

Sample Annotation File: TSA (Transcriptome Shotgun Assembly)

primary entries are from short reads registered in SRA

This line is not required for annotation

Entry	Feature	Location	Qualifier	Value
COMMON	DIVISION		division	TSA
	KEYWORD		keyword	TSA
			keyword	Transcriptome Shotgun Assembly
	DBLINK		project	PRJDB43210
			biosample	SAMD70000000
			sequence read archive	DRR999999
	SUBMITTER		contact	Hanako Mishima
			ab_name	Mishima,H.
			ab_name	Yamada,T.
			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.
			title	Glyceraldehyde-3-phosphate dehydrogenase
			status	Unpublished
			year	2017
	DATE		hold_date	20191130
	ST_COMMENT		tagset_id	Assembly-Data
			Assembly Method	Velev v. 2.0
			Sequencing Technology	454 GS FLX; ABI 3730
FA01	source	1..E	organism	Homo sapiens
			mol_type	mRNA
			submitter_seqid	hs_liv_FA01
			tissue_type	liver
			ff_definition	@@[organism]@@ RNA, @@[submitter_seqid]@@
	CDS	73..669	gene	GAPD
			product	glyceraldehyde-3-phosphate dehydrogenase
			codon_start	1
FA02	source	1..E	organism	Homo sapiens
			mol_type	mRNA
			tissue_type	liver
			submitter_seqid	hs_liv_FA02
			ff_definition	@@[organism]@@ RNA, @@[submitter_seqid]@@

Common information of all entries

Enter DIVISION "TSA"

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

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

"PRIMARY_CONTIG" lines are not needed when the TSA sequence is assembled by raw read sequence deposited in the SRA database.

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

Enter the ST_COMMENT by which depends on the submitted sequences. Please see the Mass Submission System Making Files (COMMENT/ST_COMMENT) for details.

Enter the contig name using "submitter_seqid" qualifier.

First entry

Second entry

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, submitter_seqid, in ff_definition. Please visit the following site for detail. http://www.ddbj.nig.ac.jp/sub/mss/file_format-e.html#annotation-15