



MAR 09, 2023

Submitting Genomes

emma.pearce¹¹UCSF

emma.pearce

ABSTRACT

Steps to submit a genome to NCBI through Bankit

OPEN ACCESS

External link:

<https://www.ncbi.nlm.nih.gov/WebSub/?form=history&tool=genbank>

Protocol Citation: emma.pearce 2023. Submitting Genomes. **protocols.io**
<https://protocols.io/view/submitting-genomes-cpfmvjk6>

License: This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Protocol status: In development
We are still developing and optimizing this protocol

Created: Feb 14, 2023**Last Modified:** Mar 09, 2023**PROTOCOL integer ID:**
77005**Keywords:** bankit, submitting, ncbi

Submitting to Bankit

1 Log into Bankit with UCSF username and password:

- Follow this link: <https://www.ncbi.nlm.nih.gov/WebSub/?form=history&tool=genbank>
- Choose more login options and select University of California, San Francisco

2 Select "Start Bankit Submission"

3 Fill out the contact information

4 **Sequence Authors:**

List all sequence authors (use the Add button for more than one)

Reference Information #1:

Select publication status (unpublished, in-press, or Published)

- If in-press add reference title, journal title, year, volume, issue, and page numbers
- If published add reference title, journal title, year, volume, issue, page numbers, and PubMed ID

- Optional: if unpublished add reference title

Select reference authors as "Same as Sequence Authors" or "Specify New Authors"

- If specify new authors, list authors

(Optional) Add Another Reference:

Follow Reference Information #1 steps

5 **Sequencing Technology:**

Select the sequencing technology (or other and specify)

Select unassembled sequence reads or assembled sequences (consisting of two or more sequence reads)

List assembly program and version or date

Example: Illumina, Geneious v. Geneious Prime 2023.0.1

6 **Submission Release Date:**

Select "Immediately after processing" or "Release date"

- If Release Date is selected, specify date in DD-Mon-YYYY format

Sequence(s) and Definition Line(s):

Choose molecule type, linear or circular, if it is a complete sequence, and fasta or alignment format

Either download sequence file or copy and paste it in the box

- Note: make sure the first line follows this format; make everything in bold specific to your submission

>Seq#[organism=**genus species**] **species strain**info

Example: >Seq1[organism=Enterovirus rhinovirus] Rhinovirus C17 strain RvC17/USA/2019

7 Submission Category:
Select "Original" or "Third Party Annotation"

8 Source Modifiers:
Choose organelle/location if applicable
Choose source modifiers and list information in value column, add as many as desired

Example: Strain = RvC17/USA/2019, host = homo sapiens, tissue_type = Lung, country = USA, collection_date = 2019

9 Features (Overview):
Select "Add features by completing input forms"
Select "Coding Region (CDS) / Gene / mRNA"
Select "providing intervals"
Click Add

10 Features (Detail):
Choose if the CDS is on the + or - strand
If the CDS is not complete, select 5' or 3' for which end it is incomplete at
Select "Entire Sequence" or "Specific Spans" for Nucleotide Interval Spans
- If Specific Spans, specify start and stop and which strand it is on
List protein name (optional: also list protein description and EC number)
Click accept

Example: specific spans: start = 19 stop = 6498 strand = -minus; protein name = polyprotein

11 Review Submission:
Make sure everything looks good
If resubmitting check the box under the resubmission section