

Sample Annotation File: Coding Sequence

This line is not required for annotation file.

	Entry	Feature	Location	Qualifier	Value
Common information of all entries	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	Aquaporin gene	
			status	Unpublished	
			year	2017	
	DATE		hold_date	20191130	
First entry	ENT01	source	1..E	organism	Homo sapiens
				isolate	FA01
				mol_type	mRNA
				tissue_type	liver
		CDS	217..1104	gene	AQP9
				product	aquaporin 9
	3'UTR	1105..2878			
Second entry	ENT02	source	1..E	organism	Shigella flexneri
				strain	BM123
				mol_type	genomic DNA
		CDS	<1..1051	gene	APQZ
				product	aquaporin Z
				transl_table	11
			codon_start	2	

“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.

When translation should start at second or third nt, enter “2” or “3”. Default is

When the end of the feature is truncated, add “<” or “>”.

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.

When translation should start at second or third nt, enter "2" or "3". Default is

When the end of the feature is truncated, add "<" or ">".

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

Enter translation table code for the organism, in this case for bacteria "11". Default is "1". Please visit a following site for detail; ["http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi?mode=c"](http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi?mode=c).

Generally, email, phone, fax are not shown on DDBJ flat file.
If you wish to disclose any of the three items, please enter Qualifier: email_pub, phone_pub, fax_pub in Feature: SUBMITTER.
Please see the following site on Mass Submission System Making Files
"SUBMITT http://www.ddbj.nig.ac.jp/sub/mss/file_format-i.html#annotation-5

