Sample Annotation File: TSA (Transcriptome Shotgun Assembly) primary entries are from EST

This line is not required for annotation file.

Entry	Feature	Location	Qualifier	Value
COMMON	DIVISION		division	TSA
	KEYWORD		keyword	TSA
			keyword	Transcriptome Shotgun Assembly
	DBLINK		project	PRJDB43210
			biosample	SAMD80000000
	SUBMITTER		contact	Hanako Mishima
			ab_name	Mishima,H.
			ab_name	Yamada,T.
			email	mishima@ddbj.nig.ac.jp
			phone	81-55-981-6853
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			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.
			title	Glyceraldehy
			status	Unpublished
			year	2017
	DATE		hold_date	20191130
FA01	PRIMARY_CONTIG	1..598	entry	ZZ000004.1
			primary_bases	2..599
	PRIMARY_CONTIG	1..669	entry	ZZ000005.1
			primary_bases	11..679
	PRIMARY_CONTIG	2..596	entry	ZZ000006.0
			primary_bases	1..595
	PRIMARY_CONTIG	2..575	entry	ZZ000007.1
			primary_bases	1..574
	PRIMARY_CONTIG	5..676	entry	ZZ000008.1
			primary_bases	1..672
	PRIMARY_CONTIG	6..725	entry	ZZ000009.1
			primary_bases	1..720
	PRIMARY_CONTIG	59..369	entry	ZZ000010.1
			primary_bases	13..322
	PRIMARY_CONTIG	605..800	entry	ZZ000011.1
			primary_bases	1..196
			complement	
	source	1..E	organism	Homo sapiens
			mol_type	mRNA
			tissue_type	liver
			submitter_seqid	est_FA01
	CDS	73..669	gene	GAPD
			product	glyceraldehyde-3-phosphate dehydrogenase
			codon_start	1

Common information of all entries

First entry

Enter DIVISION "TSA".

KEYWORD "TSA" and "Transcriptome Shotgun Assembly" must be indicated.

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 location on the TSA sequence corresponding to the "primary" sequences.

Enter two qualifiers, "project" for BioProject ID and "biosample" for BioSample ID, on DBLINK line, respectively.

"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.

Enter the accession number (with version) of "primary" sequences.

If primary entry is not yet publicized, enter the accession number with version "0".

Enter the location on each "primary" sequence that contributes to the TSA sequence.

If primary sequence is corresponding to reverse strand in the TSA sequence, enter "complement" qualifier.

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