**From:** gb-admin@ncbi.nlm.nih.gov
**To:** [redacted]
**Subject:** DELETION Submissions grp 7385146

Dear GenBank Submitter,

As per our previous correspondence, we have deleted the following sequence submission(s) from our processing queue:

Received on Dec 28, 2019:
BankIt2298002 Coronavirus/Wuhan/2019/WH01

Sincerely,

The GenBank Submissions Staff
Bethesda, Maryland USA
**********************************************************************
gb-admin@ncbi.nlm.nih.gov (for replies and updates to current records)
info@ncbi.nlm.nih.gov (for general questions regarding GenBank)
**********************************************************************

**From:** gb-admin@ncbi.nlm.nih.gov
**To:** [redacted]
**Subject:** AUTODELETED group 7385146

Groups deleted (use these grids to undelete if necessary):
7385146[redacted]

**From:** [redacted]
**To:** [redacted]
**Subject:** WebSub 2298002 [BANKIT]

Comment: [redacted]
TOTAL # OF SEQS:1

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  contact {
   contact {
    name name {
     last "Xiang",
     first "Lili"
    },
    affil std {
     affil "Institute of Pathogen Biology, Chinese Academy of Medical
Sciences & Peking Union Medical College",
     div "Christophe Merieux Laboratory",
     city "Beijing",
     country "China",
     street "Dongdan santiao",
     email "[redacted]",
     postal-code "100730"
    }
   }
  },
  cit {
   authors {
    names std {
     {
      name name {
       last "Wu",
       first "Chao",
       initials "C."
      }
     },
     {
      name name {
       last "Liu",
       first "Yiwei",
       initials "Y."
      }
     },
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      name name {
       last "Guo",
       first "Li",
       initials "L."
      }
     }
    },
    affil std {
     affil "Institute of Pathogen Biology, Chinese Academy of Medical
Sciences & Peking Union Medical College",
     div "Christophe Merieux Laboratory",
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        country "China",
        street "Dongdan santiao",
        postal-code "100730"
      }
    },
    medium email,
    date std {
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      month 12,
      day 28,
      hour 3,
      minute 51,
      second 39
    }
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    month 12,
    day 31
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  tool "BankIt 5.0",
  comment "BankIt2298002"
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  set {
    class nuc-prot,
    descr {
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        org {
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          common "human",
          db {
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              db "taxon",
              tag id 9606
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          },
          orgname {
            name binomial {
              genus "Homo",
              species "sapiens"
            },
            attrib "specified",
            mod {
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                subtype strain,
                subname "Coronavirus/Wuhan/2019/WH01"
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                subname "Coronavirus/Wuhan/2019/WH01"
              },
              {
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        subname "Homo sapiens"
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      mgcode 2,
      div "PRI"
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      name "China"
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     {
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      data int 1
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        data int 28
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        data int 2019
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    month 12,
    day 28,
    hour 3,
    minute 54,
    second 12
  }
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      general {
        db "BankIt",
        tag str "2298002/Coronavirus/Wuhan/2019/WH01"
      }
    },
    descr {
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        biomol genomic,
        completeness complete
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            data str "fasta"
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    type str "StructuredComment",
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        data str "##Assembly-Data-START##"
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        label str "Assembly Method",
        data str "MEGA v. MEGA7.0"
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        data str "Mega"
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      {
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        data str "##Assembly-Data-END##"
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  },
  user {
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    data {
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        data str "LocalID:Coronavirus/Wuhan/2019/WH01"
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    }
  }
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  mol rna,
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Message

**From:** gb-admin@ncbi.nlm.nih.gov [gb-admin@ncbi.nlm.nih.gov]
**Sent:** 12/31/2019 12:07:37 PM
**To:** [redacted]
**BCC:** [redacted]
**Subject:** GenBank Submissions grp 7385146
**Attachments:** annotating_source_modifiers_bankit.txt; unique_information.txt

Dear Dr. Ren, Xiang:

We have received the following 1 sequence submission(s) from you:

BankIt2298002 :  (1)

Complete feature annotation has not been included for some or all of the sequence(s) you have submitted.

A. Please resubmit your sequence(s) with relevant features such as:

- coding regions (CDS features), partial or complete, including nucleotide spans and reading frame. Using this information, our software will add the amino acid translations for you.
- structural RNAs such as rRNAs, tRNAs, misc_RNAs, with nucleotide spans
- features which may describe your sequence, such as repeat_regions, UTRs, promoters with nucleotide spans

If we do not hear from you by Jan 14, 2020, all of your submission(s) will be deleted from the processing queue.

We have appended a list of a few common methods for adding features to records. We cannot accept annotation in text format; you must resubmit.

B. If you are unsure how to add the annotation, please contact GenBank Users Services at: info@ncbi.nlm.nih.gov and include this message with your request.

C. If you are unable to determine the feature annotation, please provide a biological reason for the lack of annotation. Alternatively, you may choose to unverify your records and the following comment will be added:

COMMENT  GenBank staff is unable to verify sequence and/or annotation provided by the submitter.

The commented record(s) will indicate that the data are unverified and your sequence(s) will not be included in NCBI BLAST databases.

For more information about annotating your submission, please see:

https://www.ncbi.nlm.nih.gov/books/NBK53711/

Please analyze your data prior to resubmission. In order to avoid delays in receiving your accession numbers, ensure that your submission does not have:

- internal stop codons or reading frame shifts in any coding regions
- sequences less than 200 bp
- sequences containing vector contamination
- untrimmed low-quality sequencing read ends

In addition, include:

- unique identifying information for each sample, such as strain isolate, clone, specimen voucher or laboratory identifier
- properly fielded source information using the correct source modifiers

Details about adding identifiers and other source information are attached.

Send your reply to: gb-admin@ncbi.nlm.nih.gov and your resubmitted
sequence(s) through Bankit.

Thank you for your attention. We will not assign GenBank Accession Numbers or further process your submissions until we hear from you.

For your reference, please find your preliminary records below.

Please reply using the current Subject line.

Sincerely,

[redacted]

The GenBank Submissions Staff
Bethesda, Maryland USA

******************************************************************

gb-admin@ncbi.nlm.nih.gov (for replies and updates to current records)
info@ncbi.nlm.nih.gov (for general questions regarding GenBank)

******************************************************************

The "Features" Page in BankIt:
https://www.ncbi.nlm.nih.gov/books/NBK53711/#gbankquickstart.Feature_Annotation_Using

Formatting your Submission:
https://www.ncbi.nlm.nih.gov/books/NBK53702/

adding annotation using Bankit:

[1] You must start a new BankIt submission; do not send an email with the annotation.

[2] If you upoaded a nucleotide FASTA file, features can be added in BankIt on the 'Features' page by choosing either the 'Forms' or the 'Files' option.

If you uploaded a nucleotide alignment file, you will have the option to use Feature Propagate to annotate features. Feature Propagate allows you to annotate just one sequence via 'Files' or 'Forms' and then features are applied to the other sequences in the alignment automatically.

i.Choosing 'Files' allows you to upload a 5-column feature table file, which is described at: https://www.ncbi.nlm.nih.gov/Sequin/table.html#Table Layout

ii. Choosing 'Forms' allows you to input information for your choice of features from the following types:

- Coding Region (CDS, with applicable Gene and/or mRNA)
- RNA Features (tRNA, rRNA, etc)
- Repeat Region (for simple repeats, mobile elements, satellites)
- Other Features (5''UTR, 3''UTR, exons, introns, promoters, etc)

Once you have chosen a specific feature, follow the instructions to input the features descriptive information (nucleotide intervals, protein name, rRNA name, gene name etc).

[3] On the Review and Correct page, check the box in point 2 to indicate you are resubmitting and provide the previous bankit xxxxxxx or group number ###### in the text box.

Click on Finish Submission to submit your record(s).

******************************************************************

preliminary GenBank flatfiles:

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LOCUS       Coronavirus/Wuhan/2019/WH0129684 bp    RNA    linear   PRI 28-DEC-2019
DEFINITION  Homo sapiens strain Coronavirus/Wuhan/2019/WH01 isolate
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ACCESSION
VERSION
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 29684)
  AUTHORS   Wu,C., Liu,Y. and Guo,L.
```

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  TITLE     Direct Submission
  JOURNAL   Submitted (28-DEC-2019) Christophe Merieux Laboratory, Institute of
            Pathogen Biology, Chinese Academy of Medical Sciences & Peking
            Union Medical College, Dongdan santiao, Beijing 100730, China
COMMENT     Bankit Comment: LocalID:Coronavirus/Wuhan/2019/WH01.
            Bankit Comment: BankIt2298002.

            ##Assembly-Data-START##
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            ##Assembly-Data-END##
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annotating source modifiers:

Providing source information in your submission:

https://www.ncbi.nlm.nih.gov/books/NBK53701/

Annotating nucleotide FASTA definitions with source modifiers:

https://www.ncbi.nlm.nih.gov/books/NBK53702/#gbankquickstart.how_do_i_format_a_fasta

The ?Source Modifiers? Page in BankIt:

https://www.ncbi.nlm.nih.gov/books/NBK293914/#BankItUserGuide.The__Source_Modifiers_Se

Importing and Adding Source Modifiers with Table:

https://www.ncbi.nlm.nih.gov/books/NBK53702/#gbankquickstart.can_you_give_me_stepbyst_1

https://www.ncbi.nlm.nih.gov/WebSub/html/help/genbank-source-table.html

Common Mistakes:

https://www.ncbi.nlm.nih.gov/books/NBK293914/#BankItUserGuide.Common_Mistakes_Made_Whi_
4