

Sample Annotation File: Microsatellite Marker

| | Entry | Feature | Location | Qualifier | Value |
|-----------------------------------|--------|---------------|----------------------|----------------|--|
| Common information of all entries | COMMON | SUBMITTER | | contact | Hanako Mishima |
| | | | | ab_name | Mishima,H. |
| | | | | ab_name | Yamada,T. |
| | | | | email | mishima@ddbj.n |
| | | | | 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. |
| First entry | | | | title | Bovine microsatellite markers |
| | | | | status | Unpublished |
| | | | | year | 2017 |
| | | DATE | | hold_date | 20191130 |
| | | DIVISION | | division | STS |
| | | KEYWORD | | keyword | STS |
| | ENT01 | source | 1..E | organism | Bos taurus |
| | | | | chromosome | 11 |
| | | | | map | 11p |
| | | | | mol_type | genomic DNA |
| Second entry | | | | rpt_type | tandem |
| | | | | rpt_unit_seq | ta |
| | | | | satellite | microsatellite: 3456P |
| | | primer_bind | 20..40 | PCR_conditions | denaturation 94degC 2 min; 30 cycles 94degC 30 sec, 56degC 1 min, 72degC 1 min; final extension 72degC 1 min |
| | | | | note | forward primer |
| | | primer_bind | complement(254..274) | note | reverse primer |
| | ENT02 | source | 1..E | organism | Bos taurus |
| | | | | chromosome | 11 |
| | | | | map | 11p |
| | | | | mol_type | genomic DNA |
| | | repeat_region | 60..200 | rpt_type | tandem |
| | | | | rpt_unit_seq | ta |
| | | | | satellite | microsatellite: 3458P |
| | | | | PCR_conditions | denaturation 94degC 2 min; 30 cycles 94degC 30 sec, 56degC 1 min, 72degC 1 min; final extension 72degC 1 min |
| | | | | note | forward primer |
| | | primer_bind | complement(210..230) | note | reverse primer |

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