	B6-1-2-4-2	Streptococcus agalactiae	[AF302131]	

12	Ygta	6	Wcca	13	@Hgtg	16	Qttg	14	Lcaa	82	~?CDS	---	---	---	---	B6-1-2-4-2	Streptococcus mutans UA159	[AE014870]	
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	309	SAG0'	---	---	---	---	B6-1-2-4-2	Streptococcus agalactiae 2603V/R	[AE014202]	
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	410	SAG0'	---	---	---	---	B6-1-2-4-2	Streptococcus agalactiae 2603V/R	[AF014195]	
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	410	SAG0'	####	SAG0'	403	16S	->	B6-1-2-4-2	Streptococcus agalactiae	[AE009948]
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	309	SAG0'	####	yfia	329	16S	->	B6-1-2-4-2	Streptococcus agalactiae	[AE009948]
12	Ygta	6	Wcca	13	@Hgtg	16	Qttg	14	Lcaa	82	~SMU'	####	SMU'	104	~Scga	->	B6-1-2-4-2	Streptococcus mutans UA159	[AE014133]
12	Ygta	4	Wcca	14	@Hgtg	10	Qttg	9	Lcaa	106	SP20'	---	---	---	---	B6-1-2-4-2	Streptococcus pneumoniae TIGR4	[AE007495*]	
12	Ygta	4	Wcca	14	@Hgtg	10	Qttg	9	Lcaa	106	SP20'	####	SP20'	93	Ettc	->	B6-1-2-4-2	Streptococcus pneumoniae	[AF005672*]
19	Ygta	6	Wcca	11	@Hgtg	8	Qttg	19	Lcaa	1767	SPs0'	####	SPs0'	1096	16S	->	B6-1-2-4-2	Streptococcus pyogenes SSI-1	[AP005141]
19	Ygta	6	Wcca	11	@Hgtg	8	Qttg	19	Lcaa	1767	SPs0'	####	SPs0'	1096	16S	->	B6-1-2-4-2	Streptococcus pyogenes SSI-1	[BA000034]
19	Ygta	6	Wcca	11	@Hgtg	9	Qttg	19	Lcaa	259	SPy0'	---	---	---	---	B6-1-2-4-2	Streptococcus pyogenes M1 GAS	[AE006479]	
19	Ygta	6	Wcca	11	@Hgtg	9	Qttg	19	Lcaa	259	SPy0'	####	oppF	1089	16S	->	B6-1-2-4-2	Streptococcus pyogenes	[AE004092]
19	Ygta	6	Wcca	11	@Hgtg	8	Qttg	19	Lcaa	259	SPyM'	---	---	---	---	B6-1-2-4-2	Streptococcus pyogenes MGAS315	[AF014137]	
19	Ygta	6	Wcca	11	@Hgtg	8	Qttg	19	Lcaa	259	SPyM'	####	oppF	1096	16S	->	B6-1-2-4-2	Streptococcus pyogenes MGAS315	[AE014074]
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	413	gbs0'	---	---	---	---	B6-1-2-4-2	Streptococcus agalactiae NEM316	[AL766843]	
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	141	gbs0'	####	gbs0'	369	16S	->	B6-1-2-4-2	Streptococcus agalactiae NEM316	[AL732656]
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	141	gbs0'	####	gbs0'	369	16S	->	B6-1-2-4-2	Streptococcus agalactiae NEM316	[AL766844]
11	Ygta	6	Wcca	14	@Hgtg	6	Qttg	10	Lcaa	413	gbs0'	####	gbs0'	445	16S	->	B6-1-2-4-2	Streptococcus agalactiae NEM316	[AL732656]
12	Ygta	4	Wcca	14	@Hgtg	10	Qttg	9	Lcaa	106	sprl'	---	---	---	---	B6-1-2-4-2	Streptococcus pneumoniae R6	[AF008551*]	
12	Ygta	4	Wcca	14	@Hgtg	10	Qttg	9	Lcaa	106	sprl'	####	comX	93	Ettc	->	B6-1-2-4-2	Streptococcus pneumoniae	[AE007317*]
---	---	---	---	---	@Hgtg	23	Qttg	28	Ltag	---	---	---	---	---	---	B6-1-3-1-1-1	Acholeplasma laidlawii	[X61067]	
---	ackA	46	Sgga	443	@Hgtg	88	Qttg	53	Ltag	23	Wcca	431	?CDS	####	pepP	->	B6-1-3-1-1-2	Onion yellows phytoplasma OY-M	[AF006628]
---	ackA	46	Sgga	443	@Hgtg	88	Qttg	53	Ltag	23	Wcca	431	PAML'	####	pepP	->	B6-1-3-1-1-2	Onion yellows phytoplasma	[AF006628]
---	?CDS	146	Ptgg	22	@Hgtg	20	Rtgc	44	~?CDS	####	~?CDS	25	Qttg	85	Mcat	->	B12-5-1-2-1	Helicobacter hepaticus ATCC 51449	[AF017144]
---	HH003	146	Ptgg	22	@Hgtg	20	Rtgc	44	~HH003	####	~HH02'	25	Qttg	85	Mcat	->	B12-5-1-2-1	Helicobacter hepaticus ATCC 51449	[AE017125]
---	HP041	-230	Ptgg	68	@Hgtg	60	Rtgc	25	Rtct	29	HP04'	---	---	---	---	B12-5-1-2-1	Helicobacter pylori 26695	[AE000557]	
53393	HP041	-230	Ptgg	68	@Hgtg	60	Rtgc	25	Rtct	29	HP04'	####	~HP04'	648	23S	->	B12-5-1-2-1	Helicobacter pylori 26695	[AE000511]
34566	CJ166	42	Ptgg	24	@Hgtg	3	Rtgc	14	Rtct	4	Ltag	174	CJ16'	####	~ribD	->	B12-5-1-1-1	Campylobacter jejuni	[AL111168*]
34678	CJ166	42	Ptgg	24	@Hgtg	3	Rtgc	14	Rtct	4	Ltag	174	CJ16'	####	~ribD	->	B12-5-1-1-1	Campylobacter jejuni subsp. jejuni NCTC 11168	[AL139079*]
88	Gtcc	14	Rtct	14	@Hgtg	8	Rtgc	73	TM019	---	---	---	---	---	---	B3-1-1-1	Thermotoga maritima	[AF001704*]	
88	Gtcc	14	Rtct	14	@Hgtg	8	Rtgc	73	TM019	####	~TM01'	48	~5S	37	~23S	->	B3-1-1-1	Thermotoga maritima	[AE000512*]
---	---	---	---	---	@Hgtg	14	Rtgc	80	TP063	---	---	---	---	---	---	B10-1-2-2	Treponema pallidum subsp. pallidum str. Nichols	[AE001239*]	
1E+05	~TP063	-30	~Fgaa	136	@Hgtg	14	Rtgc	80	TP063	####	~TP05'	159	Mcat	69	Dgtc	->	B10-1-2-2	Treponema pallidum	[AE000520*]
---	---	---	---	---	@Hgtg	32	Rtgc	106	rpsD	---	---	---	---	---	---	B10-1-2-2	Treponema denticola ATCC 35405	[AF017252*]	

Effective procedure to develop alternative annotations of bacterial tRNA genes by means of deductive inference on the basis of characteristic tandems of tRNA genes

Table 3. (2) Candidates of characteristic tRNA-gene tandems whose headings begin with H. (for His)

Heading	Class code	bacterial name
@Hgtg	Hatg	Chlamydomonadales
@Hgtg	16S Atgc 23S	Methanocaldococcus jannaschii
@Hgtg	Ettc	Chlorobium tepidum
@Hgtg	Ggcc	Borrelia burgdorferi
@Hgtg	Gtcc	Bacillus, Listeria
@Hgtg	Gtcc Igat	Bacillus, Listeria
@Hgtg	Gtcc Igat Nggt	Bacillus, Listeria
@Hgtg	Gtcc Igat Nggt Sgct	Bacillus, Listeria
@Hgtg	Gtcc Igat Nggt Sgct Ettc	Bacillus, Listeria
@Hgtg	Gtcc Nggt	Staphylococcus
@Hgtg	Gtcc Nggt Ettc	Staphylococcus
@Hgtg	Gtcc Nggt Ettc Sgga	Staphylococcus
@Hgtg	Hgtg	Chromobacterium violaceum
@Hgtg	Hgtg Hgtg	Chromobacterium violaceum
@Hgtg	Kctt	Fusobacterium, Xanthomonas, Xylella
@Hgtg	Kctt Lttag	Fusobacterium, Xanthomonas
@Hgtg	Kttt Lttag Qttg	Fusobacterium nucleatum
@Hgtg	Lcag	Aeromonas, Blochmannia, Escherichia, Photorhabdus, Pseudomonas, Salmonella, Shigella, Yersinia
@Hgtg	Lcag Ptgg	Aeromonas, Blochmannia, Escherichia, Photorhabdus, Salmonella, Shigella, Yersinia
@Hgtg	Lcag Ptgg Lcag	Escherichia coli
@Hgtg	Lcag Ptgg Lcag Ptgg	Escherichia coli
@Hgtg	Ltag	Deinococcus, Thermus; Bacillus ; Geobacter, Pseudomonas
@Hgtg	Ltag Ggcc	Bacillus
@Hgtg	Ltag Ggcc Lttaa	Bacillus
@Hgtg	Ltag Ggcc Lttaa Racg	Bacillus
@Hgtg	Ltag Ggcc Lttaa Racg Ptgg	Bacillus
@Hgtg	Ltag Hgtg	Pseudomonas aeruginosa
@Hgtg	Mcat	Oceanobacillus iheyensis
@Hgtg	Mcat Stga	Oceanobacillus iheyensis
@Hgtg	Mcat Stga Fgaa	Oceanobacillus iheyensis
@Hgtg	Ptgg	Buchnera, Haemophilus, Photobacterium, Shewanella, Vibrio
@Hgtg	Ptgg 16S	Haemophilus ducreyi
@Hgtg	Ptgg 16S Ettc	Haemophilus ducreyi
@Hgtg	Ptgg 16S Ettc 23S	Haemophilus ducreyi
@Hgtg	Ptgg 16S Ettc 23S 5S	Haemophilus ducreyi
@Hgtg	Ptgg Hgtg	Vibrio
@Hgtg	Ptgg Hgtg Ptgg	Vibrio
@Hgtg	Ptgg Ptgg	B11, B12 Photobacterium, Shewanella
@Hgtg	Ptgg Ptgg Hgtg	Photobacterium phosphoreum
@Hgtg	Ptgg Ptgg Ptgg	Photobacterium phosphoreum
@Hgtg	Qttg	Enterococcus, Lactobacillus, Staphylococcus

@Hgtg	Qttg	Cgca		B6-1	Enterococcus, Lactobacillu, Staphylococcus
@Hgtg	Qttg	Cgca	Gtcc	B6-1-1-4-1	Staphylococcus
@Hgtg	Qttg	Cgca	Gtcc	B6-1-1-4-1	Staphylococcus
@Hgtg	Qttg	Cgca	Gtcc	B6-1-1-4-1	Staphylococcus epidermidis
@Hgtg	Qttg	Cgca	Gtcc	B6-1-1-4-1	Staphylococcus epidermidis
@Hgtg	Qttg	Cgca	Gtcc	Lcaa	Staphylococcus aureus
@Hgtg	Qttg	Cgca	Lcaa	B6-1-2	Enterococcus, Lactobacillus
@Hgtg	Qttg	Ggcc		B6-1-1	Bacillus, Listeria, Oceanobacillus
@Hgtg	Qttg	Ggcc	Cgca	B6-1-1	Bacillus, Listeria, Oceanobacillus
@Hgtg	Qttg	Ggcc	Cgca	B6-1-1	Bacillus, Listeria, Oceanobacillus
@Hgtg	Qttg	Ggcc	Cgca	Lcaa	Bacillus subtilis
@Hgtg	Qttg	Ggcc	Cgca	Lcaa	Bacillus subtilis
@Hgtg	Qttg	Ggcc	Cgca	Ltaa	Bacillus halodurans
@Hgtg	Qttg	Ggcc	Racy	B6-1-1-1-1	Bacillus halodurans
@Hgtg	Qttg	Ggcc	Racy	B6-1-1-1-1	Bacillus halodurans
@Hgtg	Qttg	Ggcc	Racy	B6-1-1-1-1	Bacillus halodurans
@Hgtg	Qttg	Kttt		B6-1-4-1	Clostridium, Thermoaerobacter
@Hgtg	Qttg	Kttt	Kttt	B6-1-4-1	Clostridium, Thermoaerobacter
@Hgtg	Qttg	Kttt	Kttt	B6-1-4-1	Clostridium, Thermoaerobacter
@Hgtg	Qttg	Kttt	Kttt	B6-1-4-1	Clostridium, Thermoaerobacter
@Hgtg	Qttg	Kttt	Kttt	B6-1-4-1-2-1	Clostridium
@Hgtg	Qttg	Kttt	Ltag	B6-1-4-1-2-1	Clostridium
@Hgtg	Qttg	Kttt	Ltag	B6-1-4-1-2-1	Clostridium
@Hgtg	Qttg	Kttt	Ltag	B6-1-4-1-2-1	Clostridium
@Hgtg	Qttg	Lcaa		B6-1-2-4-2	Streptococcus
@Hgtg	Qttg	Ltag		B6-1-3-1-1	Acholeplasma, Phytoplasma
@Hgtg	Qttg	Ltag	Wcca	B6-1-3-1-1-2	Onion yellows phytoplasma
@Hgtg	Rtctg			B3, B10, B12	Tehrnotoga, Treponema, Campylobacter, Helicobacter
@Hgtg	Rtctg	Rtct		B12-5-1-2-1	Campylobacter, Helicobacter
@Hgtg	Rtctg	Rtct	Ltag	B12-5-1-1-1	Campylobacter Jejuni

Effective procedure to develop alternative annotations of bacterial tRNA genes by means of deductive inference on the basis of characteristic tandems of tRNA genes

Table 4. Examples of putative genes newly detected  
Accession tRNA and/or rRNA gene tandem  
No.

AB013377 AStea(1300-1388gta)Mcat(1574-1646acca)YHQttg(1844-1914acca)GR  
 AB031213 NSEVDLLRPtgg(2595-2667acca)GI  $\Sigma$   $\wedge$   $\Phi$   
 AB031215 GRacg(9668-9740gccca)  
 AB071783  $\Sigma$  IAtgc(320-394acca)  $\wedge$  [Cf. // A(455-531)/]  
 AE000052 CPM|cat(6625-6696)SMDF  
 AE000129 Atgc(5476-5547aaca), Dgtc(8906-8986gccca) [Cf. (A or B)tgc(5476-5551), (D or V)gtc(8906-8990)]  
 AE000406 complement Atgc(tggt5721-5792) [Cf. //(A or B)tgc//]  
 AE000453 Dgtc(3233-3305gccca)W [Cf. //(D or OTHER)gtc//]  
 AE001652 G(1733-1802)E(4945-5019)K(5045-5117) [Cf. complement G(1733-1803),and complement EK ]  
 AE006473  $\Sigma$   $\wedge$   $\Phi$ (9535-9649)VDKLTGLRP  
 AE006474  $\Sigma$   $\wedge$   $\Phi$ (5002-5116)VGIESMFGIS  
 AE006479  $\Sigma$   $\wedge$   $\Phi$ (5551-5661)VGIESMFYWHQL  
 AE006496  $\Sigma$   $\wedge$   $\Phi$ (5937-6051)NR  
 AE006592 complement EITLKDV  $\Phi$ (6697-6891)  $\wedge$   $\Sigma$   
 AE006615 complement, RN  $\Phi$ (932-1046)  $\wedge$   $\Sigma$   
 AE007319  $\Sigma$   $\wedge$   $\Phi$ (5764-5878)N, [ Cf. //  $\Phi$ (5755-5902)N(5883-// overlap( $\Phi$  & N))]  
 AE008706 Igat(10816-10888)Atgc(11002-11073) [Cf. I(10826-10899)[A or B](11012-11084)]  
 AE014136  $\Sigma$   $\wedge$   $\Phi$ (22026-22140)VDKLTGLRP,  $\Sigma$   $\wedge$   $\Phi$ (28028-28143)VDKLTGLRPMMSMFGIS,  
 AE014137  $\Sigma$   $\wedge$   $\Phi$ (33169-33283)VGIESMFYWHQL  
 AE014141  $\Sigma$   $\wedge$   $\Phi$ (5613-5717)NR  
 AE014162 complement EITLKDV  $\Phi$ (22529-22743)  $\wedge$   $\Sigma$   
 AE014168 complement, RN  $\Phi$ (933-1047)  $\wedge$   $\Sigma$   
 AE014192  $\Phi$ (10-124)VDKLTGLRP  $\Sigma$   $\wedge$   $\Phi$ (5841-5955)VDKLTGLRPMMSMFGIS  
 AE014195  $\Sigma$   $\wedge$   $\Phi$ (17811-17925)VDKLTIE  
 AE014202  $\Sigma$   $\wedge$   $\Phi$ (17813-17927)VGIESMFYWHQL  
 AE014207  $\Sigma$   $\wedge$   $\Phi$ (9537-9654)N [Cf. //  $\Phi$ (9519-9679)N(9660-// overlap( $\Phi$  & N))]  
 AE014210  $\Sigma$   $\wedge$   $\Phi$ (1048810602)VGIE  
 AE015714 complement Kittt(869-1049) long D-loop (tgccctagctttataaaaaag:22 n) Not a tRNA or ctttataaaaaag to be deleted  
 AE016998  $\Sigma$   $\wedge$   $\Phi$ (155848-155961)NTEVYQ  
 AE016999  $\Sigma$   $\wedge$   $\Phi$ (207456-207570)NSEVMDFTYWHQGCL  
 AE017000  $\Sigma$   $\wedge$   $\Phi$ (114882-114995)VYKLOGLRPASSMDFTWNE  
 AE017013 complement ESNIGKTFDMSMMAPLGLHTV  $\Phi$ (269750-269861)  $\wedge$   $\Sigma$   
 AE017205 complement N  $\Phi$   $\wedge$  (146140-146905)  $\Sigma$  [Cf. //  $\Phi$ (-145978)  $\wedge$  (145965-149015)// overlap( $\Phi$  &  $\wedge$ )]  
 AE017205 complement N  $\Phi$   $\wedge$  (152807-155682)  $\Sigma$  [Cf. //  $\Phi$ (-152645)  $\wedge$  (152632-155682)// overlap( $\Phi$  &  $\wedge$ )]  
 AE017205 complement N  $\Phi$   $\wedge$  (167256-170131)  $\Sigma$  [Cf. //  $\Phi$ (-167094)  $\wedge$  (167081-170131)// overlap( $\Phi$  &  $\wedge$ )]  
 AE017280 complement E(GAA)(t32876-32946)S(AGC)(tggc32957-33043)N(AAC)(tggc33055-33125)(AUC)(tggt33137-33209)  
 [Cf. E(32875-32946)S(32953-33043)N(33051-33125)(33133-33209)]  
 AE017280 complement G(GGA)(a33221-33290)K(AAA)(tggt33308-33379)T(ACA)(tggt33394-33465)F(uuc)(tggt33484-33555)

- [Cf. G(33220-33290)K(33304-33379)T(33390-33465)F(33480-33555)D(33568-33643)]  
 AE017280 complement D(GAC)(tggc33572-33643)M(AUG)(tgg33649-33721)S(UCA)(tgg33753-33841)M(AUG)(tgg33863-33935)  
 [Cf. M(33645-33721)S(33749-33841)M(33859-33935)]  
 AE017280 complement M(AUG)(tgg33944-34016)A(GCA)(t34038-34109)P(CCA)(t34126-34198)R(CGU)(c34210-34282)  
 [Cf. M(33940-34016)A(34037-34109)P(34125-34198)R(34209-34282)]  
 AE017280 complement L(UUA)(tgg34290-34374)G(GGC)(tgg34395-34465)L(UUA)(t34496-34575)H(CAC)(tgg34602-34673)  
 [Cf. L(34286-34374)G(34391-34465)L(34465-34575)H(34598-34673)]  
 AE017280 complement I(ACA)(tgg34687-34758)V(GUA)(tgg34767-34838)S(34845-34959)A(35061-37969)Σ(38144-39652)  
 [Cf. T(34683-34758)V(34763-34838)Σ(34846-34956)A(35061-37969)Φ(38145-39652)]  
 AE017281 complement F(TTC)(t300444-300515)D(GAC)(tgg300561-300632)E(GAA)(t300655-300725)K(AAA)(tgg300743-300814)  
 [Cf. F(300443-300515)D(300632)E(300654-300725)K(300739-300814)]  
 AF074828 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)(136-192:57 n) I: A-arm pair 5(caccc)/4(ggtg)]  
 AF074829 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)(136-192:57 n) I: A-arm pair 5(cacbc)/4(ggtg)]  
 AF074830 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)(136-192:57 n) I: A-arm pair 5(caccc)/4(ggtg)]  
 AF074831 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)(136-192:57 n) I: A-arm pair 5(caccc)/4(ggtg)]  
 AF074832 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)(136-192:57 n) I: A-arm pair 5(caccc)/4(ggtg)]  
 AF074833 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)(136-192:57 n) I: A-arm pair 5(caccc)/4(ggtg)]  
 AF074834 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)(136-192:57 n) I: A-arm pair 5(caccc)/4(ggtg)]  
 AF074835 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)(136-192:57 n) I: A-arm pair 5(caccc)/4(ggtg)]  
 AF074836 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)(136-192:57 n) I: A-arm pair 5(caccc)/4(ggtg)]  
 AF074837 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)(136-192:57 n) I: A-arm pair 5(caccc)/4(ggtg)]  
 AF074838 A(52-123acca)Igat(135-206acca) [Cf. A(51-127)(135-191:57 n) I: A-arm pair 5(caccc)/4(ggtg)]  
 AF074839 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)(136-192:57 n) I: A-arm pair 5(caccc)/4(ggtg)]  
 AF074840 A(52-123acca)Igat(136-206acca) [Cf. A(51-127)(136-192:57 n) I: with A-arm pair 5(caccc)/4(ggtg)]  
 AF074841 A(52-123acca)Igat(136-207acca) [Cf. A(51-127)(136-192:57 n) I: with A-arm pair 5(caccc)/4(ggtg)]  
 AF130462 Ygta(431-512ac)TTMeat(1573-1642accg)W  
 AF223396 Σ Igat(252-323acca) A Λ Igat: A-arm pair 4(ccgc)/5(ccgtg)  
 AF223397 Σ Igat(252-323acca) A Λ Igat: A-arm pair 4(ccgc)/5(ccgtg)  
 AF223398 Σ Igat(252-323acca) A Λ Igat: A-arm pair 4(ccgc)/5(ccgtg)  
 AF223399 Σ Igat(252-323acca) Atgg Λ Igat: A-arm pair 4(ccgc)/5(ccgtg) Atgg(anticodon)  
 AF268429 Σ Atggc(98-174acca)Igat(200-273acca) Λ [Cf. //A(98-278, 181 n)(200-// overlap (Atgc and Igat)]  
 AF302130 Λ Φ(562-676)Gtcc(757-827)Igat(865-937)Ettc(949-1019)Stag(1034-1125)Lcaa(1136-1209)  
 [Cf. Λ Φ(489-740)G(757-838)D(896-941)E(949-1219)S(1034-1114)M(1137-1210)]  
 AF302130 Egaa(1213-1284)Ygta(1297-1376)Wcaa(1384-1453)Hgtg(1470-1540)Gttg(1548-1618)Lcaa(1621->1680)  
 [Cf. F(1213-1284)W(1383-1451)H(1470-1451)Q(1548-1622)L(1622->1680)]  
 AF302131 Λ Φ(563-677)Kttt(833-904)Ltag(914-995)Tgt(1006-1077)Igat(1108-1181)Ettc(1193-1263)  
 [Cf. Λ Φ(490-741)(837-894:58n)(961-1003:43n)K(1012-1068:57n)D(1140-1185:46 n)E(1193-1273)]  
 AF302131 Mcat(1381-1455)Ygta(1542-1613)Hgtg(1715-1785) Meat A-arm pair 5(tgggg)/6(accgga); Mcat, Ygta and Hgtg: E-loop 4n  
 [Cf. MY(1542-1593:52 n)H(1716-1786)]  
 AF312492 Σ (<1-18)Igat(342-414acca)Atgc(540-611acca) [Cf. I(166-242)A(568-643)]  
 AF312493 Igat(319-391acca)Atgc(517-588acca) [Cf. I(166-242)A(568-643)]  
 AF312494 Igat(319-392acca)Atgc(517-588acca) Igat: A-arm pair 6(ccgcga)/5(gcgtg) [Cf. I(166-242)A(568-643)]



Effective procedure to develop alternative annotations of bacterial tRNA genes by means of deductive inference on the basis of characteristic tandems of tRNA genes

AF312495  $\Sigma$  (<1-93)?(447-512)Atgc(875-945)  
 AF338860 Igat(167-239acca)A  $\wedge$  [Cf. //I(157-243)//]  
 AF338862 Igat(164-237acca)A  $\wedge$  [Cf. //I(155-241)//]  
 AF338864 Igat(167-239acca)A  $\wedge$  [Cf. //I(157-243)//]  
 AF375994  $\Sigma$  Igat(1687-1760acca)Atgc(1785-1856acca)  $\wedge$  [Cf. //I(1687-1762)A(1744-1858:115 n)//]  
 AF397709  $\Sigma$  Igat Atgg.  $\wedge$  Atgg (anticodon?)  
 AF397714  $\Sigma$  Igat Atcc.  $\wedge$  Atcc(anticodon?)  
 AF440225  $\Sigma$  Igat A Igat:A-arm pair 6(egccgc)/5(scgtg)  
 AF510361  $\Sigma$  Igat Atgt  $\wedge$  Atgt(anticodon?)  
 AJ012700  $\Sigma$  Igat A  $\wedge$  [Cf. //Icca//]  
 AJ012701  $\Sigma$  Igat Atgc  $\wedge$  [Cf. //lataAgca//]  
 AJ012702  $\Sigma$  Igat Atgc  $\wedge$  [Cf. //lataAgca//]  
 AJ012703  $\Sigma$  Igat Atgc  $\wedge$  [Cf. //lataAgca//]  
 AJ012704  $\Sigma$  AtgcI  $\wedge$  [Cf. //Acat//]  
 AJ012705  $\Sigma$  Igat Atgc  $\wedge$  [Cf. //lataAgca//]  
 AJ012706  $\Sigma$  Igat Atgc.  $\wedge$  [Cf. //lataAgca//]  
 AJ012707  $\Sigma$  Igat Atgc  $\wedge$  [Cf. //lataAgca//]  
 AJ248283 complement G(GCA)(tggt149923-149996)F(UUC)(agcg15008-15080) [Cf. complement G(TCC)F(UCU)]  
 AJ248285 complement M(AUG)N(AAG) [Cf. complement M(TTA)N(TTA)]  
 AJ293101 Igat(AUC)A [Cf. I(AUA)A]  
 AP002547 Fttc(183943-184016a)Kttt(184043-184114a) [Cf. complement E(183943-184017)K(184043-184115)]  
 AP003363 complement MD(GAG)F D(GAC): A-arm pair 5(cctgc)/6(gcagg) [Cf. M?D]  
 AP003604 complement ARVG(GGA)TMLKLLPLQGNFRY?X G(GGA): E-loop 4 n; [Cf. //QQNFRYS(TCG)X//]  
 AP005141  $\Sigma$  A  $\wedge$   $\Phi$  (22026-22140)VDKLTGLRPMMSMFGIS,  $\Sigma$  A  $\wedge$   $\Phi$  (79005-79119)VGIEMFYWHQL,  $\Sigma$  A  $\wedge$   $\Phi$  (255060-255174)NR  
 AP005142  $\Sigma$  A  $\wedge$   $\Phi$  (230646-230760)VDKLTIE  
 AP005146 complement NR $\Phi$ (65033-65147)  $\wedge$   $\Sigma$   
 AP005274 Igat(14851-14923acca)Atgc(14939-15007tcca), Atgc(23500-23568tcca)Igat(23903-23975acca)Atgc(23991-24059tcca)  
 [Cf. I(GAT)A(TGC), A(TGC)I(GAT)A(TGC)]  
 AP005274 Lcag(49705-49787acca). Stga(221750-221833gca). Sgct(233409-233496g)Racg(233527-233598acca)  
 [Cf. L(CAG), S(TGA), S(GCT)R(ACG)]  
 AP005274 Sgca(244294-244380acca), complement S(UCC)(ttgc256226-256309), complement P(CCG)(ttgc292470-295442)  
 [Cf. S(CGA), complement S(GGA), complement P(CGG)]  
 AP005274 Tcgt(329629-329700tcca) [Cf. T(CGT)]  
 AP005275 Yeta(155249-155330aaca)Tggt(155954-156020)Tggt(156279-156351)Mcat(156390-156460accg)Wcca(1565558-156629gcaa)  
 [Cf. Y(GTA)T(GGT)T(GGT)M(CAT)W(CCA)]  
 AP005278 Qctg(32543-32613a)Ectc(32653-32724a)Qctg(32792-32862a)Ectc(32901-32872a). Ectc(34523-34598acca).  
 [Cf. Q(CTG)E(CTC)Q(CTG)E(CTG), E(CTC)]  
 AP005278 complement L(TTG)(tggt80519-80591), complement P(CCC)(ttgt187177-182249).  
 [Cf. comolent L(CAA), complement P(GGG)]  
 AP005278 Lgag(276372-276456ac)Lgag(276544-276628acca) [Cf. L(GAG)I(GAG)]  
 AP005279 complement G(GCC)(ttga104527-104598)V(GUC)(tggt104636-104706)C(UGG)(aggt104721-104787)  
 [Cf. G(GCC)V(GAC)C(GCA)G(GCC)]  
 AP005279 complement G(GGC)(acca104833-104901)Y(GUC)(tggt104939-105059)G(GGC)(a105044-105115).

- [Cf. complement G(GCC)V(GAC)G(GCC)]
- AP005279 V(GUG)(105463-105520acca) [Cf. V(CAC)]  
 AY190662  $\Sigma$  Igat(235-307acca)Atgc(341-413acca)  $\wedge$  [Cf. //I(255-329)A(359-434)//]  
 AY224382  $\Sigma$   $\wedge$   $\Phi$ NTtctc(5985-6055acca) VYQKGA [Cf. //Q(CAA)(5985-6059)//]  
 AY277896  $\Sigma$  Igat(524-596acca)Atgc(936-1007acca)  $\wedge$  [Cf. //I(AUU)//]  
 AY531069 Igat(67-139acca)Atgc(185-256)Vtac(274-356acca) [Cf. //I(AUC)A(GCA)V(GUA)//]  
 AY591324  $\Sigma$  Igat(144-216acca)Atgc(275-346acca)  $\wedge$  [Cf.  $\Sigma$  A(161-217: 57 n)(275-347)  $\wedge$ ] Inversion (1 & A)  
 AY591325  $\Sigma$  Igat(140-212acca)Atgc(271-343acca)  $\wedge$  [Cf.  $\Sigma$  A(157-213: 57 n)(271-343)  $\wedge$ ] Inversion (1 & A)  
 AY591326  $\Sigma$  Igat(132-204acca)Atgc(263-334acca)  $\wedge$  [Cf.  $\Sigma$  A(149-205: 57 n)(263-335)  $\wedge$ ] Inversion (1 & A)  
 AY591327  $\Sigma$  Igat(140-212acca)Atgc(271-342acca)  $\wedge$  [Cf.  $\Sigma$  A(571-213: 57 n)(271-343)  $\wedge$ ] Inversion (1 & A)  
 AY591328  $\Sigma$  Igat(140-212acca)Atgc(271-343acca)  $\wedge$  [Cf.  $\Sigma$  A(571-213: 57 n)(271-344)  $\wedge$ ] Inversion (1 & A)  
 BX248585 Kctt(206786-206853acca), complement S(206999-207082) [Cf. complement K(206786-206853)S]  
 BX248585 Scga(255174--255257acca), complement S(a255635-255722), Ngtt(255897-255969g)  
 [Cf. Complement Sega(255174-255261) S(255635-255722), Ngtt(255896-255968)]  
 BX248586 Vtac(44868-44939a)Kttt(44984-44056) [Cf. complement V(44868-44940)K(44984-44056)]  
 CR378668 complement G(GGA)(tggga182119-182189)I(ACA)(tggg-182203-182283) [Cf. complement G(TCC)I(TGT)]  
 CR378674 complement I(ACC)(tggg597225-59801)G(GCA)(tggga59818-59888) T(ACC) A-arm pair 6(cacccc)/5(gggtg)  
 [Cf. complement T(CAC)G(CAG)]
- D88802 Dgtc(26423-26495gcca) [Cf. D(26423-26989: 567 n)] [Cf. //Q(CCU)M(CUA)QQ(AAU)]  
 J01713 MLQQttg(487-557gcca)Mecat(577-647acca)QQctg(813-883gcca)  
 K01983  $\Sigma$  Igat(324-396a)A [Cf. //I(UCA)//]  
 L00194  $\Sigma$  Igat(552-626acca)Atgc(685-755acca)  $\wedge$  [Cf.  $\Sigma$  IgccAgca  $\wedge$ ]  
 L08236  $\wedge$   $\Phi$  Mecat(265-337acca)Dgtc(402-474) [Cf.  $\wedge$   $\Phi$ M(ACC)D(AAC)]  
 L26364  $\Sigma$  Igat(386-458acca)A  $\wedge$  [Cf.  $\Sigma$  I(CUG)A  $\wedge$ ]  
 L28159  $\Sigma$  IgatAtgc  $\wedge$  Igat: A-arm pair 5(cacccc)/4(ggtg)  
 L28159  $\Sigma$  IgatAtgc  $\wedge$  Igat: A-arm pair 5(cacccc)/4(ggtg)  
 L28154  $\Sigma$  IA(321-391acca)  $\wedge$  [Cf.  $\Sigma$  IA(324-399)  $\wedge$ ]  
 L28156  $\Sigma$  IgatAtgc  $\wedge$  [Cf.  $\Sigma$  IataAgca  $\wedge$ ]  
 L28157  $\Sigma$  IgatAtgc  $\wedge$  [Cf.  $\Sigma$  ItgaAcaa  $\wedge$ ]  
 L28159  $\Sigma$  IgatAtgc  $\wedge$  Igat: A-arm pair 5(cacccc)/4(ggtg)  
 L28160  $\Sigma$  IgatAtgc  $\wedge$  Igat: A-arm pair 5(cacccc)/4(ggtg)  
 L28161  $\Sigma$  IgatAtgc  $\wedge$  Igat: A-arm pair 5(cacccc)/4(ggtg)  
 L28162  $\Sigma$  IgatAtgc  $\wedge$  Igat: A-arm pair 5(cacccc)/4(ggtg)  
 L35100  $\Sigma$  IgatAtgc  $\wedge$  [Cf.  $\Sigma$  I(ATT)A(TTG)  $\wedge$ ]  
 L35101  $\Sigma$  IgatAtgc  $\wedge$  [Cf. GenBank  $\Sigma$  I(AUU)A(AGCU)  $\wedge$ ]; EMBL  $\Sigma$  I(UUA)A(GCU)  $\wedge$  ]  
 L35102  $\Sigma$  Iatgc  $\wedge$  [Cf.  $\Sigma$  I(ATC)A(TTG)  $\wedge$ ]  
 L35103  $\Sigma$  IgatA  $\wedge$  [Cf.  $\Sigma$  I(UUA)A  $\wedge$ ]  
 L36472  $\wedge$ (5208-8130) [Cf.  $\wedge$  or  $\Phi$  ]  
 L42976 A Igat(77->133) [Cf. //I or A//]  
 M13687 complement Kttt(tggg1225-1296)VtacVtacVtac [Cf. K(GAT)V(CCT)V(CCT)V(CCT)]  
 In early days, description of position of the anticodon for Kttt was 1-3.  
 M23210 Vtac(22-93acca)Tgt(130-201acca)Kttt(243-314acca)Cag(329-411acca)Ggcc(421-491tcca)Ltaa(510-59a)R

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M65195 [Cf. V(ACG)T(UUA)K(AUU)L(AUU)G(ACG)G(ACG)L(AUU)R  
 Gtcc(22-82a)P [Cf. G(GTT)P]  
 M91385 Wtea(1046-1117gccca)WS [Cf. W(AAA)WS]  
 U15182 Ettc(37225-37296)Egtc(37328-37400)Fgaa(37342-37509) [Cf. D(ATC)(37219-372919)F(GGC)(37596-37845)  
 U60278  $\Sigma$  Igat (71-143acca)A [Cf. //I(UCA)//]  
 U60279  $\Sigma$  Igat (71-143acca)A [Cf. //I(UCA)//]  
 U60280  $\Sigma$  Igat (71-143acca)A [Cf. //I(UCA)//]  
 U60281  $\Sigma$  Igat (71-143acca)A [Cf. //I(UCA)//]  
 X04108  $\Sigma$  ?? [Cf.  $\Sigma$  (<1-42) A(GCA)(144-219)L(CUA)(228-304)]  
 X06727 Kttt(94-165acca)Ltag(172-251-acca) [Cf. K(UUU)L(AUG)]

tRNA and/or rRNA genes that we discovered or whose description we modified

[Cf. Original relevant data]

Note :  $\Lambda$  : Large subunit (23S) rRNA,  $\Sigma$  : Small subunit rRNA (16S) rRNA, and  $\Phi$  : 5S rRNA

**Accession Number index****Accession No(s) . Bacterial name**

[AB013377] to [AB031215]	<i>Bacillus halodurans</i> C-125
[AB071783]	<i>Saprosira</i> sp. SS91-40
[AE000052]	<i>Mycoplasma pneumoniae</i> M129
[AE000129] to [AE000453]	<i>Escherichia coli</i> K12 MG1655
[AE001652]	<i>Chlamydomydia pneumoniae</i> CWL029
[AE006473] to [AE006615]	<i>Streptococcus pyogenes</i> M1 GAS
[AE007319]	<i>Streptococcus pneumoniae</i> TIGR4
[AE008706]	<i>Salmonella thphimurium</i> LT2
[AE014136] to [AE014168]	<i>Streptococcus pyogenes</i> MGAS315
[AE014192] to [AE014210]	<i>Streptococcus agalactiae</i> 2603V/R
[AE015714]	<i>Shewanella oneidensis</i> MR-1
[AE016998] to [AE017013]	<i>Bacillus cereus</i> ATCC 14579
[AE017205]	<i>Lactobacillus johnsonii</i> NCC533
[AE017280] to [AE017281]	<i>Bacillus cereus</i> ATCC 10987
[AF074828]	<i>Campylobacter jejuni</i> NCTC11168
[AF074829]	<i>Campylobacter jejuni</i> NCTC11392
[AF074830]	<i>Campylobacter jejuni</i> KJ7
[AF074831]	<i>Campylobacter jejuni</i> JEO2677(3-1 a)
[AF074832]	<i>Campylobacter jejuni</i> JEO2677(3-1 a)
[AF074833]	<i>Campylobacter jejuni</i> JEO2693(125883/87)
[AF074834]	<i>Campylobacter jejuni</i> JEO2759(16-1 b)
[AF074835]	<i>Campylobacter jejuni</i> JEO2762(22-5 b)
[AF074836]	<i>Campylobacter jejuni</i> NCTC11951 T
[AF074837]	<i>Campylobacter coli</i> NCTC11366 T
[AF074838]	<i>Campylobacter coli</i> NCTC11353
[AF074839]	<i>Campylobacter coli</i> JEO2772(11-8)
[AF074840]	<i>Campylobacter coli</i> JEO2777 (783)
[AF074841]	<i>Campylobacter lari</i> CCUG29406
[AF130462]	<i>Corynebacterium glutamicum</i> ATCC 13032
[AF223396]	<i>Neisseria gonorrhoeae</i> 1245-1
[AF223397]	<i>Neisseria gonorrhoeae</i> 1199-1
[AF223398]	<i>Neisseria gonorrhoeae</i> 1021-1
[AF223399]	<i>Neisseria gonorrhoeae</i> 1231-1
[AF268429]	uncultured bacterium NAZ4
[AF302130]	<i>Streptococcus agalactiae</i> L41
[AF302131]	<i>Streptococcus agalactiae</i> L48
[AF312492]	<i>Bartonella bacilliformis</i> isolate Cuzco 14
[AF312493]	<i>Bartonella bacilliformis</i> isolate MONZON 269
[AF312494]	<i>Bartonella bacilliformis</i> isolate MONZON 812

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[AF312495]	<i>Bartonella bacilliformis</i> isolate URBHLLY 8
[AF338860]	<i>Bradyrhizobium</i> sp. MSDJ 5493
[AF338862]	<i>Bradyrhizobium</i> sp. MSDJ 5730
[AF338864]	<i>Bradyrhizobium</i> sp. MSDJ 5726
[AF375994]	<i>Candidatus Brocadia anammoxidans</i>
[AF397709]	<i>Synechococcus</i> sp. WH 8012
[AF397714]	<i>Synechococcus</i> sp. WH 8112
[AF440225]	<i>Bartonella</i> sp. N40
[AF510361]	<i>Mesorhizobium</i> sp. vgn-4
[AJ012700]	<i>Roseovarius tolerans</i> EL-172
[AJ012701]	<i>Roseovarius tolerans</i> EL-164
[AJ012702]	<i>Roseovarius tolerans</i> EL-171
[AJ012703]	<i>Roseovarius tolerans</i> EL-222
[AJ012704]	<i>Antarctobacter heliothermus</i> EL-219
[AJ012705]	<i>Rosenbacter algicola</i> DSM 10251
[AJ012706]	<i>Roseovarius denitrificans</i> DSM 7001
[AJ012707]	<i>Rosenbacter litoralis</i> DSM 6996
[AJ248283]	<i>Pyrococcus abyssi</i> Orsay
[AJ248285]	<i>Pyrococcus abyssi</i> Orsay
[AJ293101]	<i>Anabaena lemmermannii</i> 262
[AP002547]	<i>Chlamydomphila pneumoniae</i> J138
[AP003363]	<i>Staphylococcus aureus</i> substr. aures Mu 50
[AP003604]	<i>Nostoc</i> sp. PCC 7120
[AP005141] to [AP005146]	<i>Streptococcus pyogenes</i> SSI-1
[AP005274] to [AP005279]	<i>Corynebacterium glutamicum</i> ATCC 13032
[AY190662]	<i>Polyangium cellulorum</i> So9881
[AY224382]	<i>Bacillus cereus</i> BGSC 6A5
[AY277896]	<i>Bartonella</i> sp. Rt222sm
[AY531069]	<i>Vibrio parahaemolyticus</i> RIMD2210856
[AY591324] to [AY591328]	<i>Enterococcus faecium</i>
[BX248585] to [EX148586]	<i>Candidatus Blochjmannia floridanus</i>
[CR378668] to [CR378674]	<i>Photobacterium profundum</i> SS9
[D88802]	<i>Batillis subtilis</i> 168
[J01713]	<i>Escherichia coli</i>
[K01983]	<i>Synechococcus</i> sp. PCC 6301
[L00194]	<i>Caulobacter vibrioides</i> CB13
[L08236]	<i>Bacillus subtilis</i> 168T
[L26364]	<i>Bartonella bacilliformis</i> KC584
[L28154]	<i>Burkholderia cepacia</i>
[L28148] to [L28149]	<i>Pseudomonas aeruginosa</i>
[L28156] to [L28158]	<i>Burkholderia gladioli</i>
[L28159] to [L18162]	<i>Psuedmonas mendocina</i>
[L35100]	<i>Bartonella quintana</i> Fuller

[L35101]	<i>Bartonella henselae</i> Houston
[L35102]	<i>Bartonella vinsonii</i> Baker
[L35103]	<i>Bartonella elizabethae</i> F9251
[L36472]	<i>Staphylococcus aureus</i>
[L42976]	<i>Xanthomonas albilineans</i>
[M13687]	<i>Escherichia coli</i> K12
[M23210]	<i>Bacillus subtilis</i>
[M65195]	<i>Mycobacterium smegmatis</i>
[M91385]	<i>Spiroplasma citri</i> R8A2
[U15182]	<i>Mycobacterium leprae</i>
[U60278]	<i>Acinetobacter calcoaceticus</i> ATCC 23055
[U60279]	<i>Acinetobacter baumannii</i> ATCC 19606
[U60280]	<i>Acinetobacter genomosp. 3</i> ATCC 19004
[U60281]	<i>Acinetobacter genomosp. 13</i> ATCC 17903
[X04108]	<i>Campylobacter jejuni</i> N941
[X06727]	<i>Mycoplasma capricolum</i> Carifornia kid(ATCC27343)

E(GAA)VYQK of [AE016750] (*Staphylococcus*: B6-1-1-4-1), [AE016998] and [AE017334] (*Bacillus cereus*) and [AE017024] (*Bacillus anthracis*). We found E(GAA) just on the Q(CAA)

A clue [TTW] [AF130462] (*Corynebacterium*: B6-2-2-2-3-1-1). The clue was compared with YTTMW [AP005275] (*Corynebacterium*), and as a consequence, corresponding Y and M were found.

Two clues [GDE] and [SMFW] [AF302130] (*Streptococcus agalactiae* B6-1-2-4-2). The first clue was compared with GIE of [AE016947] (*Enterococcus faecalis* B6-1-2-2-1) and [AE006474] (*Streptococcus pyogenes*). We found Igat just on the site of the D. The second clue was compared with SMFYW of [AE006479] (*Streptococcus pyogenes*). Then we found Ygta between the F and the W.

#### 4.1.2 tRNA genes (Inverted tandems)

Sometimes “unfamiliarity” of a clue becomes a clue for detection of annotation errors.

A clue [5' KE 3'] [AE001652] (*Chlamydomonas pneumoniae* B11-2-1-1-2). The clue is popular in genera of *Bacillus* (B6-1-1-1), *Leptospira* (B10-1-1-1), and *Geobacter* (B12-4-2-1), but neither in genera of *Chlamydomonas* (B11-2-1-1-2) nor *Clamylidia* (B11-2-1-1-1). Therefore we examined the sequence of the annotated 5' KE 3', and found that it matches with the complement of 3' KE 5'. A complement tandem 3' EK 5' [AP002547] (*Chlamydomonas pneumoniae*) should be read as 5' EK3'.

A clue [5' FDEK 3'] [AE017281] (*Bacillus* B6-1-1-1-1). Unlike 3' FDEK 5', the clue is not familiar in many *Bacillus* species. Therefore we tried to search for its complement sequence, and found a four genes which form a tetragene tandem 3' FDEK 5'. This means that each template form was interpreted as a complement one.

A clue [5' ESNIGKTFDMSMAPRLGLHTV  $\Sigma \Lambda \Phi$  3'] [AE017280] (*Bacillus cereus* B6-1-1-1-1). In a similar process, we found twenty two genes which form a 22-gene tandem 3' ESNIGKTFDMSMAPRLGLHTV 5' and 3'  $\Phi \Lambda$

$\Sigma$  5' just on the 5'  $\Sigma \Lambda \Phi$  3', which is hold also in [AE017039] *Bacillus anthracis*.

There are some other examples as follows: A sequence for a complement tandem for 3'GDKT5' [AE001652] should be read as 5'GDK3' and 3'T5'. An apparent complete tandems 3'KS5' and 3'SSN5' [BX248585] (*Candidatus Blochmannia floridanus*) should be read as (5'K3' and 3'S5'), and (5'S3', 3'S5' and 5'N3'), respectively. A complement tandem 3'VK5' [BX248586] (*Candidatus Blochmannia floridanus*) should be read as 5'VK3'.

#### 4.1.3 Expansion to rRNA genes

The first stage: A clue [ $\Lambda \Phi$  VLKDE] [AF302131] (*Streptococcus agalactiae*). The clue was compared with a template VDKLTIE of [AE014195] (the same bacterium), and we found new V (not the inherent V), new D (not the inherent D), new K (not the inherent K, instead of the inherent V to be denied), L (instead of the inherent L to be denied, but up shift about 50 b), T (instead of the inherent K to be denied), and I (instead of the inherent D to be denied) to form a new tandem  $\Lambda \Phi$  VDKLTIE.

The second stage: A clue [ $\Lambda$  V] of the tandem mentioned above  $\Lambda$  VDKLTIE [AE014195] (*Streptococcus agalactiae*). The clue was compared with the hot template  $\Lambda \Phi$  V of [AF302131], and we found  $\Phi$ .

A clue [ $\Lambda$  N] ([AE006615], [AE014141], [AE014168], [AP005141] and [AP005146]) (*Streptococcus pyogenes* B6-1-2-4-2), [AE016999] (*Bacillus cereus* B6-1-1-1-1) and [AE016998] (*Bacillus cereus* B6-1-1-1-1). The clue was compared with  $\Lambda \Phi$  N of [AE017024] (*Bacillus anthracis* B6-1-1-1-1), [AB109772] (*Fingoldia magne* B6-1-4-1-4-1), [AF007319] (*Streptococcus pneumoniae* B6-1-2-4-2) and [AJ010599] (*Listeria monocytogenes* B6-1-1-3-1). We found  $\Phi$  in each species.

A clue [ $\Lambda$  V] [AE016998] to [AE017000] (*Bacillus cereus* B6-1-1-1-1), [AE06474] and [AE06479] (*Streptococcus pyogenes* B6-1-2-4-2),

and [AE014192] (*Streptococcus agalactiae* B6-1-2-4-2). The clue was compared with a tandem  $\Lambda\Phi V$  of [AF302131] (*Streptococcus agalactiae* B6-1-2-4-2) and [AE017205] (*Lactobacillus johnsoii* B6-1-2-3-1), and respective corresponding  $\Phi$  genes were found.

Now we have found several rRNA genes ( $\Lambda$ ,  $\Sigma$  and  $\Phi$ ) shown in Table 4.

## 4.5 Some problems to be dissolved

### 4.5.1 Arbitrariness of annotation

About ten years ago, after asking DDBJ the reason why it gave a single bacteria of [X03715] two different names, *melifenum* and *melliferum*, the former was revised and an EMBL person apologized us. Because we knew that the original paper used the two, we answered that the venter did not need to apologize. However, the true reason, maybe was misselection of a single and important keyword in database search at that time. Also today a similar case remains in [L35101]: *Bartonella* and *Baronella*. After asking DDBJ the original word of an amino acid "Ara" of [AB100740] to [AB100760], in summer 2003 we found it was changed to "Ala" several months later. If possible, we want to be informed that the reasons why a word was adopted and abandoned just when it was abandoned.

Generally, the Annotations appear to treat codon/anticodon of tRNA genes a little too lightly. For example, data in [L35000] to [L35003] were cited from the same pair of references. However, anticodons/codons that we can obtain by literal translation from DNA sequences of cloverleaf structures are Igat(AUC) and Atgc(GCA). On the other hand the Annotations are as follows:

	Up-date		Igat(AUC)		Atgc(GCA)	
	G	E	G	E	G	E
[L35000]	1996	1999	AUU	TTA	UUG	TTG
[L35001]	1996	2000	AUU	UUA	GCU	UCG
[L35002]	1996	1999	AUC	ATC	UUG	TTG
[L35003]	1996	2000	AUU	UUA	GCA	GCA

G: GenBank E: EMBL

This suggests that update do not always afford correct annotations.

Whereas a literal translation of a sequence of a tRNA gene yields

M(AUG)L(CUA)Q(CAA)Q(CAA)M(AUG)Q(CAG)Q(CAG),

[J01713] gives the annotation

M(AUG)L(CUA)Q(CAA) Q(CCU)M(CUA) Q(CAG-)Q(AAU).

### 4.5.2 Arbitrariness or systematic errors

When T(175-260) of [M87888] was treated as T[75-250], it was, maybe mechanically, put upstream of V(90-170). In the present day, as seen in [AJ010599], CDS(464..1201) is arranged after and before tRNA(139..214) and tRNA(232..314) in GenBank and EMBL, respectively. This fact may suggest difference between their policies.

Several other entries of Table 4 as well as [L35000] to [L35003] consist of I and/or A. They were yielded from investigation of the 16S-23S intergenic regions,<sup>8)</sup> which were inquired from a viewpoint of phylogenetic relationship among bacterial species, where annotations of individual tRNA genes involving differentiation of codon/anticodon would be not so important. Although one<sup>8a)</sup> of the papers mentioned that by alignment of four DNA sequences from the same genera but different species, a mutation of a nucleotide of anticodon of A (c to g, namely Atgc to Atgg) was detected, it dismissed such a change as a trivial mutation which has no effect on study their bacteria. It did not discuss change of tRNA from Atgc to Ptgg. There are some tendencies from unknown causes. For example, in a group of [AF074828] to [AF074841], Igtc was shortened about 15 b. Another group of [AF223326] to [AF322329] are of A-arm 45. In [AF312492] to [AF312495], there are both Igtc and Atgc at the positions different from those indicated by the Annotations. Whereas our literal translation gives



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IgatAtgc, each of [AY591324] and [AY591325] adopt AI.

The above mentioned AI in [AY591324] to [AY591328] (*Enterococcus fecium* B6-1-2-2-1) is popular in other genera of B6 and B12: *Ethanoligenbacterium* (B6-1-4-1-3-1), *Clostridium* (B6-1-4-1-2-1), *Campylobacter* (B12-5-1-1-1), *Xanthomonas* (B12-3-11-1-2), *Helicobacter* (B12-5-1-2-1), *Antractobacter* (B12-1-2-1-1), *Xylolla* (B12-3-11-1-2), but very rare (or may be no other example) in *Enterococcus*. Actually it is not  $\Sigma AI \Delta$  but  $\Sigma$  IgatAtgc  $\Delta$  which is frequently investigated as a tandem of the 16S-23S intergenic region. We would like to know why the order of the genes were such inverted in every case. In addition, all tandems, “tRNA-Ile”s are very short against their true lengths. We guess it would be due to some systematic error.

In each sequence of [AE014207] *Streptococcus agalactiae*, [AF268479] Uncultured bacterium NAZ4, and (old) [M87888] *Bacillus subtilis*, two genes overlap with each other. Our alternative and reasonable annotations are shown as follows:

T(75-250) over V(95-170)  
 --> T(175-250) [M87888] (corrected)  
 $\Phi$ (9518-9679) over Ngtt(9660-9733)  
 -->  $\Phi$ (9537-9654) [AE014207]  
 A(98-278) over I(200-277)  
 --> A(98-178) [AF248479]

In fact, there is a problem of confliction of description as exemplified as follows:

[AE008706 ]  
 14864-14937 tRNA  
 /gene= "aspU"  
 /note="tRNA-Val"

### 4.5.3 Systematic error or clerical careless mistake

In addition, we cannot avoid careless mistake exemplified in Appendix 2. “Heliobacter” still survive instead of “Helicobacter” ([L25079],

[M88140], [M88155], and so on).

Confusion of “Ara” with Ala ([AB100740] to [AB100760]) was dissolved in 2003, but another confusion of *Chlamydophila pneumoniae* with *Chlamydia pneumoniae* began ([AE001585] to [AE001687]). We would like to avoid such careless and severe mistakes as much as possible.

### 4.5.4 International mutual aid

Finally, in order to hope long continuance of the ongoing irreplaceable treasure, DDBJ/GenBank/EMBL, we cannot but say that we have to stop easy use of easy answers afforded by easy computer softwares without any discussion. Some tRNA genes were reported to be very long (in Table 4. Cf. Dgtc [D88802], Atgc[AF268429] and so others) or very short (in 46, of [AF074828]). Nevertheless, it is a kind of simple careless mistakes. More serious problem is a systematic error as exemplified in misassignment of positions of anticodon/codon, which, maybe, lead to misassignment of anticodon/codon. We indicated the same thing in the case of introns of mRNAs. We guess that most of the unbelievable and miserable results are due to such rashy behavior. We cannot and must not judge whether an unfamiliar annotation is true or false. Only person who can correct wrong data is its producer. The others only can call the producer’s attention. Appendix 2 is a part of such suspects we picked up. We would like to emphasize that the present exposure of mistakes and errors also is one of the results of our systematic induction-deduction system and not causal accidents.

We recommend that all of you should begin to consider how to help to maintain and improve the quality of the DDBJ/GenBank/EMBL database. One of them is to stop easy use of easy answers produced with easy computer softwares without any discussion. Another is to establish any good ways to internationally hold a set of a question and answers, opinions, criticism, and so on resulted from this in hold. We told this also in our

another paper on introns of human mRNAs<sup>9)</sup>.

## 5. Conclusion

We made the existence of tRNA and rRNA gene-tandems that are characteristic of a various level of bacterial classes, and proved that it can be used to deductively dig up hidden and putative tRNA and rRNA genes from genome DNA sequences. In order to maintain and improve the DDBJ/GenBank/EMBL, which is valuable and irreplaceable treasure, as effectively and efficiently much as possible, we insist some ideas.

## 6. References

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- 8) Volker Gurtler and Vilma A. Stanisich, *Microbiology*, 1996,142,4. And many relevant papers have been published, for example:
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**Appendix 1**(1) A cloverleaf structure<sup>1)</sup> and a frame

Usually, a cloverleaf structure of tRNA gene contain 73 or more (up to W76) as follows:

	0 <sup>3)</sup>	1 or less
Aminoacyl stem	1 to 7, 66 to 72	7 pairs
D-stem	10 to 13, 22 to 25	4 pairs
D-loop	14 to 21	8 or more
A-stem	27-to 31, 39 to 43	5 pairs
A-loop	32 to 38 (anticodon 34 to 36)	7
E-loop	44 to 48	5 or more
TF stem	49 to 53, 61 to 65	5 pairs
TF-loop	54 to 60	7
ACCA	73 (up to 76)	1 to 4

We define a frame. Its range is only 1 to 72.

In fact, as shown even in the 1989 compilation by Sprinzl et al.<sup>2)</sup> there have been many tRNA genes a little deviating from the "standard". We mention them in Table 4, as exemplified as A-stem 54, which means that 1 nucleotide is missing from the standarad(A-stem 55).

## (2) Description of a frame

A frame is illustrated as follows:

Ex. 1 tRNA (1002...1073): 1002ggt----acctgc1073acca

Ex. 2 tRNA complement(2002..2073) : tggt 2002gcaggt-----acctg2073

## (3) A tRNA gene

A tRNA gene can be described as combination of a relevant amino acids with anticodon and/or codon, as exemplified with Mcat(AUG), Mcat(ATG), or simply Mcat, and/or M(AUG), M(ATG). Three rRNA genes are mentioned as simply. A (tRNA-gene) tandem is a sequence consisting of more than one tRNA(and rRNA) gene. A DNA data (a sequence, annotation and so on) is indicated with its Accession number of the DDBJ/GenBank/EMBL.

## References

- 1) In Transfer-RNA:Structure, Properties and Recognition, P.R. Schimmel, D. Soll, J.N. Abelson, Eds, 1979, Cold Spring Harbor Laboratory, N.Y. pp.518-519 (Cited as Reference No. 1 in Ref. 3.)
- 2) Mathius Sprinzl et al., Nucleic Acid Res. 1989, 17,r1.
- 3) Sergey Steinbeg et al., ibid, 1993,21,3011.

## Appendix 2

For	Read	Location (Examples)
Baronella	Bartonella	[L35101]
Heliobacter	Helicobacter	[M88156], [M88140], [M88155] and [L25079]
Chlamydia	Chlamydophila	[AE001585] to [AE001687]
n (numeral) in anticodon=(pos: n..[n+2], aa: )		
	n-1	[AJ012701] to [AJ02703], [L28150],
	n-2	[AJ012704], [L35100],
	n+1	[U60278] to [U60281]
	n+4	[L00194]
"codon recognized:GAT"	"anticodon recognized:GAT"	[AP005275], [L08236], [M23210], [L35101] (part)
(Already corrected)		
Ara	Ala	[AB100740] to [AB100760]
tRNA complement(1221..1296) /anticodon=(pos:1..3.aa:OTHER)	tRNA complement(1221..1296) /gene="valU"	[M13687]
/note=codon recognized=GAT"	/product="tRNA-Val"	
/gene="valU"		
/product="tRNA-OTHER"		
tRNA 75-250 Thr	175-250 Thr	[M87888]