Sample Annotation File: HTG (High-Throughput Genomic Sequences) unfinished

This line is not required for annotation

Entry	Feature	Location	Qualifier	Value
COMMON	SUBMITTER		contact	Hanako Mishima
			ab_name	Mishima,H.
			ab_name	Yamada,T.
			ab_name	Park,C.S.
			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	Arabidopsis thaliana DNA
			status	Unpublished
			year	2017
	DATE		hold_date	20191130
	DIVISION		division	HTG
	KEYWORD		keyword	HTG
			keyword	HTGS_PHASE1
ENT001	source	1..E	clone	CIC5D1
			clone_lib	AT01 BAC
			organism	Arabidopsis thaliana
			mol_type	genomic DNA
			chromosome	1
			ecotype	columbia
			ff_definition	@@[organism]@@ DNA, BAC clone: @@[clone]@@, chromosome @@[chromosome]@@, *** SEQUENCING IN PROGRESS ***
	assembly_gap	5001..5100	estimated_length	unknown
			gap_type	within scaffold
			linkage_evidence	within clone
	assembly_gap	24001..24100	estimated_length	unknown
			gap_type	within scaffold
			linkage_evidence	within clone
	assembly_gap	32001..32100	estimated_length	unknown
			gap_type	within scaffold
			linkage_evidence	within clone
	assembly_gap	55001..55100	estimated_length	unknown
			gap_type	within scaffold
			linkage_evidence	within clone
ENT002	source	1..E	clone	CIC6D5
			clone_lib	AT01 BAC
			organism	Arabidopsis thaliana
			mol_type	genomic DNA
			chromosome	6
			ecotype	columbia
			ff_definition	@@[organism]@@ DNA, BAC clone: @@[clone]@@, chromosome @@[chromosome]@@, *** SEQUENCING IN PROGRESS ***
			estimated_length	unknown
			gap_type	within scaffol
			linkage_evidence	within clone
	assembly_gap	28001..28100	estimated_length	unknown
			gap_type	within scaffol
			linkage_evidence	within clone
	assembly_gap	36001..36100	estimated_length	unknown
			gap_type	within scaffol
			linkage_evidence	within clone
	assembly_gap	65001..65100	estimated_length	unknown
			gap_type	within scaffold
			linkage_evidence	within clone
	assembly_gap	83001..83100	estimated_length	unknown
			gap_type	within scaffold
			linkage_evidence	within clone

Common information of all entries

First

Second entry

Annotation notes:

"contact" is mandatory. Enter the full name.

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

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

In addtion to "HTG", enter the additional keyword(s) which depends on situation of sequeces. Keywords are listed on the following webpage, http://www.insdc.org/documents/methodological-keywords

"*** SEQUENCING IN PROGRESS ***" has to be included in ff_definition for unfinished HTG entry.

Two qualifiers, "estimated_length", "gap_type" are mandatory for describeing an assembly_gap feature. "linkage_evidence" are mandatory only , if value of "gap_type" is "within scaffold" or "repeat within scaffold".

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

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

DDBJ DNA Data Bank of Japan