Sample Annotation File: WGS (Whole Genome Shotgun) in

Common information of all entries

Entry	Feature	Location	Qualifier	Value
COMMON	DATATYPE		type	WGS
	KEYWORD		keyword	WGS
			keyword	STANDARD_DRAFT
	DBLINK		project	PRJDB90001
			biosample	SAMD90000000
			sequence read archive	DRR999900
	SUBMITTER		contact	Hanako Mishima
			consrtm	Streptomyces flavus genome
			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
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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.
			ab_name	Kim,K.-H.
			ab_name	Park,C.S.
			ab_name	Liu,G.Q.
			title	Streptomyces flavus NBRC 12345 whole genome shotgun sequence
			status	Unpublished
			year	2017
	DATE		hold_date	20191130
	COMMENT		line	Please visit our web page
			line	URL:http://www.ddbj.nig.ac.jp/
	ST_COMMENT		tagset_id	Genome-Assembly-Data
			Assembly Method	Velevt v. 2.0
			Assembly Name	Sfl_assembly01
			Genome Coverage	60x
			Sequencing Technology	454 GS FLX; ABI 3730
	source	1..E	organism	Streptomyces flavus
			mol_type	genomic DNA
			culture_collection	NBRC:12345
			strain	NBRC 12345
			ff_definition	@@[organism]@@ @@[strain]@@ DNA, @@[submitter_seqid]@@
			submitter_seqid	@@[entry]@@

Annotations:

- Enter DATATYPE and KEYWORD "WGS".
- Use consrtm "qualifier" for group name.
- In case of submission, entry name is not necessary. Header description for each entry in sequence file is reflected as contig name (value of /submitter_seq_id) on a publicized flat file.
- Select the KEYWORD from list of methodological KEYWORD. Keywords are listed on the following webpage, http://www.insdc.org/documents/methodological-
- Enter two qualifiers, "project" for BioProject ID and "biosample" for BioSample ID, on DBLINK line, respectively. When the sequeces is assembled by using short reads which were output from NGS, accession number of the Run Data issued by SRA database should be described
- Enter the full name for contact qualifier .
- 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. For eukaryotic genome entry(ies), "Assembly Name" qualifier is mandatory. Please see the Mass Submission System Making Files (COMMENT/ST_COMMENT) for details.
- Enter the contig name using "submitter_seqid" qualifier.
- Metadecription, @@[entry]@@, can be used to describe value for some qualifiers, such as clone, isolate, if entry name repesents clone or islate name. 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
- Source feature can be described on a submissio which all information, feature, qualifer and its value are same for all

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