

Sample Annotation File: TPA (Third Party Data)

This line is not required for annotation file.

Entry	Feature	Location	Qualifier	Value
COMMON	DATATYPE		type	TPA
	KEYWORD		keyword	Third Party Data
	KEYWORD		keyword	TPA
	KEYWORD		keyword	TPA:experimental
	SUBMITTER		contact	Hanako Mishima
	ab_name		ab_name	Mishima,H.
	ab_name		ab_name	Yamada,T.
	email		email	mishima@ddbj.nig.ac.jp
	phone		phone	81-55-981-6853
	fax		fax	81-55-981-6849
	institute		institute	National Institute of Genetics
	department		department	DNA Data Bank of Japan
	country		country	Japan
	state		state	Shizuoka
	city		city	Mishima
	street		street	Yata 1111
	zip		zip	411-8540
	REFERENCE		ab_name	Mishima,H.
			ab_name	Yamada,T.
			title	Comparative genomic analysis of
			year	2015
			status	Unpublished
FA01	PRIMARY_CONTIG	1..552	entry	ZZ000001.1
			primary_bases	54872..55422
	PRIMARY_CONTIG	553..705	entry	ZZ000002.5
			primary_bases	1..153
	source	1..705	organism	Homo sapiens
			mol_type	mRNA
			tissue_type	liver
		1..705	gene	AQP9
			product	aquaporin 9
			codon_start	1
BM123	PRIMARY_CONTIG	1..438	entry	ZZ000010.1
			primary_bases	1..438
	PRIMARY_CONTIG	377..695	entry	ZZ000011.1
			primary_bases	1..320
			complement	
	PRIMARY_CONTIG	411..784	entry	ZZ000021.12
			primary_bases	1..398
	PRIMARY_CONTIG	790..1190	entry	ZZ000022.0
			primary_bases	1..401
	source	1..1191	organism	Shigella flexneri
			strain	BM123
			mol_type	genomic DNA
	CDS	122..1069	gene	APQZ
			product	aquaporin 2
			transl_table	11
			codon_start	1

Common information of all entries

First entry

Second entry

Enter DATATYPE "TPA".

KEYWORD "Third Party Data" and "TPA" must be indicated. In Addition, either TPA:experimental or TPA:inferential is needed.

Do not enter hold_date for TPA entry.

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

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

Enter the location on the TPA sequence corresponding to the "primary" sequences.

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

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