

Sample Annotation File: EST (expressed sequence tag)

This line is not required for annotation file.

Common information of all entries

First entry

Second entry

Entry	Feature	Location	Qualifier	Value
COMMON	SUBMITTER		contact	Hanako Mishima
			ab_name	Mishima,H.
			ab_name	Yamada,T.
			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	Mus musculus EST
			status	Unpublished
			year	2017
	DATE		hold_date	20191130
	DIVISION		division	EST
	KEYWORD		keyword	EST
			keyword	3'-end sequence (3'-EST)
	COMMENT		line	3'-EST sequences are presented as anti-sense strand.
2310009A01_r	source	1..E	clone	2310009A01
			clone_lib	full-length enriched mouse cDNA library
			organism	Mus musculus
			mol_type	mRNA
			tissue_type	tongue
			dev_stage	adult
			ff_definition	@@[organism]@@ mRNA, clone: @@[clone]@@, 3' end sequence, expressed in tongue
			sex	male
2310009A02_r	source	1..E	clone	2310009A02
			clone_lib	full-length enriched mouse cDNA library
			organism	Mus musculus
			mol_type	mRNA
			tissue_type	tongue
			dev_stage	adult
			ff_definition	@@[organism]@@ mRNA, clone: @@[clone]@@, 3' end sequence, expressed in tongue
			sex	male

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

"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.

"5'-end sequence (5'-EST)", "3'-end sequence (3'-EST)", or "unspecified EST" must be specified in keyword.

In the case of "3'-EST", enter the COMMENT for either "anti-sense" or "sense" strand.

"clone" is mandatory for EST

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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

Metadescription can be used to represent value for some qualifiers, such as organism, clone, in ff_definition. Please visit the following site for detail.
http://www.ddbj.nig.ac.jp/sub/mss/file_format-e.html#annotation-15