Sample Annotation File: Ribosomal RNA

This line is not required for annotation file.

Entry	Feature	Location	Qualifier	Value
COMMON	SUBMITTER		contact	Hanako Mishima
			ab_name	Mishima,H.
			ab_name	Yamada,T.
			ab_name	Kim,K.-H.
			ab_name	Liu,G.Q.
			email	mishima@ddbj.nig.ac.jp
			phone	81-55-981-6853
			fax	81-55-981-6849
			institute	National Institute of Genetics
			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.
			ab_name	Park,C.S.
			ab_name	Liu,G.Q.
			title	16S rRNA of Pseudomonas sp. isolated from the rice plant
			status	Unpublished
			year	2017
	DATE		hold_date	20191130
ENT01	source	1..E	strain	YCL-001
			organism	Pseudomonas sp. YCL-001
			mol_type	genomic DNA
			isolation_source	root of rice plant
			country	Japan:Okinawa
	rRNA	<1..>1475	product	16S rRNA
ENT02	source	1..E	strain	YCL-002
			organism	Pseudomonas sp. YCL-002
			mol_type	genomic DNA
			isolation_source	rice paddy
			country	Taiwan:Tainan
	rRNA	<1..>1480	product	16S rRNA

Common information of all entries

First entry

Second entry

"contact" is mandatory. Enter the full name.

Enter the date to withhold your data. If the data should be publicized immediately, delete the DATE line.

Entry name should be unique to all entries, i.e. clone name, isolate name, etc. and identical to the one in the sequence file.

When the end of the feature is truncated, add "<" or ">".

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

The organism name that ends with 'sp.' should include strain, isolate or clone information in order to make the organism unique.

DDBJ DNA Data Bank of Japan