

Sample Annotation File: Mitochondrial sequence

	Entry	Feature	Location	Qualifier	Value
Common information of all entries	COMMON	SUBMITTER		contact	Hanako Mishima
				ab_name	Mishima,H.
				ab_name	Yamada,T.
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				department	DNA Data Bank of Japan
				country	Japan
				state	Shizuoka
				city	Mishima
				street	Yata 1111
				zip	411-8540
		REFERENCE		ab_name	Mishima,H.
				ab_name	Yamada,T.
First entry				title	Plant mitochondrial DNA
				status	Unpublished
				year	2017
		DATE		hold_date	20191130
		TOPOLOGY		circular	
	ENT01	source	1..E	organelle	mitochondrion
				organism	Abies nordmanniana subsp. equi-trojani
				mol_type	genomic DNA
				isolate	SM08
				sub_species	equi-trojani
		CDS	8607..9390	gene	COX3
				note	TAA stop codon is completed by the addition of 3' A residues to the mRNA
				product	cytochrome oxidase subunit 3
				transl_except	(pos:9390,aa:TERM)
				transl_table	1
Second entry		tRNA	9391..9458	anticodon	(pos:9421..9423,aa:Gly)
				note	codon recognized:GGA
				product	tRNA-Gly
		CDS	9459..9806	gene	ND3
				product	NADH dehydrogenase subunit 3
				transl_table	1
		tRNA	complement(9808..9875)	anticodon	(pos:complement(9838..9840),aa:Arg)
				product	tRNA-Arg
	ENT02	source	1..E	organelle	mitochondrion
				organism	Abies nordmanniana
				mol_type	genomic DNA
				isolate	SM09
		CDS	8607..9390	gene	COX3
				note	TAA stop codon is completed by the addition of 3' A residues to the mRNA
				product	cytochrome oxidase subunit 3
				transl_except	(pos:9390,aa:TERM)
				transl_table	1

Meta-base position, "E", can be used to describe location of a feature instead of numerical number of sequence end point, if a given feature, including source, spans full length of a submitted sequence. Please visit a following site for detail, http://www.ddbj.nig.ac.jp/sub/mss/file_format-e.html#annotation-4

Enter "translation table code" for the organism, in this case for plants. Default is "1". Visit for detail: <http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi?mode=c>