# Sample Annotation File: CON entries for WGS scaffold

This line is not required for annotation file.

| Entry | Feature | Location | Qualifier | Value |
|---|---|---|---|---|
| COMMON | DATATYPE | | type | WGS |
| | DIVISION | | division | CON |
| | KEYWORD | | keyword | WGS |
| | | | keyword | NON_CONTIGUOU... |
| | DBLINK | | project | PRJDB12345 |
| | | | biosample | SAMD90000001 |
| | | | sequence read archive | DRR990000 |
| | SUBMITTER | | contact | Hanako Mishima... |
| | | | consrtm | Mouse genome se... |
| | | | ab_name | Mishima,H. |
| | | | ab_name | Yamada,T. |
| | | | ab_name | Kim,K.H. |
| | | | ab_name | Park,C.S. |
| | | | ab_name | Liu,G.Q. |
| | | | email | mishima@ddbj.nig... |
| | | | 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 | Kim,K.H. |
| | | | ab_name | Park,C.S. |
| | | | ab_name | Liu,G.Q. |
| | | | title | Mouse whole genom... |
| | | | status | Unpublished |
| | | | year | 2017 |
| | DATE | | hold_date | 20191130 |
| | COMMENT | | line | Please visit our web... |
| | | | line | URL:http://www.ddb... |
| | ST_COMMENT | | tagset_id | Genome-Assembly-Data |
| | | | Assembly Method | Velevt v. 2.0 |
| | | | Assembly Name | Mmus_assembly01 |
| | | | Genome Coverage | 60x |
| | | | Sequencing Technology | 454 GS FLX; ABI 3730 |
| scaffold1 | source | 1..E | organism | Mus musculus |
| | | | mol_type | genomic DNA |
| | | | strain | 15706 |
| | | | ff_definition | @@[organism]@@ @@[strain]@@ DNA, @@[submitter_seqid]@@ |
| | | | submitter_seqid | scaffold_contig001 |
| | assembly_gap | 12005..12500 | estimated_length | known |
| | | | gap_type | within scaffold |
| | | | linkage_evidence | align genus |
| | assembly_gap | 30001..30100 | estimated_length | unknown |
| | | | gap_type | within scaffold |
| | | | linkage_evidence | paired-ends |
| scaffold2 | source | 1..E | organism | Mus musculus |
| | | | mol_type | genomic DNA |
| | | | strain | 15706 |
| | | | ff_definition | @@[organism]@@ @@[strain]@@ DNA, @@[submitter_seqid]@@ |
| | | | submitter_seqid | scaffold_contig002 |

Common information of all entries

First entry

Second entry

**Callouts:**

Select the KEYWORD from list of methodological KEYWORD. Keywords are listed on the following webpage, http://www.insdc.org/documents/methodological-keywords.

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 outpit from NGS, accession number of the Run Data issued by SRA database should be described in "sequence read archive".

Enter "WGS" for DATATYPE, KEYWORD and "CON" for DIVISION.

Use consrtm qualifier for group name.

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.

Entry name should be unique to all entries, and identical to the one in the sequence file.

Enter the contig name using submitter_seqid qualifier. If an entry name represents value of submitter_id qualfiier, you can use metadescription, @@[entry]@@, to show sequence name, instead of concrete sequence name, respectively.

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

Metadecription can be used to represent value for some qualifiers, such as organism, submitter_seqid, in ff_definition. Please visit the following site for deatil. http://www.ddbj.nig.ac.jp/sub/mss/file_format-e.html#annotation-15

DDBJ
DNA Data Bank of Japan