

## [Ext] GenBank MW434077-MW434122, MW434124-MW434134, MW434221-MW435021

**gb-admin@ncbi.nlm.nih.gov** <gb-admin@ncbi.nlm.nih.gov> To: amy.kistler@czbiohub.org

Fri, Feb 19, 2021 at 9:36 AM

Dear GenBank Submitter:

Thank you for your submission.

Based on the data submitted to us, the scheduled release date for your submission is:

Feb 24, 2021

If this date is not correct, let us know as soon as possible, otherwise this submission will be released on the date indicated above. The data will become available from our different servers within a few days of release. The data are simultaneously made available to ENA in Europe and the DNA Data Bank of Japan.

Due to the size of your submission, we have not included your GenBank flatfiles with this letter.

If you would like to see representative records for your review before your sequences are released, please let us know.

Changes may have been made to your original submission in order to conform to database annotation conventions including:

- Strings of N's, low quality sequence, vector or linker trimmed from ends
- Feature spans corrected and descriptions modified for all feature types including coding regions
- Nomenclature edited to 'official' gene names, product labels, etc.
- Exon spans adjusted to conform to the splice donor/acceptor consensus sequences, GT and AG, respectively
- Any mRNA or ribosomal RNA sequences submitted on the minus-strand have been reverse-complemented
- Taxonomic and source data edited, including unpublished organism names changed to temporary names. Please notify us when the organism names are published and we will update them accordingly.

If your submission needs revision, do not submit a new sequence. Instead, follow the directions to update a sequence record at: https://www.ncbi.nlm.nih.gov/Genbank/update.html Since the flatfile record is a display format only and is not an editable format of the data, do not make changes directly to a flatfile. Send properly formatted updates to: gb-admin@ncbi.nlm.nih.gov

An accession number has been assigned to each nucleotide sequence and was previously provided to you. During the processing, we have assigned protein identifiers to any proteins within the submission. This is fielded as /protein\_id.

We strongly recommend that these numbers appear in any publication which reports or discusses these data, so that readers may easily retrieve your data from our databases.

Please reply using the current Subject line.

Sincerely,

Linda Frisse, PhD GenBank Direct Submission Staff gb-admin@ncbi.nlm.nih.gov