

From: [Myles, Renate \(NIH/OD\) \[E\]](#)
To: [Nathaniel Weixel](#)
Cc: [Fine, Amanda \(NIH/OD\) \[E\]](#); [Emma Wojtowicz](#)
Subject: RE: Statement on database deletion?
Date: Wednesday, June 23, 2021 5:14:00 PM

Hi Nathaniel:

Thanks for checking with us. The below statement is attributable to NIH generally. Off the record: we think this WaPo story does a good job characterizing the situation:

https://www.washingtonpost.com/health/coronavirus-origin-nih-gene-sequence-deletion/2021/06/23/186e87d0-d437-11eb-a53a-3b5450fdca7a_story.html

NIH is aware of Dr. Bloom's preprint submission. Staff at the National Library of Medicine (NLM), which hosts the Sequence Read Archive (SRA), have reviewed the submitting investigator's request to withdraw the data. These SARS-CoV-2 sequences were submitted for posting in SRA in March 2020 and subsequently requested to be withdrawn by the submitting investigator in June 2020. The requestor indicated the sequence information had been updated, was being submitted to another database, and wanted the data removed from SRA to avoid version control issues. The submitting investigator published relevant information about these sequences [by preprint in March, 2020](#) and in a [journal in June, 2020](#). Submitting investigators hold the rights to their data and can request withdrawal of the data.

Currently, NLM has no plans to change the policy that recognizes submitters rights to their own data and the right to petition that their data be withdrawn from the SRA. The National Center for Biotechnology Information (NCBI), part of the NLM that manages the database, is the U.S. participating member of the International Nucleotide Sequence Database Collaboration (INSDC), which provides guidelines for withdrawing data: <http://www.insdc.org/documents/insdc-status-document>. NLM/NCBI can't speculate on motive beyond a submitter's stated intentions.

Thanks,
Renate

Renate Myles, MBA

Acting Associate Director for Communications and Public Liaison
Acting Director, Office of Communications and Public Liaison
National Institutes of Health
Tel: (b) (6)



From: Nathaniel Weixel <nweixel@thehill.com>
Sent: Wednesday, June 23, 2021 4:46 PM
To: Myles, Renate (NIH/OD) [E] (b) (6)
Subject: Statement on database deletion?

Hi Renate, does NIH have a response to the deletion of SRA data on the genetic sequence of SARS-CoV-2, as alleged in this preprint? Is it standard for the agency to grant such a request?

<https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1.full.pdf>

Thanks,

--

Nathaniel Weixel
Healthcare Reporter
The Hill
Cell: (b) (6)

From: [Myles, Renate \(NIH/OD\) \[E\]](#)
To: [Salzman, Sony](#)
Cc: [Strauss, Eric M.](#); [Fine, Amanda \(NIH/OD\) \[E\]](#); [Emma Wojtowicz](#)
Subject: RE: Request for comment on Dr. Bloom's recent paper
Date: Wednesday, June 23, 2021 5:09:00 PM

Hi Sony:

Thanks for checking with us. The below statement is attributable to NIH generally. Off the record: the WaPo story is much more even-keeled than the NYT piece:

https://www.washingtonpost.com/health/coronavirus-origin-nih-gene-sequence-deletion/2021/06/23/186e87d0-d437-11eb-a53a-3b5450fdca7a_story.html

NIH is aware of Dr. Bloom's preprint submission. Staff at the National Library of Medicine (NLM), which hosts the Sequence Read Archive (SRA), have reviewed the submitting investigator's request to withdraw the data. These SARS-CoV-2 sequences were submitted for posting in SRA in March 2020 and subsequently requested to be withdrawn by the submitting investigator in June 2020. The requestor indicated the sequence information had been updated, was being submitted to another database, and wanted the data removed from SRA to avoid version control issues. The submitting investigator published relevant information about these sequences [by preprint in March, 2020](#) and in a [journal in June, 2020](#). Submitting investigators hold the rights to their data and can request withdrawal of the data.

Currently, NLM has no plans to change the policy that recognizes submitters rights to their own data and the right to petition that their data be withdrawn from the SRA. The National Center for Biotechnology Information (NCBI), part of the NLM that manages the database, is the U.S. participating member of the International Nucleotide Sequence Database Collaboration (INSDC), which provides guidelines for withdrawing data: <http://www.insdc.org/documents/insdc-status-document>. NLM/NCBI can't speculate on motive beyond a submitter's stated intentions.

Thanks,
Renate

Renate Myles, MBA

Acting Associate Director for Communications and Public Liaison
Acting Director, Office of Communications and Public Liaison
National Institutes of Health
Tel: (b) (6)



From: Salzman, Sony <Sony.Salzman@abc.com>

Sent: Wednesday, June 23, 2021 4:59 PM

To: Myles, Renate (NIH/OD) [E] (b) (6)

Cc: Strauss, Eric M. <Eric.M.Strauss@abc.com>

Subject: Request for comment on Dr. Bloom's recent paper

Hi Reneta,

I'm the coordinating producer of ABC's Medical Unit. Would you mind sharing a statement about the deleted raw data from the SRA database, recently described in a preprint from Dr. Jesse Bloom at FredHutch?

I believe you explained to NYT and others that the sequences were submitted and then requested to be withdrawn. And - just checking - would you be willing to share more information about who made the request?

Thank you in advance,

Sony Salzman

Coordinating Producer

ABC News Medical Unit

From: [Myles, Renate \(NIH/OD\) \[E\]](#)
To: [Carl Zimmer](#); [Wojtowicz, Emma \(NIH/OD\) \[E\]](#)
Cc: [Fine, Amanda \(NIH/OD\) \[E\]](#); [Virginia Hughes](#)
Subject: RE: FW: Query from New York Times journalist about preprint on sequences deleted from SRA
Date: Wednesday, June 23, 2021 4:49:00 PM

Hi Carl:

I saw your story. Just noting that it isn't a mystery. The researcher asked for it be withdrawn and it was withdrawn. Also, it didn't disappear; it was removed per the submitter's request. Off the record: I know that Dr. Bloom is making the mystery part of the narrative of his paper, but we expected reporters not hype language.

Also, just to clarify, NLM conducted an analysis and found that eight SARS-COV-2 submission packages were withdrawn upon request of the submitter since the beginning of the pandemic. This included one requested by the submitter from China and the rest from submitters predominantly in the U.S.

Thanks,
Renate

From: Carl Zimmer <carl.zimmer@nytimes.com>
Sent: Wednesday, June 23, 2021 4:35 PM
To: Wojtowicz, Emma (NIH/OD) [E] [REDACTED] (b) (6)
Cc: Myles, Renate (NIH/OD) [E] [REDACTED] (b) (6); Fine, Amanda (NIH/OD) [E] [REDACTED] (b) (6); Virginia Hughes <virginia.hughes@nytimes.com>
Subject: Re: FW: Query from New York Times journalist about preprint on sequences deleted from SRA

Thanks! I will get her name fixed ASAP.

c

Carl Zimmer
Columnist
[REDACTED]
carl.zimmer@nytimes.com
Author website carlzimmer.com

On Wed, Jun 23, 2021 at 3:45 PM Wojtowicz, Emma (NIH/OD) [E] [REDACTED] (b) (6) wrote:

Hi Carl-

We see your [story](#) ran. Please note that you spelled Renate's name wrong. The correct spelling is Renate, not Renata; please correct the spelling of her name.

Regarding your question about the requestor, you will have to submit a FOIA request. And in follow up to your other question about how common is it:

Over a one year period from March 2020-2021, there were 2.4 million submissions processed of all types of sequence data (not just SARS-CoV-2) and posted to the SRA. 0.19% have been withdrawn.

Thank you-
Emma

From: Carl Zimmer <carl.zimmer@nytimes.com>

Sent: Wednesday, June 23, 2021 1:54 PM

To: Myles, Renate (NIH/OD) [E] [REDACTED] (b) (6)

Cc: Fine, Amanda (NIH/OD) [E] [REDACTED] (b) (6); Wojtowicz, Emma (NIH/OD) [E] [REDACTED] (b) (6)

Subject: Re: FW: Query from New York Times journalist about preprint on sequences deleted from SRA

In the spreadsheet where these sequences are listed in a PeerJ paper, the contact name is Aisi Fu of Wuhan University. Can you confirm that this is also the name of the person who requested the sequences be deleted from SRA?

Thank you.

Best wishes,

Carl

Carl Zimmer
Columnist

[REDACTED]

carl.zimmer@nytimes.com

Author website carlzimmer.com

On Wed, Jun 23, 2021 at 11:34 AM Myles, Renate (NIH/OD) [E] [REDACTED] (b) (6) wrote:

Hi Carl:

Thanks for checking with us and hope you're well.

NIH is aware of Dr. Bloom's preprint submission. Staff at the National Library of Medicine (NLM), which hosts the Sequence Read Archive (SRA), have reviewed the submitting investigator's request to withdraw the data. These SARS-CoV-2 sequences

were submitted for posting in SRA in March 2020 and subsequently requested to be withdrawn by the submitting investigator in June 2020. The requestor indicated the sequence information had been updated, was being submitted to another database, and wanted the data removed from SRA to avoid version control issues. The submitting investigator published relevant information about these sequences [by preprint in March, 2020](#) and in a [journal in June, 2020](#). Submitting investigators hold the rights to their data and can request withdrawal of the data.

Currently, NLM has no plans to change the policy that recognizes submitters rights to their own data and the right to petition that their data be withdrawn from the SRA. The National Center for Biotechnology Information (NCBI), part of the NLM that manages the database, is the U.S. participating member of the International Nucleotide Sequence Database Collaboration (INSDC), which provides guidelines for withdrawing data: <http://www.insdc.org/documents/insdc-status-document>. NLM/NCBI can't speculate on motive beyond a submitter's stated intentions.

In terms of your last question, yes, other requests for deletions have occurred, consistent with what is outlined in the INSDC link. I'll have to see if it's other SARS-CoV-2 sequence data. Will get back to you.

Thanks,
Renate

Renate Myles, MBA

Acting Associate Director for Communications and Public Liaison
Acting Director, Office of Communications and Public Liaison
National Institutes of Health
Tel: (b) (6)



From: Carl Zimmer <carl.zimmer@nytimes.com>

Sent: Wednesday, June 23, 2021 9:48 AM

To: NLM Communications <NLMCommunications@nlm.nih.gov>; Crutchman, Alise (NIH/NLM)

[E] (b) (6)

Subject: Query from New York Times journalist about preprint on sequences deleted from SRA

Greetings:

Last night a preprint was published by Jesse Bloom, a virologist at the Fred Hutchinson Cancer Institute, on how he recovered SARS-CoV-2 sequences originally stored on SRA: <https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1>

Dr. Bloom mentioned that he had spoken to Dr. Stephen Sherry of NCBI about the request from the authors to delete the sequences.

I'm writing about the preprint. If possible, I'd like to see a copy of the email from the scientists who requested the deletion. The project is Bio-Project PRJNA612766 by Aisu Fu and colleagues at Wuhan University.

I'd like to know why they requested its deletion, if they gave any reason.

I was also wondering how common it is for scientists to request removal of sequences from SRA. Also, have other SARS-Cov-2 sequences been removed?

Thanks for your help.

Best wishes,

Carl Zimmer

Columnist

carl.zimmer@nytimes.com

Author website carlzimmer.com

From: [Myles, Renate \(NIH/OD\) \[E\]](#)
To: [Jon Cohen](#)
Cc: [Fine, Amanda \(NIH/OD\) \[E\]](#); [Emma Wojtowicz](#)
Subject: RE: Status Update for Request #56587
Date: Wednesday, June 23, 2021 10:56:00 AM

Hi Jon:

Thanks for reaching out and hope you're well. I'll ask the FOIA office if they can expedite the actual email exchange, but in the meantime the below statement captures it. The statement is attributable to NIH generally:

NIH is aware of Dr. Bloom's preprint submission. Staff at the National Library of Medicine, which hosts the Sequence Read Archive (SRA), have reviewed the submitting investigator's request to withdraw the data. These SARS-CoV-2 sequences were submitted for posting in SRA in March 2020 and subsequently requested to be withdrawn by the submitting investigator in June 2020. The requestor indicated the sequence information had been updated, was being submitted to another database, and wanted the data removed from SRA to avoid version control issues. The submitting investigator published relevant information about these sequences [by preprint in March, 2020](#) and in a [journal in June, 2020](#). Submitting investigators hold the rights to their data and can request withdrawal of the data.

Thanks,
Renate

Renate Myles, MBA

Acting Associate Director for Communications and Public Liaison
Acting Director, Office of Communications and Public Liaison
National Institutes of Health
Tel: (b) (6)



From: Jon Cohen <jcohen@aaas.org>
Sent: Wednesday, June 23, 2021 10:47 AM
To: Myles, Renate (NIH/OD) [E] (b) (6)
Subject: Fwd: Status Update for Request #56587

Hi Renate,

I filed this request for the e-mail exchange between NCBI and Chinese researchers who had SARS-CoV-2 sequence data in the SRA removed, which Jesse Bloom writes about here:

<https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1>.

Any chance you could help expedite?

I've heard, too, that NIH is planning to release a statement?

Thanks for the help.

Best,

Jon

Begin forwarded message:

From: FOIA_noreply@nih.gov
Subject: Status Update for Request #56587
Date: June 23, 2021 at 6:50:25 AM PDT
To: jcohen@aaas.org

[EXTERNAL EMAIL]

Dear Jon Cohen,

The status of your FOIA request #56587 has been updated to the following status 'Received'. To log into the NIH FOIA Public Portal click on the Application URL below.

<https://foiaportal.nih.gov>

Sincerely,
National
Institutes of Health

From: [Alison Young](#)
To: [Myles, Renate \(NIH/OD\) \[E\]](#)
Subject: Re: Seeking NIH comment/interview on deleted early SARS-CoV-2 sequences
Date: Wednesday, June 23, 2021 8:48:23 AM

Thanks, Renate.

On Wed, Jun 23, 2021 at 8:44 AM Myles, Renate (NIH/OD) [E] [REDACTED] (b) (6) wrote:

The submitter did not provide that information.

From: Alison Young [REDACTED] (b) (6)
Sent: Wednesday, June 23, 2021 8:36 AM
To: Myles, Renate (NIH/OD) [E] [REDACTED] (b) (6)
Cc: Fine, Amanda (NIH/OD) [E] [REDACTED] (b) (6); Wojtowicz, Emma (NIH/OD) [E] [REDACTED] (b) (6); Crutchman, Alise (NIH/NLM) [E]
Subject: Re: Seeking NIH comment/interview on deleted early SARS-CoV-2 sequences

Thanks, Renate.

Can you also tell me what database the scientists said they were moving the data to when they requested the deletion?

Alison

On Wed, Jun 23, 2021 at 8:32 AM Myles, Renate (NIH/OD) [E] [REDACTED] (b) (6) wrote:

Hi Alison:

The response below is attributable to NIH generally:

Currently, the National Library of Medicine (NLM) has no plans to change the policy that recognizes submitters rights to their own data and the right to petition that their data be withdrawn from the Sequence Read Archive (SRA). The National Center for

Biotechnology Information (NCBI), part of the NLM that manages the database, is the U.S. participating member of the International Nucleotide Sequence Database Collaboration, which provides guidelines for withdrawing data: <http://www.insdc.org/documents/insdc-status-document>. NLM/NCBI can't speculate on motive beyond a submitter's stated intentions.

Also, just a note that Elizabeth Weise also reached out to us.

Thanks,

Renate

From: Myles, Renate (NIH/OD) [E]
Sent: Tuesday, June 22, 2021 10:04 PM
To: Alison Young (b) (6)
Cc: Fine, Amanda (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6); Crutchman, Alise (NIH/NLM) [E] (b) (6)
Subject: RE: Seeking NIH comment/interview on deleted early SARS-CoV-2 sequences

Hi Alison:

I'm checking for you.

Renate

From: Alison Young (b) (6)
Sent: Tuesday, June 22, 2021 9:47 PM
To: Myles, Renate (NIH/OD) [E] (b) (6)
Cc: Fine, Amanda (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6); Crutchman, Alise (NIH/NLM) [E] (b) (6)
Subject: Re: Seeking NIH comment/interview on deleted early SARS-CoV-2 sequences

Thanks, Renate. Can you say anything about whether NIH is doing any analysis or examination to look for any other SARS-CoV-2 sequence data that has been deleted from that database? And is NIH discussing any potential policy changes related to the future management of this data?

Alison

On Tue, Jun 22, 2021 at 9:39 PM Myles, Renate (NIH/OD) [E] (b) (6)
wrote:

Hi Alison:

Thanks for checking with us. The below statement is attributable to NIH directly:

NIH is aware of Dr. Bloom's preprint submission. Staff at the National Library of Medicine, which hosts the Sequence Read Archive (SRA), have reviewed the submitting investigator's request to withdraw the data. These SARS-CoV-2 sequences were submitted for posting in SRA in March 2020 and subsequently requested to be withdrawn by the submitting investigator in June 2020. The requestor indicated the sequence information had been updated, was being submitted to another database, and wanted the data removed from SRA to avoid version control issues. The submitting investigator published relevant information about these sequences [by preprint in March, 2020](#) and in a [journal in June, 2020](#). Submitting investigators hold the rights to their data and can request withdrawal of the data.

NIH can't speculate on motive beyond the investigator's stated intentions.

Thanks,

Renate

Renate Myles, MBA

Acting Associate Director for Communications and Public Liaison

Acting Director, Office of Communications and Public Liaison

National Institutes of Health

Tel: (b) (6)



From: Alison Young [REDACTED] (b) (6)
Sent: Tuesday, June 22, 2021 7:41 PM
To: Myles, Renate (NIH/OD) [E] [REDACTED] (b) (6); Fine, Amanda (NIH/OD) [E] [REDACTED] (b) (6); Wojtowicz, Emma (NIH/OD) [E] [REDACTED] (b) (6); Crutchman, Alise (NIH/NLM) [E] [REDACTED] (b) (6)
Subject: Seeking NIH comment/interview on deleted early SARS-CoV-2 sequences

Renate, Amanda, Emma and Alise:

I apologize for the late email. Jesse Bloom, an evolutionary biologist at the Fred Hutchinson Cancer Research Center, has posted on a pre-print site (and a very long Twitter thread) in which he details how he discovered that someone went into a repository of virus sequences (called the Sequence Read Archive) and deleted entries from early Wuhan case samples.

Dr. Bloom has indicated that NIH Director Collins and officials at NCBI are aware of what has occurred and that they shared the information with him. But Bloom wrote on Twitter that he "will let them share more widely."

So I'm reaching out to find out what can Dr. Collins and NCBI officials say about:

- Who deleted the sequences from Sequence Read Archive that were discovered by Dr. Bloom? The person's name, affiliation, title, country of residence/work?
- What was the stated reason for the deletions at the time they were removed? (Has NIH reached the individual(s) since Dr. Bloom raised concerns? Has any additional explanation been provided?)
- On what date were the sequences deleted?
- When did NIH become aware of these deletions?
- How significant are these deleted sequences to understanding the origins of SARS2? Would they have changed potentially the conclusions in the Proximal Origins paper (Andersen et. al.) that has so far been seen as the most important

- analysis of the virus' genome?
- What follow-up has NIH done since being alerted to the deletions of these sequences? Have any other deleted sequences been identified that involve SARS-CoV-2?
 - From Dr. Collins/NIH's perspective, what are the potential implications of Dr. Bloom's findings of the deleted sequences -- and his further analysis of the recovered data?
 - Does NIH have any plans to change how data deletions are handled in the future?

Here is Dr. Bloom's Twitter thread, which includes a link to the pre-print paper: https://twitter.com/jbloom_lab/status/1407445604029009923

In it he says:

The ability for scientists to delete data from the SRA "may have been used to obscure sequences informative for understanding early #SARSCoV2," he wrote on Twitter. "It is important to examine if other trust-based systems in science conceivably may have also been used to hide data relevant to origins / early spread of #SARSCoV2..."

In his Twitter string, Dr. Bloom notes that the database has "rigorous data tracking" enabling the systems officials at NIH to determine when data was deleted and the justification by the authors.

Thank you in advance for any interview or comment you all can provide.

Alison

--

Alison Young

Independent Journalist, bylines in USA TODAY, ProPublica and more

AlisonYoungReports.com

Mobile: (b) (6)

(b) (6)

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Alison Young

Mobile: [REDACTED] (b) (6)

AlisonYoungReports.com

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Alison Young

Mobile: [REDACTED] (b) (6)

AlisonYoungReports.com

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Alison Young

Mobile: [REDACTED] (b) (6)

AlisonYoungReports.com

From: [Myles, Renate \(NIH/OD\) \[E\]](#)
To: [Fox, Maggie; Fine, Amanda \(NIH/OD\) \[E\]](#)
Cc: [Burklow, John \(NIH/OD\) \[E\]](#); [Wojtowicz, Emma \(NIH/OD\) \[E\]](#); [Brodd, Lauren \(NIH/OD\) \[E\]](#)
Subject: RE: Jesse Bloom and missing SARS-Cov2-2 genetic sequences
Date: Wednesday, June 23, 2021 8:36:00 AM

Hi Maggie:

Hope you're well. Dr. Collins is out on vacation this week, so isn't available. Here is a statement attributable to NIH generally.

NIH is aware of Dr. Bloom's preprint submission. Staff at the National Library of Medicine, which hosts the Sequence Read Archive (SRA), have reviewed the submitting investigator's request to withdraw the data. These SARS-CoV-2 sequences were submitted for posting in SRA in March 2020 and subsequently requested to be withdrawn by the submitting investigator in June 2020. The requestor indicated the sequence information had been updated, was being submitted to another database, and wanted the data removed from SRA to avoid version control issues. The submitting investigator published relevant information about these sequences [by preprint in March, 2020](#) and in a [journal in June, 2020](#). Submitting investigators hold the rights to their data and can request withdrawal of the data.

Currently, the National Library of Medicine (NLM) has no plans to change the policy that recognizes submitters rights to their own data and the right to petition that their data be withdrawn from the Sequence Read Archive (SRA). The National Center for Biotechnology Information (NCBI), part of the NLM that manages the database, is the U.S. participating member of the International Nucleotide Sequence Database Collaboration, which provides guidelines for withdrawing data: <http://www.insdc.org/documents/insdc-status-document>. NLM/NCBI can't speculate on motive beyond a submitter's stated intentions.

Thanks much,
Renate

From: Fox, Maggie <Maggie.Fox@cnn.com>
Sent: Wednesday, June 23, 2021 12:00 AM
To: Fine, Amanda (NIH/OD) [E] (b) (6)
Cc: Burklow, John (NIH/OD) [E] (b) (6); Myles, Renate (NIH/OD) [E]
(b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6)
Subject: Jesse Bloom and missing SARS-Cov2-2 genetic sequences

Hi y'all-

Jesse Bloom, geneticist at Fred Hutchinson Cancer Center, published this preprint and has been all over Twitter tonight saying early sequences of coronavirus samples from Wuhan were somehow deleted from the NIH database. He says Dr Collins confirmed this and was helping him track it down? <https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1.full.pdf>

Can you all confirm this and may I speak to Dr. Collins about it?

Thank you so much!

Maggie Fox
Senior Editor, Health

CNN

404-333-4509

From: [Nurik, Jody \(NIH/NLM\) \[E\]](#)
To: [Myles, Renate \(NIH/OD\) \[E\]](#); [Tuncer, Diane \(NIH/NLM\) \[E\]](#)
Cc: [Fine, Amanda \(NIH/OD\) \[E\]](#); [Wojtowicz, Emma \(NIH/OD\) \[E\]](#)
Subject: RE: FLAGGING: SARS-CoV-2 data deleted from the NIH/NCBI SRA
Date: Tuesday, June 22, 2021 10:42:20 AM
Attachments: [image001.png](#)

Thanks, Renate! Let us know if we can help out in anyway.

Jody

Jody Nurik
Communications Director, Office of Communications and Public Liaison
National Library of Medicine | National Institutes of Health
Office: (b) (6)



From: Myles, Renate (NIH/OD) [E] (b) (6)
Sent: Tuesday, June 22, 2021 9:56 AM
To: Nurik, Jody (NIH/NLM) [E] (b) (6); Tuncer, Diane (NIH/NLM) [E]
(b) (6)
Cc: Fine, Amanda (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E]
(b) (6)
Subject: RE: FLAGGING: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Thanks, Jody. We'll need lots of eyes. Also, I made a light tweak to the response. We'll handle it here.

NIH is aware of Dr. Bloom's preprint submission. Staff at the National Library of Medicine, which hosts the Sequence Read Archive (SRA), have reviewed the submitting investigator's request to withdraw the data. These SARS-CoV-2 sequences were submitted for posting in SRA in March 2020 and subsequently requested to be withdrawn by the submitting investigator in June 2020. The requestor indicated the sequence information had been updated, was being submitted to another database, and wanted the data removed from SRA to avoid version control issues. The submitting investigator published relevant information about these sequences [by preprint in March, 2020](#) and in a [journal in June, 2020](#). Submitting investigators hold the rights to their data and can request withdrawal of the data.

Was there any motive for the investigator to remove the data?

NIH can't speculate on motive beyond the investigator's stated intentions.

Are investigators allowed to request that data be deleted from SRA?

Submitting investigators hold rights to their data and can request withdrawal of the data

From: Nurik, Jody (NIH/NLM) [E] (b) (6)
Sent: Monday, June 21, 2021 6:26 PM
To: Myles, Renate (NIH/OD) [E] (b) (6); Tuncer, Diane (NIH/NLM) [E]
(b) (6)
Cc: Fine, Amanda (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E]
(b) (6)
Subject: Re: FLAGGING: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Thanks, Renate - we will also be keeping an eye out for the paper.

Have a good evening,

Jody

From: "Myles, Renate (NIH/OD) [E]" (b) (6)
Date: Monday, June 21, 2021 at 6:22:37 PM
To: "Tuncer, Diane (NIH/NLM) [E]" (b) (6), "Nurik, Jody (NIH/NLM) [E]"
(b) (6)
Cc: "Fine, Amanda (NIH/OD) [E]" (b) (6), "Wojtowicz, Emma (NIH/OD) [E]"
(b) (6)
Subject: RE: FLAGGING: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Hi Diane:

Spoke with Patti and below is what we agreed on. So far, paper still hasn't posted. We're keeping an eye out for it.

(b) (5)



Was there any motive for the investigator to remove the data?

(b) (5)

Are investigators allowed to request that data be deleted from SRA?

(b) (5)

Thanks,
Renate

From: Myles, Renate (NIH/OD) [E]
Sent: Monday, June 21, 2021 4:20 PM
To: Tuncer, Diane (NIH/NLM) [E] (b) (6); Nurik, Jody (NIH/NLM) [E]
(b) (6)
Cc: Fine, Amanda (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E]
(b) (6)
Subject: RE: FLAGGING: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Okay, thanks. Yes, I have a call with her. (b) (5)

From: Tuncer, Diane (NIH/NLM) [E] (b) (6)
Sent: Monday, June 21, 2021 4:19 PM
To: Myles, Renate (NIH/OD) [E] (b) (6); Nurik, Jody (NIH/NLM) [E]
(b) (6)
Cc: Fine, Amanda (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E]
(b) (6)
Subject: RE: FLAGGING: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Hi Renate,

We shared the language below with Dr. Brennan (b) (5) We were informed that you and Dr. Brennan will be talking today at 5pm to discuss further.

In the meantime, here are some facts that Dr. Brennan asked us to share:

Since March of 2020, SRA received 4.6M sequence submissions (4,668,926). Fewer than 2% of these have been withdrawn. The only way that sequences are removed is when removal is requested by submitters. NLM is reviewing the submission and withdraw process for verification.

Diane

From: Myles, Renate (NIH/OD) [E] (b) (6)
Sent: Monday, June 21, 2021 2:25 PM
To: Tuncer, Diane (NIH/NLM) [E] (b) (6); Nurik, Jody (NIH/NLM) [E]
(b) (6)
Cc: Fine, Amanda (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E]
(b) (6)
Subject: FLAGGING: SARS-CoV-2 data deleted from the NIH/NCBI SRA
Importance: High

Hi all:

The attached paper was submitted to BioRx for preprint. The researcher is focusing on early genome sequence data on SARS-CoV-2 that the submitter requested be deleted. Unfortunately, the author of the paper is assigning motive and suggesting that the purpose of deletion was to obscure its existence. Below are reactive statement and QA in case we get media interest. Please let me know ASAP if NLM has any concerns with this language.

[Redacted content]

(b) (5)

Was there any motive for the investigator to remove the data?

[Redacted content]

(b) (5)

Are investigators allowed to request that data be deleted from SRA?

[Redacted content]

(b) (5)

[Redacted content]

Thanks,
Renate

bioprojecthelp at ncbi.nlm.nih.gov
Mon Mar 16 06:19:45 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your submission:

SubmissionID: SUB7147304
BioProject ID: PRJNA612766
Title:

has been successfully registered with the BioProject database. After review by the database staff, your project information will be accessible with the following link, usually within a few days of the release date that you set (or the release of linked data, whichever is first):

<http://www.ncbi.nlm.nih.gov/bioproject/612766>

Please use the BioProject ID PRJNA612766 with your correspondence and your data submissions.

Send questions to bioprojecthelp at ncbi.nlm.nih.gov, and include the BioProject ID and organism name.

Regards,

NCBI BioProject Submissions Staff
Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

bioprojecthelp at ncbi.nlm.nih.gov (for BioProject questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

biosamplehelp at ncbi.nlm.nih.gov
Mon Mar 16 06:30:03 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your submission has been successfully registered with the BioSample database:

Temporary SubmissionID: SUB7147304
Release date: as soon as processing is complete

Attached is a list of the sample names you submitted.

Database staff will review your submission within the next few days and will contact you if problems are identified.

Once processing is complete, you will receive another email with assigned accession numbers.

Send questions and update requests to biosamplehelp at ncbi.nlm.nih.gov.

Regards,

NCBI BioSample Submissions Staff
Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

biosamplehelp at ncbi.nlm.nih.gov (for BioSample questions/replies) info at
ncbi.nlm.nih.gov (for general questions regarding NCBI)

----- next part -----

Object IDs and corresponding URLs:

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14381199: <https://www.ncbi.nlm.nih.gov/sra/14381199>
14381200: <https://www.ncbi.nlm.nih.gov/sra/14381200>
14381201: <https://www.ncbi.nlm.nih.gov/sra/14381201>
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14381311: <https://www.ncbi.nlm.nih.gov/sra/14381311>

----- next part -----

| Sample Name | SPUID | Organism | Tax ID | Isolate |
|-------------|-----------|---|---------|---------|
| A12-10min | A12-10min | Severe acute respiratory syndrome coronavirus 2 | | |
| 2697049 | A12-10min | | | |
| A12-4h | A12-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A12-4h |
| A1-10min | A1-10min | Severe acute respiratory syndrome coronavirus 2 | | |
| 2697049 | A1-10min | | | |
| A1-4h | A1-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A1-4h |
| A2-10min | A2-10min | Severe acute respiratory syndrome coronavirus 2 | | |
| 2697049 | A2-10min | | | |
| A2-4h | A2-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A2-4h |
| A3-10min | A3-10min | Severe acute respiratory syndrome coronavirus 2 | | |
| 2697049 | A3-10min | | | |
| A3-4h | A3-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A3-4h |
| A4-10min | A4-10min | Severe acute respiratory syndrome coronavirus 2 | | |
| 2697049 | A4-10min | | | |
| A4-4h | A4-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A4-4h |
| A5-10min | A5-10min | Severe acute respiratory syndrome coronavirus 2 | | |
| 2697049 | A5-10min | | | |

A5-4h A5-4h Severe acute respiratory syndrome coronavirus 2 2697049 A5-4h
A6-10min A6-10min Severe acute respiratory syndrome coronavirus 2
2697049 A6-10min
A6-4h A6-4h Severe acute respiratory syndrome coronavirus 2 2697049 A6-4h
A7-10min A7-10min Severe acute respiratory syndrome coronavirus 2
2697049 A7-10min
A7-4h A7-4h Severe acute respiratory syndrome coronavirus 2 2697049 A7-4h
A8-10min A8-10min Severe acute respiratory syndrome coronavirus 2
2697049 A8-10min
A8-4h A8-4h Severe acute respiratory syndrome coronavirus 2 2697049 A8-4h
A9-10min A9-10min Severe acute respiratory syndrome coronavirus 2
2697049 A9-10min
A9-4h A9-4h Severe acute respiratory syndrome coronavirus 2 2697049 A9-4h
B4-10min B4-10min Severe acute respiratory syndrome coronavirus 2
2697049 B4-10min
B4-4h B4-4h Severe acute respiratory syndrome coronavirus 2 2697049 B4-4h
C11-10min C11-10min Severe acute respiratory syndrome coronavirus 2
2697049 C11-10min
C11-4h C11-4h Severe acute respiratory syndrome coronavirus 2 2697049 C11-4h
C1-10min C1-10min Severe acute respiratory syndrome coronavirus 2
2697049 C1-10min
C1-4h C1-4h Severe acute respiratory syndrome coronavirus 2 2697049 C1-4h
C2-10min C2-10min Severe acute respiratory syndrome coronavirus 2
2697049 C2-10min
C2-4h C2-4h Severe acute respiratory syndrome coronavirus 2 2697049 C2-4h
D10-10min D10-10min Severe acute respiratory syndrome coronavirus 2
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D10-4h D10-4h Severe acute respiratory syndrome coronavirus 2 2697049 D10-4h
D12-10min D12-10min Severe acute respiratory syndrome coronavirus 2
2697049 D12-10min
D12-4h D12-4h Severe acute respiratory syndrome coronavirus 2 2697049 D12-4h
D2-10min D2-10min Severe acute respiratory syndrome coronavirus 2
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D2-4h D2-4h Severe acute respiratory syndrome coronavirus 2 2697049 D2-4h
E1-10min E1-10min Severe acute respiratory syndrome coronavirus 2
2697049 E1-10min
E1-4h E1-4h Severe acute respiratory syndrome coronavirus 2 2697049 E1-4h
E5-10min E5-10min Severe acute respiratory syndrome coronavirus 2
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E5-4h E5-4h Severe acute respiratory syndrome coronavirus 2 2697049 E5-4h
F12-10min F12-10min Severe acute respiratory syndrome coronavirus 2
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F12-4h F12-4h Severe acute respiratory syndrome coronavirus 2 2697049 F12-4h
F5-10min F5-10min Severe acute respiratory syndrome coronavirus 2
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F5-4h F5-4h Severe acute respiratory syndrome coronavirus 2 2697049 F5-4h
G1-10min G1-10min Severe acute respiratory syndrome coronavirus 2
2697049 G1-10min
G1-4h G1-4h Severe acute respiratory syndrome coronavirus 2 2697049 G1-4h
H12-10min H12-10min Severe acute respiratory syndrome coronavirus 2
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H12-4h H12-4h Severe acute respiratory syndrome coronavirus 2 2697049 H12-4h
H9-10min H9-10min Severe acute respiratory syndrome coronavirus 2
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H9-4h H9-4h Severe acute respiratory syndrome coronavirus 2 2697049 H9-4h
NC1-10min NC1-10min Severe acute respiratory syndrome coronavirus 2
2697049 NC1-10min
NC1-4h NC1-4h Severe acute respiratory syndrome coronavirus 2 2697049 NC1-4h
PC1-10min PC1-10min Severe acute respiratory syndrome coronavirus 2
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PC1-4h PC1-4h Severe acute respiratory syndrome coronavirus 2 2697049 PC1-4h
A10-10min A10-10min Severe acute respiratory syndrome coronavirus 2
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A11-10min A11-10min Severe acute respiratory syndrome coronavirus 2
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A11-4h A11-4h Severe acute respiratory syndrome coronavirus 2 2697049 A11-4h
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B3-10min B3-10min Severe acute respiratory syndrome coronavirus 2
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B5-4h B5-4h Severe acute respiratory syndrome coronavirus 2 2697049 B5-4h
B9-10min B9-10min Severe acute respiratory syndrome coronavirus 2
2697049 B9-10min
B9-4h B9-4h Severe acute respiratory syndrome coronavirus 2 2697049 B9-4h
C12-10min C12-10min Severe acute respiratory syndrome coronavirus 2
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C12-4h C12-4h Severe acute respiratory syndrome coronavirus 2 2697049 C12-4h

C9-10min C9-10min Severe acute respiratory syndrome coronavirus 2
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C9-4h C9-4h Severe acute respiratory syndrome coronavirus 2 2697049 C9-
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D11-10min D11-10min Severe acute respiratory syndrome coronavirus 2
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D11-4h D11-4h Severe acute respiratory syndrome coronavirus 2 2697049 D11-
4h
D9-10min D9-10min Severe acute respiratory syndrome coronavirus 2
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D9-4h D9-4h Severe acute respiratory syndrome coronavirus 2 2697049 D9-
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E6-4h E6-4h Severe acute respiratory syndrome coronavirus 2 2697049 E6-
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F11-10min F11-10min Severe acute respiratory syndrome coronavirus 2
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F11-4h F11-4h Severe acute respiratory syndrome coronavirus 2 2697049 F11-
4h
F8-10min F8-10min Severe acute respiratory syndrome coronavirus 2
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G12-4h G12-4h Severe acute respiratory syndrome coronavirus 2 2697049 G12-
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G6-10min G6-10min Severe acute respiratory syndrome coronavirus 2
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G6-4h G6-4h Severe acute respiratory syndrome coronavirus 2 2697049 G6-
4h
H3-10min H3-10min Severe acute respiratory syndrome coronavirus 2
2697049 H3-10min
H3-4h H3-4h Severe acute respiratory syndrome coronavirus 2 2697049 H3-
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NC2-4h NC2-4h Severe acute respiratory syndrome coronavirus 2 2697049 NC2-
4h
PC2-10min PC2-10min Severe acute respiratory syndrome coronavirus 2
2697049 PC2-10min

PC2-4h PC2-4h Severe acute respiratory syndrome coronavirus 2 2697049 PC2-4h
R01-10min R01-10min Severe acute respiratory syndrome coronavirus 2
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R01-4h R01-4h Severe acute respiratory syndrome coronavirus 2 2697049 R01-4h
R02-10min R02-10min Severe acute respiratory syndrome coronavirus 2
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R02-4h R02-4h Severe acute respiratory syndrome coronavirus 2 2697049 R02-4h
R03-10min R03-10min Severe acute respiratory syndrome coronavirus 2
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R03-4h R03-4h Severe acute respiratory syndrome coronavirus 2 2697049 R03-4h
R04-4h R04-4h Severe acute respiratory syndrome coronavirus 2 2697049 R04-4h
R05-10min R05-10min Severe acute respiratory syndrome coronavirus 2
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R05-4h R05-4h Severe acute respiratory syndrome coronavirus 2 2697049 R05-4h
R06-10min R06-10min Severe acute respiratory syndrome coronavirus 2
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R06-4h R06-4h Severe acute respiratory syndrome coronavirus 2 2697049 R06-4h
R07-10min R07-10min Severe acute respiratory syndrome coronavirus 2
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R07-4h R07-4h Severe acute respiratory syndrome coronavirus 2 2697049 R07-4h
R08-10min R08-10min Severe acute respiratory syndrome coronavirus 2
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R08-4h R08-4h Severe acute respiratory syndrome coronavirus 2 2697049 R08-4h
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R15-10min R15-10min Severe acute respiratory syndrome coronavirus 2
2697049 R15-10min
R15-4h R15-4h Severe acute respiratory syndrome coronavirus 2 2697049 R15-
4h
R16-10min R16-10min Severe acute respiratory syndrome coronavirus 2
2697049 R16-10min
R16-4h R16-4h Severe acute respiratory syndrome coronavirus 2 2697049 R16-
4h

biosamplehelp at ncbi.nlm.nih.gov
Mon Mar 16 12:50:18 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your recent submission to the BioSample database has been successfully processed and will be released on the date specified.

BioSample accessions: SAMN14381071, SAMN14381072, SAMN14381073,
SAMN14381074, SAMN14381075, SAMN14381076, SAMN14381077, SAMN14381078,
SAMN14381079, SAMN14381080, ... see attached file.
Temporary SubmissionID: SUB7147304
Release date: as soon as processing is complete

A submission summary and the links by which your BioSample records will be accessible are appended and attached.

Please reference BioSample accessions SAMN14381071, SAMN14381072,
SAMN14381073, SAMN14381074, SAMN14381075, SAMN14381076, SAMN14381077,
SAMN14381078, SAMN14381079, SAMN14381080, ... see attached file. when making
corresponding sequence data submissions.

Send questions and update requests to biosamplehelp at ncbi.nlm.nih.gov;
include the BioSample accessions SAMN14381071, SAMN14381072, SAMN14381073,
SAMN14381074, SAMN14381075, SAMN14381076, SAMN14381077, SAMN14381078,
SAMN14381079, SAMN14381080, ... see attached file. in any correspondence.

Regards,

NCBI BioSample Submissions Staff
Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

biosamplehelp at ncbi.nlm.nih.gov (for BioSample questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

| Accession ID | Sample Name | SPUID | Organism | Tax |
|--------------|-------------|-------|------------|-----|
| | Isolate | | BioProject | |

| | | | |
|---------------|-----------|-----------|-----------------------------------|
| SAMN14381071 | A12-10min | A12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A12-10min | PRJNA612766 |
| SAMN14381072 | A12-4h | A12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A12-4h | PRJNA612766 |
| SAMN14381073 | A1-10min | A1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A1-10min | PRJNA612766 |
| SAMN14381074 | A1-4h | A1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A1-4h | PRJNA612766 |
| SAMN14381075 | A2-10min | A2-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A2-10min | PRJNA612766 |
| SAMN14381076 | A2-4h | A2-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A2-4h | PRJNA612766 |
| SAMN14381077 | A3-10min | A3-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A3-10min | PRJNA612766 |
| SAMN14381078 | A3-4h | A3-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A3-4h | PRJNA612766 |
| SAMN14381079 | A4-10min | A4-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A4-10min | PRJNA612766 |
| SAMN14381080 | A4-4h | A4-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A4-4h | PRJNA612766 |
| SAMN14381081 | A5-10min | A5-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A5-10min | PRJNA612766 |
| SAMN14381082 | A5-4h | A5-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A5-4h | PRJNA612766 |
| SAMN14381083 | A6-10min | A6-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A6-10min | PRJNA612766 |
| SAMN14381084 | A6-4h | A6-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A6-4h | PRJNA612766 |
| SAMN14381085 | A7-10min | A7-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A7-10min | PRJNA612766 |
| SAMN14381086 | A7-4h | A7-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A7-4h | PRJNA612766 |
| SAMN14381087 | A8-10min | A8-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A8-10min | PRJNA612766 |
| SAMN14381088 | A8-4h | A8-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A8-4h | PRJNA612766 |
| SAMN14381089 | A9-10min | A9-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A9-10min | PRJNA612766 |
| SAMN14381090 | A9-4h | A9-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A9-4h | PRJNA612766 |
| SAMN14381091 | B4-10min | B4-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B4-10min | PRJNA612766 |
| SAMN14381092 | B4-4h | B4-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B4-4h | PRJNA612766 |
| SAMN14381093 | C11-10min | C11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C11-10min | PRJNA612766 |
| SAMN14381094 | C11-4h | C11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C11-4h | PRJNA612766 |
| SAMN14381095 | C1-10min | C1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C1-10min | PRJNA612766 |

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| SAMN14381096 | C1-4h | C1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C1-4h | PRJNA612766 |
| SAMN14381097 | C2-10min | C2-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C2-10min | PRJNA612766 |
| SAMN14381098 | C2-4h | C2-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C2-4h | PRJNA612766 |
| SAMN14381099 | D10-10min | D10-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D10-10min | PRJNA612766 |
| SAMN14381100 | D10-4h | D10-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D10-4h | PRJNA612766 |
| SAMN14381101 | D12-10min | D12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D12-10min | PRJNA612766 |
| SAMN14381102 | D12-4h | D12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D12-4h | PRJNA612766 |
| SAMN14381103 | D2-10min | D2-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D2-10min | PRJNA612766 |
| SAMN14381104 | D2-4h | D2-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D2-4h | PRJNA612766 |
| SAMN14381105 | E1-10min | E1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E1-10min | PRJNA612766 |
| SAMN14381106 | E1-4h | E1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E1-4h | PRJNA612766 |
| SAMN14381107 | E5-10min | E5-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E5-10min | PRJNA612766 |
| SAMN14381108 | E5-4h | E5-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E5-4h | PRJNA612766 |
| SAMN14381109 | F12-10min | F12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F12-10min | PRJNA612766 |
| SAMN14381110 | F12-4h | F12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F12-4h | PRJNA612766 |
| SAMN14381111 | F5-10min | F5-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F5-10min | PRJNA612766 |
| SAMN14381112 | F5-4h | F5-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F5-4h | PRJNA612766 |
| SAMN14381113 | G1-10min | G1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G1-10min | PRJNA612766 |
| SAMN14381114 | G1-4h | G1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G1-4h | PRJNA612766 |
| SAMN14381115 | H12-10min | H12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | H12-10min | PRJNA612766 |
| SAMN14381116 | H12-4h | H12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | H12-4h | PRJNA612766 |
| SAMN14381117 | H9-10min | H9-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | H9-10min | PRJNA612766 |
| SAMN14381118 | H9-4h | H9-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | H9-4h | PRJNA612766 |
| SAMN14381119 | NC1-10min | NC1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | NC1-10min | PRJNA612766 |
| SAMN14381120 | NC1-4h | NC1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | NC1-4h | PRJNA612766 |

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| SAMN14381121 | PC1-10min | PC1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | PC1-10min | PRJNA612766 |
| SAMN14381122 | PC1-4h | PC1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | PC1-4h | PRJNA612766 |
| SAMN14381123 | A10-10min | A10-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A10-10min | PRJNA612766 |
| SAMN14381124 | A10-4h | A10-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A10-4h | PRJNA612766 |
| SAMN14381125 | A11-10min | A11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A11-10min | PRJNA612766 |
| SAMN14381126 | A11-4h | A11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A11-4h | PRJNA612766 |
| SAMN14381127 | B1-10min | B1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B1-10min | PRJNA612766 |
| SAMN14381128 | B1-4h | B1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B1-4h | PRJNA612766 |
| SAMN14381129 | B2-10min | B2-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B2-10min | PRJNA612766 |
| SAMN14381130 | B2-4h | B2-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B2-4h | PRJNA612766 |
| SAMN14381131 | B3-10min | B3-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B3-10min | PRJNA612766 |
| SAMN14381132 | B3-4h | B3-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B3-4h | PRJNA612766 |
| SAMN14381133 | B5-4h | B5-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B5-4h | PRJNA612766 |
| SAMN14381134 | B9-10min | B9-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B9-10min | PRJNA612766 |
| SAMN14381135 | B9-4h | B9-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B9-4h | PRJNA612766 |
| SAMN14381136 | C12-10min | C12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C12-10min | PRJNA612766 |
| SAMN14381137 | C12-4h | C12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C12-4h | PRJNA612766 |
| SAMN14381138 | C9-10min | C9-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C9-10min | PRJNA612766 |
| SAMN14381139 | C9-4h | C9-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C9-4h | PRJNA612766 |
| SAMN14381140 | D11-10min | D11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D11-10min | PRJNA612766 |
| SAMN14381141 | D11-4h | D11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D11-4h | PRJNA612766 |
| SAMN14381142 | D9-10min | D9-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D9-10min | PRJNA612766 |
| SAMN14381143 | D9-4h | D9-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D9-4h | PRJNA612766 |
| SAMN14381144 | E11-10min | E11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E11-10min | PRJNA612766 |
| SAMN14381145 | E11-4h | E11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E11-4h | PRJNA612766 |

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| SAMN14381146 | E12-10min | E12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E12-10min | PRJNA612766 |
| SAMN14381147 | E12-4h | E12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E12-4h | PRJNA612766 |
| SAMN14381148 | E3-10min | E3-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E3-10min | PRJNA612766 |
| SAMN14381149 | E3-4h | E3-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E3-4h | PRJNA612766 |
| SAMN14381150 | E6-10min | E6-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E6-10min | PRJNA612766 |
| SAMN14381151 | E6-4h | E6-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E6-4h | PRJNA612766 |
| SAMN14381152 | F11-10min | F11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F11-10min | PRJNA612766 |
| SAMN14381153 | F11-4h | F11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F11-4h | PRJNA612766 |
| SAMN14381154 | F8-10min | F8-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F8-10min | PRJNA612766 |
| SAMN14381155 | F8-4h | F8-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F8-4h | PRJNA612766 |
| SAMN14381156 | G11-10min | G11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G11-10min | PRJNA612766 |
| SAMN14381157 | G11-4h | G11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G11-4h | PRJNA612766 |
| SAMN14381158 | G12-10min | G12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G12-10min | PRJNA612766 |
| SAMN14381159 | G12-4h | G12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G12-4h | PRJNA612766 |
| SAMN14381160 | G6-10min | G6-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G6-10min | PRJNA612766 |
| SAMN14381161 | G6-4h | G6-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G6-4h | PRJNA612766 |
| SAMN14381162 | H3-10min | H3-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | H3-10min | PRJNA612766 |
| SAMN14381163 | H3-4h | H3-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | H3-4h | PRJNA612766 |
| SAMN14381164 | NC2-4h | NC2-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | NC2-4h | PRJNA612766 |
| SAMN14381165 | PC2-10min | PC2-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | PC2-10min | PRJNA612766 |
| SAMN14381166 | PC2-4h | PC2-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | PC2-4h | PRJNA612766 |
| SAMN14381167 | R01-10min | R01-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R01-10min | PRJNA612766 |
| SAMN14381168 | R01-4h | R01-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R01-4h | PRJNA612766 |
| SAMN14381169 | R02-10min | R02-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R02-10min | PRJNA612766 |
| SAMN14381170 | R02-4h | R02-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R02-4h | PRJNA612766 |

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| SAMN14381171 | R03-10min | R03-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R03-10min | PRJNA612766 |
| SAMN14381172 | R03-4h | R03-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R03-4h | PRJNA612766 |
| SAMN14381173 | R04-4h | R04-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R04-4h | PRJNA612766 |
| SAMN14381174 | R05-10min | R05-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R05-10min | PRJNA612766 |
| SAMN14381175 | R05-4h | R05-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R05-4h | PRJNA612766 |
| SAMN14381176 | R06-10min | R06-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R06-10min | PRJNA612766 |
| SAMN14381177 | R06-4h | R06-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R06-4h | PRJNA612766 |
| SAMN14381178 | R07-10min | R07-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R07-10min | PRJNA612766 |
| SAMN14381179 | R07-4h | R07-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R07-4h | PRJNA612766 |
| SAMN14381180 | R08-10min | R08-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R08-10min | PRJNA612766 |
| SAMN14381181 | R08-4h | R08-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R08-4h | PRJNA612766 |
| SAMN14381182 | R09-10min | R09-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R09-10min | PRJNA612766 |
| SAMN14381183 | R09-4h | R09-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R09-4h | PRJNA612766 |
| SAMN14381184 | R10-10min | R10-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R10-10min | PRJNA612766 |
| SAMN14381185 | R10-4h | R10-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R10-4h | PRJNA612766 |
| SAMN14381186 | R11-10min | R11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R11-10min | PRJNA612766 |
| SAMN14381187 | R11-4h | R11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R11-4h | PRJNA612766 |
| SAMN14381188 | R12-10min | R12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R12-10min | PRJNA612766 |
| SAMN14381189 | R12-4h | R12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R12-4h | PRJNA612766 |
| SAMN14381190 | R13-10min | R13-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R13-10min | PRJNA612766 |
| SAMN14381191 | R13-4h | R13-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R13-4h | PRJNA612766 |
| SAMN14381192 | R14-10min | R14-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R14-10min | PRJNA612766 |
| SAMN14381193 | R14-4h | R14-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R14-4h | PRJNA612766 |
| SAMN14381194 | R15-10min | R15-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R15-10min | PRJNA612766 |
| SAMN14381195 | R15-4h | R15-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R15-4h | PRJNA612766 |

SAMN14381196 R16-10min R16-10min Severe acute respiratory syndrome
 coronavirus 2 2697049 R16-10min PRJNA612766
 SAMN14381197 R16-4h R16-4h Severe acute respiratory syndrome
 coronavirus 2 2697049 R16-4h PRJNA612766
 SAMN14381198 0cp-replicate01-2h 0cp-replicate01-2h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate01-
 2h PRJNA612766
 SAMN14381199 0cp-replicate01-4h 0cp-replicate01-4h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate01-
 4h PRJNA612766
 SAMN14381200 0cp-replicate02-30min 0cp-replicate02-30min Severe
 acute respiratory syndrome coronavirus 2 2697049 0cp-replicate02-
 30min PRJNA612766
 SAMN14381201 0cp-replicate02-1h 0cp-replicate02-1h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate02-
 1h PRJNA612766
 SAMN14381202 0cp-replicate02-2h 0cp-replicate02-2h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate02-
 2h PRJNA612766
 SAMN14381203 0cp-replicate02-4h 0cp-replicate02-4h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate02-
 4h PRJNA612766
 SAMN14381204 0cp-replicate03-30min 0cp-replicate03-30min Severe
 acute respiratory syndrome coronavirus 2 2697049 0cp-replicate03-
 30min PRJNA612766
 SAMN14381205 0cp-replicate03-1h 0cp-replicate03-1h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate03-
 1h PRJNA612766
 SAMN14381206 0cp-replicate03-2h 0cp-replicate03-2h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate03-
 2h PRJNA612766
 SAMN14381207 0cp-replicate03-4h 0cp-replicate03-4h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate03-
 4h PRJNA612766
 SAMN14381208 0cp-replicate04-1h 0cp-replicate04-1h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate04-
 1h PRJNA612766
 SAMN14381209 0cp-replicate04-2h 0cp-replicate04-2h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate04-
 2h PRJNA612766
 SAMN14381210 0cp-replicate04-4h 0cp-replicate04-4h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate04-
 4h PRJNA612766
 SAMN14381211 10cp-replicate01-10min 10cp-replicate01-10min Severe
 acute respiratory syndrome coronavirus 2 2697049 10cp-replicate01-
 10min PRJNA612766
 SAMN14381212 10cp-replicate01-30min 10cp-replicate01-30min Severe
 acute respiratory syndrome coronavirus 2 2697049 10cp-replicate01-
 30min PRJNA612766
 SAMN14381213 10cp-replicate01-1h 10cp-replicate01-1h Severe acute
 respiratory syndrome coronavirus 2 2697049 10cp-replicate01-
 1h PRJNA612766

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| SAMN14381214 | 10cp-replicate01-2h | 10cp-replicate01-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate01-2h | PRJNA612766 |
| SAMN14381215 | 10cp-replicate01-4h | 10cp-replicate01-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate01-4h | PRJNA612766 |
| SAMN14381216 | 10cp-replicate02-10min | 10cp-replicate02-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate02-10min | PRJNA612766 |
| SAMN14381217 | 10cp-replicate02-30min | 10cp-replicate02-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate02-30min | PRJNA612766 |
| SAMN14381218 | 10cp-replicate02-1h | 10cp-replicate02-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate02-1h | PRJNA612766 |
| SAMN14381219 | 10cp-replicate02-2h | 10cp-replicate02-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate02-2h | PRJNA612766 |
| SAMN14381220 | 10cp-replicate02-4h | 10cp-replicate02-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate02-4h | PRJNA612766 |
| SAMN14381221 | 10cp-replicate03-10min | 10cp-replicate03-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate03-10min | PRJNA612766 |
| SAMN14381222 | 10cp-replicate03-30min | 10cp-replicate03-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate03-30min | PRJNA612766 |
| SAMN14381223 | 10cp-replicate03-1h | 10cp-replicate03-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate03-1h | PRJNA612766 |
| SAMN14381224 | 10cp-replicate03-2h | 10cp-replicate03-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate03-2h | PRJNA612766 |
| SAMN14381225 | 10cp-replicate03-4h | 10cp-replicate03-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate03-4h | PRJNA612766 |
| SAMN14381226 | 10cp-replicate04-10min | 10cp-replicate04-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate04-10min | PRJNA612766 |
| SAMN14381227 | 10cp-replicate04-30min | 10cp-replicate04-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate04-30min | PRJNA612766 |
| SAMN14381228 | 10cp-replicate04-1h | 10cp-replicate04-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate04-1h | PRJNA612766 |
| SAMN14381229 | 10cp-replicate04-2h | 10cp-replicate04-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate04-2h | PRJNA612766 |
| SAMN14381230 | 10cp-replicate04-4h | 10cp-replicate04-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 10cp-replicate04-4h | PRJNA612766 |

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| SAMN14381231 | 100cp-replicate01-10min | 100cp-replicate01-10min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate01-10min | PRJNA612766 |
| SAMN14381232 | 100cp-replicate01-30min | 100cp-replicate01-30min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate01-30min | PRJNA612766 |
| SAMN14381233 | 100cp-replicate01-1h | 100cp-replicate01-1h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate01-1h | PRJNA612766 |
| SAMN14381234 | 100cp-replicate01-2h | 100cp-replicate01-2h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate01-2h | PRJNA612766 |
| SAMN14381235 | 100cp-replicate01-4h | 100cp-replicate01-4h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate01-4h | PRJNA612766 |
| SAMN14381236 | 100cp-replicate02-10min | 100cp-replicate02-10min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate02-10min | PRJNA612766 |
| SAMN14381237 | 100cp-replicate02-30min | 100cp-replicate02-30min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate02-30min | PRJNA612766 |
| SAMN14381238 | 100cp-replicate02-1h | 100cp-replicate02-1h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate02-1h | PRJNA612766 |
| SAMN14381239 | 100cp-replicate02-2h | 100cp-replicate02-2h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate02-2h | PRJNA612766 |
| SAMN14381240 | 100cp-replicate02-4h | 100cp-replicate02-4h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate02-4h | PRJNA612766 |
| SAMN14381241 | 100cp-replicate03-10min | 100cp-replicate03-10min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate03-10min | PRJNA612766 |
| SAMN14381242 | 100cp-replicate03-30min | 100cp-replicate03-30min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate03-30min | PRJNA612766 |
| SAMN14381243 | 100cp-replicate03-1h | 100cp-replicate03-1h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate03-1h | PRJNA612766 |
| SAMN14381244 | 100cp-replicate03-2h | 100cp-replicate03-2h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate03-2h | PRJNA612766 |
| SAMN14381245 | 100cp-replicate03-4h | 100cp-replicate03-4h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate03-4h | PRJNA612766 |
| SAMN14381246 | 100cp-replicate04-30min | 100cp-replicate04-30min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate04-30min | PRJNA612766 |
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| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate04-1h | PRJNA612766 |

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| SAMN14381248 | 100cp-replicate04-2h | 100cp-replicate04-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate04-2h | PRJNA612766 |
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| SAMN14381251 | 500cp-replicate01-30min | 500cp-replicate01-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate01-30min | PRJNA612766 |
| SAMN14381252 | 500cp-replicate01-1h | 500cp-replicate01-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate01-1h | PRJNA612766 |
| SAMN14381253 | 500cp-replicate01-2h | 500cp-replicate01-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate01-2h | PRJNA612766 |
| SAMN14381254 | 500cp-replicate01-4h | 500cp-replicate01-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate01-4h | PRJNA612766 |
| SAMN14381255 | 500cp-replicate02-10min | 500cp-replicate02-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate02-10min | PRJNA612766 |
| SAMN14381256 | 500cp-replicate02-30min | 500cp-replicate02-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate02-30min | PRJNA612766 |
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| SAMN14381260 | 500cp-replicate03-10min | 500cp-replicate03-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate03-10min | PRJNA612766 |
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| SAMN14381262 | 500cp-replicate03-1h | 500cp-replicate03-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate03-1h | PRJNA612766 |
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| acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-10min | PRJNA612766 |
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| acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-30min | PRJNA612766 |
| SAMN14381267 | 500cp-replicate04-1h | 500cp-replicate04-1h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-1h | PRJNA612766 |
| SAMN14381268 | 500cp-replicate04-2h | 500cp-replicate04-2h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-2h | PRJNA612766 |
| SAMN14381269 | 500cp-replicate04-4h | 500cp-replicate04-4h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-4h | PRJNA612766 |
| SAMN14381270 | 1000cp-replicate01-10min | 1000cp-replicate01-10min | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-10min | PRJNA612766 |
| SAMN14381271 | 1000cp-replicate01-30min | 1000cp-replicate01-30min | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-30min | PRJNA612766 |
| SAMN14381272 | 1000cp-replicate01-1h | 1000cp-replicate01-1h | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-1h | PRJNA612766 |
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| acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-2h | PRJNA612766 |
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| respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate03-30min | PRJNA612766 |

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|--|--------------------------|--------------------------|--------|
| SAMN14381282 | 1000cp-replicate03-1h | 1000cp-replicate03-1h | Severe |
| acute respiratory syndrome coronavirus 2 | 1h | PRJNA612766 | |
| SAMN14381283 | 1000cp-replicate03-2h | 1000cp-replicate03-2h | Severe |
| acute respiratory syndrome coronavirus 2 | 2h | PRJNA612766 | |
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| acute respiratory syndrome coronavirus 2 | 4h | PRJNA612766 | |
| SAMN14381285 | 1000cp-replicate04-10min | 1000cp-replicate04-10min | Severe |
| acute respiratory syndrome coronavirus 2 | 10min | PRJNA612766 | |
| SAMN14381286 | 1000cp-replicate04-30min | 1000cp-replicate04-30min | Severe |
| acute respiratory syndrome coronavirus 2 | 30min | PRJNA612766 | |
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| acute respiratory syndrome coronavirus 2 | 1h | PRJNA612766 | |
| SAMN14381288 | 1000cp-replicate04-2h | 1000cp-replicate04-2h | Severe |
| acute respiratory syndrome coronavirus 2 | 2h | PRJNA612766 | |
| SAMN14381289 | 1000cp-replicate04-4h | 1000cp-replicate04-4h | Severe |
| acute respiratory syndrome coronavirus 2 | 4h | PRJNA612766 | |
| SAMN14381290 | 3000cp-replicate01-10min | 3000cp-replicate01-10min | Severe |
| acute respiratory syndrome coronavirus 2 | 10min | PRJNA612766 | |
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| acute respiratory syndrome coronavirus 2 | 30min | PRJNA612766 | |
| SAMN14381292 | 3000cp-replicate01-1h | 3000cp-replicate01-1h | Severe |
| acute respiratory syndrome coronavirus 2 | 1h | PRJNA612766 | |
| SAMN14381293 | 3000cp-replicate01-2h | 3000cp-replicate01-2h | Severe |
| acute respiratory syndrome coronavirus 2 | 2h | PRJNA612766 | |
| SAMN14381294 | 3000cp-replicate01-4h | 3000cp-replicate01-4h | Severe |
| acute respiratory syndrome coronavirus 2 | 4h | PRJNA612766 | |
| SAMN14381295 | 3000cp-replicate02-10min | 3000cp-replicate02-10min | Severe |
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| SAMN14381296 | 3000cp-replicate02-30min | 3000cp-replicate02-30min | Severe |
| acute respiratory syndrome coronavirus 2 | 30min | PRJNA612766 | |
| SAMN14381297 | 3000cp-replicate02-1h | 3000cp-replicate02-1h | Severe |
| acute respiratory syndrome coronavirus 2 | 1h | PRJNA612766 | |
| SAMN14381298 | 3000cp-replicate02-2h | 3000cp-replicate02-2h | Severe |
| acute respiratory syndrome coronavirus 2 | 2h | PRJNA612766 | |

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 10min Severe acute respiratory syndrome coronavirus
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| SAMN14381071 | A12-10min | A12-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A12-10min | PRJNA612766 |
| SAMN14381072 | A12-4h | A12-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A12-4h | PRJNA612766 |
| SAMN14381073 | A1-10min | A1-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A1-10min | PRJNA612766 |
| SAMN14381074 | A1-4h | A1-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A1-4h | PRJNA612766 |
| SAMN14381075 | A2-10min | A2-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A2-10min | PRJNA612766 |
| SAMN14381076 | A2-4h | A2-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A2-4h | PRJNA612766 |
| SAMN14381077 | A3-10min | A3-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A3-10min | PRJNA612766 |
| SAMN14381078 | A3-4h | A3-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A3-4h | PRJNA612766 |
| SAMN14381079 | A4-10min | A4-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A4-10min | PRJNA612766 |
| SAMN14381080 | A4-4h | A4-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A4-4h | PRJNA612766 |
| SAMN14381081 | A5-10min | A5-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A5-10min | PRJNA612766 |
| SAMN14381082 | A5-4h | A5-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A5-4h | PRJNA612766 |
| SAMN14381083 | A6-10min | A6-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A6-10min | PRJNA612766 |
| SAMN14381084 | A6-4h | A6-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A6-4h | PRJNA612766 |
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SAMN14381090 A9-4h A9-4h Severe acute respiratory syndrome coronavirus
2 2697049 A9-4h PRJNA612766
SAMN14381091 B4-10min B4-10min Severe acute respiratory syndrome
coronavirus 2 2697049 B4-10min PRJNA612766
SAMN14381092 B4-4h B4-4h Severe acute respiratory syndrome coronavirus
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SAMN14381093 C11-10min C11-10min Severe acute respiratory syndrome
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SAMN14381094 C11-4h C11-4h Severe acute respiratory syndrome coronavirus
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coronavirus 2 2697049 C1-10min PRJNA612766
SAMN14381096 C1-4h C1-4h Severe acute respiratory syndrome coronavirus
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SAMN14381097 C2-10min C2-10min Severe acute respiratory syndrome
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SAMN14381098 C2-4h C2-4h Severe acute respiratory syndrome coronavirus
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SAMN14381099 D10-10min D10-10min Severe acute respiratory syndrome
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2 2697049 H12-4h PRJNA612766

SAMN14381117 H9-10min H9-10min Severe acute respiratory syndrome
coronavirus 2 2697049 H9-10min PRJNA612766
SAMN14381118 H9-4h H9-4h Severe acute respiratory syndrome coronavirus
2 2697049 H9-4h PRJNA612766
SAMN14381119 NC1-10min NC1-10min Severe acute respiratory syndrome
coronavirus 2 2697049 NC1-10min PRJNA612766
SAMN14381120 NC1-4h NC1-4h Severe acute respiratory syndrome coronavirus
2 2697049 NC1-4h PRJNA612766
SAMN14381121 PC1-10min PC1-10min Severe acute respiratory syndrome
coronavirus 2 2697049 PC1-10min PRJNA612766
SAMN14381122 PC1-4h PC1-4h Severe acute respiratory syndrome coronavirus
2 2697049 PC1-4h PRJNA612766
SAMN14381123 A10-10min A10-10min Severe acute respiratory syndrome
coronavirus 2 2697049 A10-10min PRJNA612766
SAMN14381124 A10-4h A10-4h Severe acute respiratory syndrome coronavirus
2 2697049 A10-4h PRJNA612766
SAMN14381125 A11-10min A11-10min Severe acute respiratory syndrome
coronavirus 2 2697049 A11-10min PRJNA612766
SAMN14381126 A11-4h A11-4h Severe acute respiratory syndrome coronavirus
2 2697049 A11-4h PRJNA612766
SAMN14381127 B1-10min B1-10min Severe acute respiratory syndrome
coronavirus 2 2697049 B1-10min PRJNA612766
SAMN14381128 B1-4h B1-4h Severe acute respiratory syndrome coronavirus
2 2697049 B1-4h PRJNA612766
SAMN14381129 B2-10min B2-10min Severe acute respiratory syndrome
coronavirus 2 2697049 B2-10min PRJNA612766
SAMN14381130 B2-4h B2-4h Severe acute respiratory syndrome coronavirus
2 2697049 B2-4h PRJNA612766
SAMN14381131 B3-10min B3-10min Severe acute respiratory syndrome
coronavirus 2 2697049 B3-10min PRJNA612766
SAMN14381132 B3-4h B3-4h Severe acute respiratory syndrome coronavirus
2 2697049 B3-4h PRJNA612766
SAMN14381133 B5-4h B5-4h Severe acute respiratory syndrome coronavirus
2 2697049 B5-4h PRJNA612766
SAMN14381134 B9-10min B9-10min Severe acute respiratory syndrome
coronavirus 2 2697049 B9-10min PRJNA612766
SAMN14381135 B9-4h B9-4h Severe acute respiratory syndrome coronavirus
2 2697049 B9-4h PRJNA612766
SAMN14381136 C12-10min C12-10min Severe acute respiratory syndrome
coronavirus 2 2697049 C12-10min PRJNA612766
SAMN14381137 C12-4h C12-4h Severe acute respiratory syndrome coronavirus
2 2697049 C12-4h PRJNA612766
SAMN14381138 C9-10min C9-10min Severe acute respiratory syndrome
coronavirus 2 2697049 C9-10min PRJNA612766
SAMN14381139 C9-4h C9-4h Severe acute respiratory syndrome coronavirus
2 2697049 C9-4h PRJNA612766
SAMN14381140 D11-10min D11-10min Severe acute respiratory syndrome
coronavirus 2 2697049 D11-10min PRJNA612766
SAMN14381141 D11-4h D11-4h Severe acute respiratory syndrome coronavirus
2 2697049 D11-4h PRJNA612766
SAMN14381142 D9-10min D9-10min Severe acute respiratory syndrome
coronavirus 2 2697049 D9-10min PRJNA612766
SAMN14381143 D9-4h D9-4h Severe acute respiratory syndrome coronavirus
2 2697049 D9-4h PRJNA612766
SAMN14381144 E11-10min E11-10min Severe acute respiratory syndrome
coronavirus 2 2697049 E11-10min PRJNA612766

SAMN14381145 E11-4h E11-4h Severe acute respiratory syndrome coronavirus
2 2697049 E11-4h PRJNA612766
SAMN14381146 E12-10min E12-10min Severe acute respiratory syndrome
coronavirus 2 2697049 E12-10min PRJNA612766
SAMN14381147 E12-4h E12-4h Severe acute respiratory syndrome coronavirus
2 2697049 E12-4h PRJNA612766
SAMN14381148 E3-10min E3-10min Severe acute respiratory syndrome
coronavirus 2 2697049 E3-10min PRJNA612766
SAMN14381149 E3-4h E3-4h Severe acute respiratory syndrome coronavirus
2 2697049 E3-4h PRJNA612766
SAMN14381150 E6-10min E6-10min Severe acute respiratory syndrome
coronavirus 2 2697049 E6-10min PRJNA612766
SAMN14381151 E6-4h E6-4h Severe acute respiratory syndrome coronavirus
2 2697049 E6-4h PRJNA612766
SAMN14381152 F11-10min F11-10min Severe acute respiratory syndrome
coronavirus 2 2697049 F11-10min PRJNA612766
SAMN14381153 F11-4h F11-4h Severe acute respiratory syndrome coronavirus
2 2697049 F11-4h PRJNA612766
SAMN14381154 F8-10min F8-10min Severe acute respiratory syndrome
coronavirus 2 2697049 F8-10min PRJNA612766
SAMN14381155 F8-4h F8-4h Severe acute respiratory syndrome coronavirus
2 2697049 F8-4h PRJNA612766
SAMN14381156 G11-10min G11-10min Severe acute respiratory syndrome
coronavirus 2 2697049 G11-10min PRJNA612766
SAMN14381157 G11-4h G11-4h Severe acute respiratory syndrome coronavirus
2 2697049 G11-4h PRJNA612766
SAMN14381158 G12-10min G12-10min Severe acute respiratory syndrome
coronavirus 2 2697049 G12-10min PRJNA612766
SAMN14381159 G12-4h G12-4h Severe acute respiratory syndrome coronavirus
2 2697049 G12-4h PRJNA612766
SAMN14381160 G6-10min G6-10min Severe acute respiratory syndrome
coronavirus 2 2697049 G6-10min PRJNA612766
SAMN14381161 G6-4h G6-4h Severe acute respiratory syndrome coronavirus
2 2697049 G6-4h PRJNA612766
SAMN14381162 H3-10min H3-10min Severe acute respiratory syndrome
coronavirus 2 2697049 H3-10min PRJNA612766
SAMN14381163 H3-4h H3-4h Severe acute respiratory syndrome coronavirus
2 2697049 H3-4h PRJNA612766
SAMN14381164 NC2-4h NC2-4h Severe acute respiratory syndrome coronavirus
2 2697049 NC2-4h PRJNA612766
SAMN14381165 PC2-10min PC2-10min Severe acute respiratory syndrome
coronavirus 2 2697049 PC2-10min PRJNA612766
SAMN14381166 PC2-4h PC2-4h Severe acute respiratory syndrome coronavirus
2 2697049 PC2-4h PRJNA612766
SAMN14381167 R01-10min R01-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R01-10min PRJNA612766
SAMN14381168 R01-4h R01-4h Severe acute respiratory syndrome coronavirus
2 2697049 R01-4h PRJNA612766
SAMN14381169 R02-10min R02-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R02-10min PRJNA612766
SAMN14381170 R02-4h R02-4h Severe acute respiratory syndrome coronavirus
2 2697049 R02-4h PRJNA612766
SAMN14381171 R03-10min R03-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R03-10min PRJNA612766
SAMN14381172 R03-4h R03-4h Severe acute respiratory syndrome coronavirus
2 2697049 R03-4h PRJNA612766

SAMN14381173 R04-4h R04-4h Severe acute respiratory syndrome coronavirus
2 2697049 R04-4h PRJNA612766
SAMN14381174 R05-10min R05-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R05-10min PRJNA612766
SAMN14381175 R05-4h R05-4h Severe acute respiratory syndrome coronavirus
2 2697049 R05-4h PRJNA612766
SAMN14381176 R06-10min R06-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R06-10min PRJNA612766
SAMN14381177 R06-4h R06-4h Severe acute respiratory syndrome coronavirus
2 2697049 R06-4h PRJNA612766
SAMN14381178 R07-10min R07-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R07-10min PRJNA612766
SAMN14381179 R07-4h R07-4h Severe acute respiratory syndrome coronavirus
2 2697049 R07-4h PRJNA612766
SAMN14381180 R08-10min R08-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R08-10min PRJNA612766
SAMN14381181 R08-4h R08-4h Severe acute respiratory syndrome coronavirus
2 2697049 R08-4h PRJNA612766
SAMN14381182 R09-10min R09-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R09-10min PRJNA612766
SAMN14381183 R09-4h R09-4h Severe acute respiratory syndrome coronavirus
2 2697049 R09-4h PRJNA612766
SAMN14381184 R10-10min R10-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R10-10min PRJNA612766
SAMN14381185 R10-4h R10-4h Severe acute respiratory syndrome coronavirus
2 2697049 R10-4h PRJNA612766
SAMN14381186 R11-10min R11-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R11-10min PRJNA612766
SAMN14381187 R11-4h R11-4h Severe acute respiratory syndrome coronavirus
2 2697049 R11-4h PRJNA612766
SAMN14381188 R12-10min R12-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R12-10min PRJNA612766
SAMN14381189 R12-4h R12-4h Severe acute respiratory syndrome coronavirus
2 2697049 R12-4h PRJNA612766
SAMN14381190 R13-10min R13-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R13-10min PRJNA612766
SAMN14381191 R13-4h R13-4h Severe acute respiratory syndrome coronavirus
2 2697049 R13-4h PRJNA612766
SAMN14381192 R14-10min R14-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R14-10min PRJNA612766
SAMN14381193 R14-4h R14-4h Severe acute respiratory syndrome coronavirus
2 2697049 R14-4h PRJNA612766
SAMN14381194 R15-10min R15-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R15-10min PRJNA612766
SAMN14381195 R15-4h R15-4h Severe acute respiratory syndrome coronavirus
2 2697049 R15-4h PRJNA612766
SAMN14381196 R16-10min R16-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R16-10min PRJNA612766
SAMN14381197 R16-4h R16-4h Severe acute respiratory syndrome coronavirus
2 2697049 R16-4h PRJNA612766
SAMN14381198 0cp-replicate01-2h 0cp-replicate01-2h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate01-2h PRJNA612766
SAMN14381199 0cp-replicate01-4h 0cp-replicate01-4h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate01-4h PRJNA612766
SAMN14381200 0cp-replicate02-30min 0cp-replicate02-30min Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate02-30min PRJNA612766

SAMN14381201 0cp-replicate02-1h 0cp-replicate02-1h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate02-1h PRJNA612766
SAMN14381202 0cp-replicate02-2h 0cp-replicate02-2h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate02-2h PRJNA612766
SAMN14381203 0cp-replicate02-4h 0cp-replicate02-4h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate02-4h PRJNA612766
SAMN14381204 0cp-replicate03-30min 0cp-replicate03-30min Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate03-30min PRJNA612766
SAMN14381205 0cp-replicate03-1h 0cp-replicate03-1h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate03-1h PRJNA612766
SAMN14381206 0cp-replicate03-2h 0cp-replicate03-2h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate03-2h PRJNA612766
SAMN14381207 0cp-replicate03-4h 0cp-replicate03-4h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate03-4h PRJNA612766
SAMN14381208 0cp-replicate04-1h 0cp-replicate04-1h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate04-1h PRJNA612766
SAMN14381209 0cp-replicate04-2h 0cp-replicate04-2h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate04-2h PRJNA612766
SAMN14381210 0cp-replicate04-4h 0cp-replicate04-4h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate04-4h PRJNA612766
SAMN14381211 10cp-replicate01-10min 10cp-replicate01-10min Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate01-10min PRJNA612766
SAMN14381212 10cp-replicate01-30min 10cp-replicate01-30min Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate01-30min PRJNA612766
SAMN14381213 10cp-replicate01-1h 10cp-replicate01-1h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate01-1h PRJNA612766
SAMN14381214 10cp-replicate01-2h 10cp-replicate01-2h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate01-2h PRJNA612766
SAMN14381215 10cp-replicate01-4h 10cp-replicate01-4h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate01-4h PRJNA612766
SAMN14381216 10cp-replicate02-10min 10cp-replicate02-10min Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate02-10min PRJNA612766
SAMN14381217 10cp-replicate02-30min 10cp-replicate02-30min Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate02-30min PRJNA612766
SAMN14381218 10cp-replicate02-1h 10cp-replicate02-1h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate02-1h PRJNA612766
SAMN14381219 10cp-replicate02-2h 10cp-replicate02-2h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate02-2h PRJNA612766
SAMN14381220 10cp-replicate02-4h 10cp-replicate02-4h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate02-4h PRJNA612766
SAMN14381221 10cp-replicate03-10min 10cp-replicate03-10min Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate03-10min PRJNA612766
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respiratory syndrome coronavirus 2 2697049 10cp-replicate03-30min PRJNA612766
SAMN14381223 10cp-replicate03-1h 10cp-replicate03-1h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate03-1h PRJNA612766
SAMN14381224 10cp-replicate03-2h 10cp-replicate03-2h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate03-2h PRJNA612766
SAMN14381225 10cp-replicate03-4h 10cp-replicate03-4h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate03-4h PRJNA612766
SAMN14381226 10cp-replicate04-10min 10cp-replicate04-10min Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate04-10min PRJNA612766
SAMN14381227 10cp-replicate04-30min 10cp-replicate04-30min Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate04-30min PRJNA612766
SAMN14381228 10cp-replicate04-1h 10cp-replicate04-1h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate04-1h PRJNA612766

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| SAMN14381257 | 500cp-replicate02-1h | 500cp-replicate02-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate02-1h | PRJNA612766 |
| SAMN14381258 | 500cp-replicate02-2h | 500cp-replicate02-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate02-2h | PRJNA612766 |
| SAMN14381259 | 500cp-replicate02-4h | 500cp-replicate02-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate02-4h | PRJNA612766 |
| SAMN14381260 | 500cp-replicate03-10min | 500cp-replicate03-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate03-10min | PRJNA612766 |
| SAMN14381261 | 500cp-replicate03-30min | 500cp-replicate03-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate03-30min | PRJNA612766 |
| SAMN14381262 | 500cp-replicate03-1h | 500cp-replicate03-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate03-1h | PRJNA612766 |
| SAMN14381263 | 500cp-replicate03-2h | 500cp-replicate03-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate03-2h | PRJNA612766 |
| SAMN14381264 | 500cp-replicate03-4h | 500cp-replicate03-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate03-4h | PRJNA612766 |
| SAMN14381265 | 500cp-replicate04-10min | 500cp-replicate04-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-10min | PRJNA612766 |
| SAMN14381266 | 500cp-replicate04-30min | 500cp-replicate04-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-30min | PRJNA612766 |
| SAMN14381267 | 500cp-replicate04-1h | 500cp-replicate04-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-1h | PRJNA612766 |
| SAMN14381268 | 500cp-replicate04-2h | 500cp-replicate04-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-2h | PRJNA612766 |
| SAMN14381269 | 500cp-replicate04-4h | 500cp-replicate04-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-4h | PRJNA612766 |
| SAMN14381270 | 1000cp-replicate01-10min | 1000cp-replicate01-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-10min | PRJNA612766 |
| SAMN14381271 | 1000cp-replicate01-30min | 1000cp-replicate01-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-30min | PRJNA612766 |
| SAMN14381272 | 1000cp-replicate01-1h | 1000cp-replicate01-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-1h | PRJNA612766 |
| SAMN14381273 | 1000cp-replicate01-2h | 1000cp-replicate01-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-2h | PRJNA612766 |
| SAMN14381274 | 1000cp-replicate01-4h | 1000cp-replicate01-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-4h | PRJNA612766 |
| SAMN14381275 | 1000cp-replicate02-10min | 1000cp-replicate02-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate02-10min | PRJNA612766 |
| SAMN14381276 | 1000cp-replicate02-30min | 1000cp-replicate02-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate02-30min | PRJNA612766 |
| SAMN14381277 | 1000cp-replicate02-1h | 1000cp-replicate02-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate02-1h | PRJNA612766 |
| SAMN14381278 | 1000cp-replicate02-2h | 1000cp-replicate02-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate02-2h | PRJNA612766 |
| SAMN14381279 | 1000cp-replicate02-4h | 1000cp-replicate02-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate02-4h | PRJNA612766 |
| SAMN14381280 | 1000cp-replicate03-10min | 1000cp-replicate03-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate03-10min | PRJNA612766 |
| SAMN14381281 | 1000cp-replicate03-30min | 1000cp-replicate03-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate03-30min | PRJNA612766 |

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|--------------|--------------------------|--------------------------|---|---------|--------------------------|-------------|
| SAMN14381282 | 1000cp-replicate03-1h | 1000cp-replicate03-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate03-1h | PRJNA612766 |
| SAMN14381283 | 1000cp-replicate03-2h | 1000cp-replicate03-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate03-2h | PRJNA612766 |
| SAMN14381284 | 1000cp-replicate03-4h | 1000cp-replicate03-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate03-4h | PRJNA612766 |
| SAMN14381285 | 1000cp-replicate04-10min | 1000cp-replicate04-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate04-10min | PRJNA612766 |
| SAMN14381286 | 1000cp-replicate04-30min | 1000cp-replicate04-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate04-30min | PRJNA612766 |
| SAMN14381287 | 1000cp-replicate04-1h | 1000cp-replicate04-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate04-1h | PRJNA612766 |
| SAMN14381288 | 1000cp-replicate04-2h | 1000cp-replicate04-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate04-2h | PRJNA612766 |
| SAMN14381289 | 1000cp-replicate04-4h | 1000cp-replicate04-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate04-4h | PRJNA612766 |
| SAMN14381290 | 3000cp-replicate01-10min | 3000cp-replicate01-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate01-10min | PRJNA612766 |
| SAMN14381291 | 3000cp-replicate01-30min | 3000cp-replicate01-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate01-30min | PRJNA612766 |
| SAMN14381292 | 3000cp-replicate01-1h | 3000cp-replicate01-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate01-1h | PRJNA612766 |
| SAMN14381293 | 3000cp-replicate01-2h | 3000cp-replicate01-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate01-2h | PRJNA612766 |
| SAMN14381294 | 3000cp-replicate01-4h | 3000cp-replicate01-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate01-4h | PRJNA612766 |
| SAMN14381295 | 3000cp-replicate02-10min | 3000cp-replicate02-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate02-10min | PRJNA612766 |
| SAMN14381296 | 3000cp-replicate02-30min | 3000cp-replicate02-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate02-30min | PRJNA612766 |
| SAMN14381297 | 3000cp-replicate02-1h | 3000cp-replicate02-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate02-1h | PRJNA612766 |
| SAMN14381298 | 3000cp-replicate02-2h | 3000cp-replicate02-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate02-2h | PRJNA612766 |
| SAMN14381299 | 3000cp-replicate02-4h | 3000cp-replicate02-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate02-4h | PRJNA612766 |
| SAMN14381300 | 3000cp-replicate03-10min | 3000cp-replicate03-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate03-10min | PRJNA612766 |
| SAMN14381301 | 3000cp-replicate03-30min | 3000cp-replicate03-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate03-30min | PRJNA612766 |
| SAMN14381302 | 3000cp-replicate03-1h | 3000cp-replicate03-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate03-1h | PRJNA612766 |
| SAMN14381303 | 3000cp-replicate03-2h | 3000cp-replicate03-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate03-2h | PRJNA612766 |
| SAMN14381304 | 3000cp-replicate03-4h | 3000cp-replicate03-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate03-4h | PRJNA612766 |
| SAMN14381305 | 3000cp-replicate04-10min | 3000cp-replicate04-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate04-10min | PRJNA612766 |

SAMN14381306 3000cp-replicate04-30min 3000cp-replicate04-30min Severe acute respiratory syndrome coronavirus 2 2697049 3000cp-replicate04-30min PRJNA612766
SAMN14381307 3000cp-replicate04-1h 3000cp-replicate04-1h Severe acute respiratory syndrome coronavirus 2 2697049 3000cp-replicate04-1h PRJNA612766
SAMN14381308 3000cp-replicate04-2h 3000cp-replicate04-2h Severe acute respiratory syndrome coronavirus 2 2697049 3000cp-replicate04-2h PRJNA612766
SAMN14381309 3000cp-replicate04-4h 3000cp-replicate04-4h Severe acute respiratory syndrome coronavirus 2 2697049 3000cp-replicate04-4h PRJNA612766
SAMN14381310 respiratory viruses-10min respiratory viruses-10min Severe acute respiratory syndrome coronavirus 2 2697049 respiratory viruses-10min PRJNA612766
SAMN14381311 respiratory viruses-2h respiratory viruses-2h Severe acute respiratory syndrome coronavirus 2 2697049 respiratory viruses-2h PRJNA612766

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Tue Mar 17 07:44:44 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your recent submission to SRA database has been successfully processed and will be released on the date specified.

Please reference PRJNA612766 in your publication. This BioProject accession number is provided above in lieu of SRP and should be used in your publication as it will allow better searching in Entrez.

SRA accession: PRJNA612766
Temporary Submission ID: SUB7147304
Release date: 2020-03-17

Your SRA records will be accessible with the following link after the indicated release date:

<https://www.ncbi.nlm.nih.gov/sra/PRJNA612766>

Send questions and update requests to sra at ncbi.nlm.nih.gov; include the SRA accession PRJNA612766 in any correspondence.

Regards,

NCBI SRA Submissions Staff
Bethesda, Maryland USA

----- next part -----

Object IDs and corresponding URLs:

RUN:13817617: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817617>
RUN:13817616: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817616>
RUN:13817615: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817615>
RUN:13817614: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817614>
RUN:13817412: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817412>

RUN:13817557: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817557>
RUN:13817556: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817556>
RUN:13817555: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817555>
RUN:13817554: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817554>
RUN:13817553: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817553>
RUN:13817552: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817552>
RUN:13817551: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817551>
RUN:13817549: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817549>

From: (b) (6)

Received: Wed Mar 18 2020 06:01:21 GMT-0400 (Eastern Daylight Time)

To: NLM/NCBI List sra; SRA Support;

Subject: Re: SRA submission SUB7147304, "Nanopore targeted sequencing for SARS-CoV-2 and other respiratory viruses, Mar 13 '20"

Dear Staff,

Thank you for informing my submission state.

Now, I can search PRJNA612766 in BioProject, but why I can't download the raw data (.fastq file) which I uploaded in the submission. Hasn't the raw data been released yet?

Regards,

(b) (6)

(b) (6)

From: [sra](#)

Date: 2020-03-17 19:44

To: (b) (6)

Subject: SRA submission SUB7147304, "Nanopore targeted sequencing for SARS-CoV-2 and other respiratory viruses, Mar 13 '20"

Dear (b) (6)

This is an automatic acknowledgment that your recent submission to SRA database has been successfully processed and will be released on the date specified.

Please reference PRJNA612766 in your publication. This BioProject accession number is provided above in lieu of SRP and should be used in your publication as it will allow better searching in Entrez.

SRA accession: PRJNA612766
Temporary Submission ID: SUB7147304
Release date: 2020-03-17

Your SRA records will be accessible with the following link after the indicated release date:
<https://www.ncbi.nlm.nih.gov/sra/PRJNA612766>

Send questions and update requests to sra@ncbi.nlm.nih.gov; include the SRA accession PRJNA612766 in any correspondence.

Regards,

NCBI SRA Submissions Staff
Bethesda, Maryland USA

From: NLM Support <nlm-support@nlm.nih.gov>;
Received: Wed Mar 18 2020 10:28:22 GMT-0400 (Eastern Daylight Time)
To: (b) (6);
Subject: case #CAS-507212-JOB4H5: Re: SRA submission SUB7147304, "Nanopore targeted...
TRACKING:000393000005604

The raw data is public, but Entrez indexing is currently delayed. In the meantime, the data is listed publicly at the SRA Run Selector:

<https://www.ncbi.nlm.nih.gov/Traces/study/?acc=PRJNA612766>

And the accessions listed here can be used to download the sequences via the SRA toolkit.

Cheers,

(b) (6)
SRA Curator

----- Original Message -----

From: (b) (6);
Received: Wed Mar 18 2020 06:01:21 GMT-0400 (Eastern Daylight Time)
To: NLM/NCBI List sra; SRA Support;
Subject: Re: SRA submission SUB7147304, "Nanopore targeted sequencing for SARS-CoV-2 and other respiratory viruses, Mar 13 '20"

Dear Staff,

Thank you for informing my submission state.

Now, I can search PRJNA612766 in BioProject, but why I can't download the raw data (.fastq file) which I uploaded in the submission. Hasn't the raw data been released yet?

Regards,

(b) (6)

(b) (6)

From: [sra](#)

Date: 2020-03-17 19:44

To: (b) (6)

Subject: SRA submission SUB7147304, "Nanopore targeted sequencing for SARS-CoV-2 and other respiratory viruses, Mar 13 '20"

Dear (b) (6)

This is an automatic acknowledgment that your recent submission to SRA database has been successfully processed and will be released on the date specified.

Please reference PRJNA612766 in your publication. This BioProject accession number is provided above in lieu of SRP and should be used in your publication as it will allow better searching in Entrez.

SRA accession: PRJNA612766

Temporary Submission ID: SUB7147304

Release date: 2020-03-17

Your SRA records will be accessible with the following link after the indicated release date:

<https://www.ncbi.nlm.nih.gov/sra/PRJNA612766>

Send questions and update requests to sra@ncbi.nlm.nih.gov; include the SRA accession PRJNA612766 in any correspondence.

Regards,

NCBI SRA Submissions Staff
Bethesda, Maryland USA

bioprojecthelp at ncbi.nlm.nih.gov

Fri Jun 5 08:01:17 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your submission:

SubmissionID: SUB7554642

BioProject ID: PRJNA637497

Title:

has been successfully registered with the BioProject database. After review by the database staff, your project information will be accessible with the following link, usually within a few days of the release date that you set (or the release of linked data, whichever is first):

<http://www.ncbi.nlm.nih.gov/bioproject/637497>

Please use the BioProject ID PRJNA637497 with your correspondence and your data submissions.

Send questions to bioprojecthelp at ncbi.nlm.nih.gov, and include the BioProject ID and organism name.

Regards,

NCBI BioProject Submissions Staff

Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

bioprojecthelp at ncbi.nlm.nih.gov (for BioProject questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

biosamplehelp at ncbi.nlm.nih.gov

Fri Jun 5 08:10:02 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your recent submission to the BioSample database has been successfully processed and will be released on the date specified.

BioSample accession: SAMN15143806

Temporary SubmissionID: SUB7554642

Release date: as soon as processing is complete

A submission summary and the links by which your BioSample records will be accessible are appended and attached.

Please reference BioSample accession SAMN15143806 when making corresponding sequence data submissions.

Send questions and update requests to biosamplehelp at ncbi.nlm.nih.gov; include the BioSample accession SAMN15143806 in any correspondence.

Regards,

NCBI BioSample Submissions Staff

Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

biosamplehelp at ncbi.nlm.nih.gov (for BioSample questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

| Accession | Sample Name | SPUID | Organism | Tax ID | Isolate |
|--------------|-------------|--------|---|---------|---------|
| SAMN15143806 | tmp_75 | tmp_75 | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 75 |

<https://www.ncbi.nlm.nih.gov/biosample/15143806>

----- next part -----

| Accession | Sample Name | SPUID | Organism | Tax ID | Isolate |
|--------------|-------------|--------|---|---------|---------|
| SAMN15143806 | tmp_75 | tmp_75 | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 75 |

sra at ncbi.nlm.nih.gov
Fri Jun 5 08:20:05 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your recent submission to SRA database has been successfully processed and will be released on the date specified.

Please reference PRJNA637497 in your publication. This BioProject accession number is provided above in lieu of SRP and should be used in your publication as it will allow better searching in Entrez.

SRA accession: PRJNA637497
Temporary Submission ID: SUB7554642
Release date: 2020-06-05

Your SRA records will be accessible with the following link after the indicated release date:
<https://www.ncbi.nlm.nih.gov/sra/PRJNA637497>

Send questions and update requests to sra at ncbi.nlm.nih.gov; include the SRA accession PRJNA637497 in any correspondence.

Regards,

NCBI SRA Submissions Staff
Bethesda, Maryland USA

From: (b) (6)
Received: Fri Jun 05 2020 21:45:04 GMT-0400 (Eastern Daylight Time)
To: Bioproject Support <bioprojecthelp@ncbi.nlm.nih.gov>;
Subject: retract BioProject

Dear Mr/Ms,

I want to retract a submission, and the BioProject ID is PRJNA637497.
I'm sorry for my wrong submitting. Thank you for your help.

Regards



bioprojecthelp at ncbi.nlm.nih.gov
Sat Jun 6 06:20:26 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your submission:

SubmissionID: SUB7554642
BioProject ID: PRJNA637497
Title:
Locus tag prefix:
None (SAMN15143806)

has been updated, eg by the linkage of one or more BioSamples. The locus_tag prefixes for each linked BioSample are included in the locustagprefix.txt file that can be accessed from this BioProject in the submission portal:

<https://submit.ncbi.nlm.nih.gov/subs/bioproject/SUB7554642/overview>

In addition, you can view the locustagprefix.txt files for all of your BioProjects from the BioProject submission page,

<https://submit.ncbi.nlm.nih.gov/subs/bioproject/>.

Please use the BioProject ID PRJNA637497 with your correspondence and your data submissions.
Use the registered locus tag prefix when you include annotation in your submission.

Send questions to bioprojecthelp at ncbi.nlm.nih.gov, and include the BioProject ID and organism name.

Regards,

NCBI BioProject Submissions Staff
Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

bioprojecthelp at ncbi.nlm.nih.gov (for BioProject questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

----- next part -----

A non-text attachment was scrubbed...

Name: locus_tag_prefixes.csv

Type: text/csv

Size: 51 bytes

Desc: not available

URL: <<http://www.ncbi.nlm.nih.gov/mailman/pipermail/sp-mail/attachments/20200606/7379b3ea/attachment-0001.csv>>

From: NLM Support <nlm-support@nlm.nih.gov>;

Received: Mon Jun 08 2020 13:36:22 GMT-0400 (Eastern Daylight Time)

To: (b) (6)

Subject: Re: case #CAS-550133-G8S8X0: retract BioProject TRACKING:00030000004630

Dear (b) (6)

Thank you for your email. We prefer to edit an existing BioProject or change its status to "replaced by" a new BioProject, rather than delete. If you submitted another BioProject to replace this one, please provide the BioProject ID for that project and we will set the status of this project to "replaced by" the desired one.

We have implemented a new capability that allows submitters to view the current content of a BioProject and make minor edits, including updating the title and description, and changing the release date. Please go to the submission portal and click on "Manage Data" where you can access your BioProject. Click on the BioProject accession in the left ("Accession") column and you will have the opportunity to make the desired change. The updates will be processed automatically and the page should refresh with the edited information within a few minutes (typically seconds). You will then be able to make additional changes, if needed.

If you need to make changes in other fields, please email the desired changes and we will edit for you. If you do not plan to use this BioProject or submit a replacement, we can delete it.

If you have other comments or questions, please reply to bioprojecthelp@ncbi.nlm.nih.gov.

Best regards,

(b) (6)

BioProject Curation Staff

* PLEASE DO NOT MODIFY THE SUBJECT LINE OF THIS EMAIL WHEN RESPONDING TO ENSURE CORRECT TRACKING

*

Case Information:

Case #: CAS-550133-G8S8X0

Customer Name: (b) (6)

Customer Email: (b) (6)

Case Created: 2020-06-06T01:45:32Z

Summary: retract BioProject

Details:

Dear Mr/Ms,

I want to retract a submission, and the BioProject ID is PRJNA637497. I'm sorry for my wrong submitting. Thank you for your help.

Regards

(b) (6)

From: (b) (6)

Received: Mon Jun 15 2020 23:10:41 GMT-0400 (Eastern Daylight Time)

To: NLM/NCBI List sra <sra@ncbi.nlm.nih.gov>; SRA Support <sra@ncbi.nlm.nih.gov>;

Subject: Re: SUB7554642/subs/sra/SUB7554642/overview

Dear Mr/Ms,

Recently, I found that it's hard to visit my submitted SRA data, and it would also be very difficult for me to update the data. I have submitted an updated version of this SRA data to another website, so I want to withdraw the old one at NCBI in order to avoid the data version issue. The Submission ID is SUB7147304. I would appreciate your help.

Best regard,

(b) (6)

From: NLM Support <nlm-support@nlm.nih.gov>;

Received: Tue Jun 16 2020 09:00:09 GMT-0400 (Eastern Daylight Time)

To: (b) (6)

Subject: Re: case #CAS-555084-Z9T9P7: Re: SUB7554642/subs/sra/SUB7554642/overview
TRACKING:00041400006890

Dear (b) (6)

Do you want to withdraw all SRA objects created in your account?
here are 2 submissions SUB7554642 and SUB7147304.
Also, bioprojects and biosamples whould be withdrawn as well, right?

Best regards,

(b) (6)

If you have any questions or concerns regarding your **SRA** submission please don't
hesitate to contact sra@ncbi.nlm.nih.gov (applies to new
questions). We *normally* respond *within 2 business days*.

(b) (6)

The NCBI SRA database submission staff

* PLEASE DO NOT MODIFY THE SUBJECT LINE OF THIS EMAIL WHEN RESPONDING TO ENSURE CORRECT TRACKING
*

Case Information:

Case #: CAS-555084-Z9T9P7

Customer Name: (b) (6)

Customer Email: (b) (6)

Case Created: 2020-06-16T03:11:52Z

Summary: Re: SUB7554642/subs/sra/SUB7554642/overview

Details:

Dear Mr/Ms,

Recently, I found that it's hard to visit my submitted SRA data, and
it would also be very difficult for me to update the data. I have submitted an updated version of this SRA
data to another website, so I want to withdraw the old one at NCBI in order to avoid the data version
issue. The Submission ID is SUB7147304. I would appreciate your help.

Best regard,

(b) (6)

From: (b) (6)
Received: Tue Jun 16 2020 20:48:44 GMT-0400 (Eastern Daylight Time)
To: nlm-support@nlm.nih.gov <nlm-support@nlm.nih.gov>; NLM Support <nlm-support@nlm.nih.gov>; Triage Team <nlm-support@nlm.nih.gov>;
Subject: Re: Re: case #CAS-555084-Z9T9P7: Re: SUB7554642/subs/sra/SUB7554642/overview
TRACKING:000414000006890

Dear (b) (6)

Thanks for your replay. Yes, I want to withdraw both 2 submissions SUB7554642 and SUB7147304. The Bioprojects, Biosamples and all SRA objects should be withdrawn as well.

Best regards,

(b) (6)

(b) (6)

From: [NLM Support](#)
Date: 2020-06-16 21:00
To: (b) (6)
Subject: Re: case #CAS-555084-Z9T9P7: Re: SUB7554642/subs/sra/SUB7554642/overview
TRACKING:000414000006890
Dear (b) (6)

Do you want to withdraw all SRA objects created in your account?
here are 2 submissions SUB7554642 and SUB7147304.
Also, bioprojects and biosamples whould be withdrawn as well, right?

Best regards,

(b) (6)

If you have any questions or concerns regarding your **SRA** submission please don't hesitate to contact sra@ncbi.nlm.nih.gov (applies to new questions). We *normally* respond *within 2 business days*.

(b) (6)

The NCBI SRA database submission staff

* PLEASE DO NOT MODIFY THE SUBJECT LINE OF THIS EMAIL WHEN RESPONDING TO ENSURE CORRECT TRACKING
*

Case Information:
Case #: CAS-555084-Z9T9P7

Customer Name: (b) (6)
Customer Email: (b) (6)
Case Created: 2020-06-16T03:11:52Z

Summary: Re: SUB7554642/subs/sra/SUB7554642/overview

Details:

Dear Mr/Ms,

Recently, I found that it's hard to visit my submitted SRA data, and it would also be very difficult for me to update the data. I have submitted an updated version of this SRA data to another website, so I want to withdraw the old one at NCBI in order to avoid the data version issue. The Submission ID is SUB7147304. I would appreciate your help.

Best regard,

(b) (6)

From: NLM Support <nlm-support@nlm.nih.gov>;
Received: Wed Jun 17 2020 12:58:07 GMT-0400 (Eastern Daylight Time)
To: (b) (6)
Subject: Re: Re: case #CAS-555084-Z9T9P7: Re: SUB7554642/subs/sra/SUB7554642/overview
TRACKING:000414000006890

Hi (b) (6)

I had withdrawn everything.

Best regards,

(b) (6)

If you have any questions or concerns regarding your **SRA** submission please don't hesitate to contact sra@ncbi.nlm.nih.gov (applies to new questions). We *normally* respond *within 2 business days*.

(b) (6)

The NCBI SRA database submission staff

----- Original Message -----

From: (b) (6)

Received: Tue Jun 16 2020 20:48:44 GMT-0400 (Eastern Daylight Time)
To: nlm-support@nlm.nih.gov; Inbound - NLM Support; Triage Team;
Subject: Re: Re: case #CAS-555084-Z9T9P7: Re: SUB7554642/subs/sra/SUB7554642/overview
TRACKING:000414000006890

Dear (b) (6)

Thanks for your replay. Yes, I want to withdraw both 2 submissions SUB7554642 and SUB7147304. The Bioprojects, Biosamples and all SRA objects should be withdrawn as well.

Best regards,

(b) (6)

(b) (6)

From: [NLM Support](#)
Date: 2020-06-16 21:00
To: (b) (6)
Subject: Re: case #CAS-555084-Z9T9P7: Re: SUB7554642/subs/sra/SUB7554642/overview
TRACKING:000414000006890
Dear (b) (6)

Do you want to withdraw all SRA objects created in your account?
here are 2 submissions SUB7554642 and SUB7147304.
Also, bioprojects and biosamples whould be withdrawn as well, right?

Best regards,

(b) (6)

If you have any questions or concerns regarding your **SRA** submission please don't hesitate to contact sra@ncbi.nlm.nih.gov (applies to new questions). *We normally respond within 2 business days.*

(b) (6)

The NCBI SRA database submission staff

* PLEASE DO NOT MODIFY THE SUBJECT LINE OF THIS EMAIL WHEN RESPONDING TO ENSURE CORRECT TRACKING
*

Case Information:
Case #: CAS-555084-Z9T9P7
Customer Name: (b) (6)
Customer Email: (b) (6)

Case Created: 2020-06-16T03:11:52Z

Summary: Re: SUB7554642/subs/sra/SUB7554642/overview

Details:

Dear Mr/Ms,

Recently, I found that it's hard to visit my submitted SRA data, and it would also be very difficult for me to update the data. I have submitted an updated version of this SRA data to another website, so I want to withdraw the old one at NCBI in order to avoid the data version issue. The Submission ID is SUB7147304. I would appreciate your help.

Best regard,

(b) (6)

bioprojecthelp at ncbi.nlm.nih.gov
Wed Jun 17 14:40:20 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your submission:

SubmissionID: SUB7554642
BioProject ID: PRJNA637497
Title:
Locus tag prefix:
None (SAMN15143806)

has been updated, eg by the linkage of one or more BioSamples. The locus_tag prefixes for each linked BioSample are included in the locustagprefix.txt file that can be accessed from this BioProject in the submission portal:

<https://submit.ncbi.nlm.nih.gov/subs/bioproject/SUB7554642/overview>

In addition, you can view the locustagprefix.txt files for all of your BioProjects from the BioProject submission page,

<https://submit.ncbi.nlm.nih.gov/subs/bioproject/>.

Please use the BioProject ID PRJNA637497 with your correspondence and your data submissions.

Use the registered locus tag prefix when you include annotation in your submission.

Send questions to bioprojecthelp at ncbi.nlm.nih.gov, and include the BioProject ID and organism name.

Regards,

NCBI BioProject Submissions Staff
Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

bioprojecthelp at ncbi.nlm.nih.gov (for BioProject questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

----- next part -----

A non-text attachment was scrubbed...

Name: locus_tag_prefixes.csv

Type: text/csv

Size: 51 bytes

Desc: not available

URL: <<http://www.ncbi.nlm.nih.gov/mailman/pipermail/sp-mail/attachments/20200617/763bf2f8/attachment-0001.csv>>

bioprojecthelp at ncbi.nlm.nih.gov

Wed Jun 17 14:40:23 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your submission:

SubmissionID: SUB7147304

BioProject ID: PRJNA612766

Title:

Locus tag prefixes:

None (SAMN14381071)

None (SAMN14381072)

has been updated, eg by the linkage of one or more BioSamples. The locus_tag prefixes for

each linked BioSample are included in the locustagprefix.txt file that can accessed

from this BioProject in the submission portal:

<https://submit.ncbi.nlm.nih.gov/subs/bioproject/SUB7147304/overview>

In addition, you can view the locustagprefix.txt files for all of your BioProjects from the BioProject submission page,

<https://submit.ncbi.nlm.nih.gov/subs/bioproject/>.

Please use the BioProject ID PRJNA612766 with your correspondence and your data submissions.

Use the registered locus tag prefixes when you include annotation in your submission.

Send questions to bioprojecthelp at ncbi.nlm.nih.gov, and include the BioProject ID and organism name.

Regards,

NCBI BioProject Submissions Staff

Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

bioprojecthelp at ncbi.nlm.nih.gov (for BioProject questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

----- next part -----

A non-text attachment was scrubbed...

Name: locus_tag_prefixes.csv

Type: text/csv

Size: 65 bytes

Desc: not available

URL: <<http://www.ncbi.nlm.nih.gov/mailman/pipermail/sp-mail/attachments/20200617/29ac3592/attachment-0001.csv>>

From: Yankie, Linda (NIH/NLM/NCBI) [E]
Sent: Fri, 13 Aug 2021 10:01:26 -0400
To: Pruitt, Kim (NIH/NLM/NCBI) [E]; Zayas Caban, Teresa (NIH/NLM) [E]; Sherry, Steve (NIH/NLM/NCBI) [E]; Mizrachi, Ilene (NIH/NLM/NCBI) [E]
Subject: RE: genome assemblies from Jesse Bloom
Attachments: bloom.letter.txt

The attached was sent Wednesday. He did not reply as of yet.

-ly

*Linda Yankie, PhD
Staff Scientist
Information Engineering Branch, NCBI/NLM/NIH*

From: Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6)
Sent: Friday, August 13, 2021 9:56 AM
To: Zayas Caban, Teresa (NIH/NLM) [E] (b) (6); Yankie, Linda (NIH/NLM/NCBI) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Mizrachi, Ilene (NIH/NLM/NCBI) [E] (b) (6)
Subject: RE: genome assemblies from Jesse Bloom

Linda,
Do you know if we responded to Jessie Bloom? Can you send us the response that was sent out?

Kim

Kim D. Pruitt, Ph.D.
Chief, Information Engineering Branch, NCBI
National Library of Medicine | National Institutes of Health
Telework hours: 8:30-5:30

From: Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Sent: Monday, August 09, 2021 7:21 PM
To: Yankie, Linda (NIH/NLM/NCBI) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Mizrachi, Ilene (NIH/NLM/NCBI) [E] (b) (6); Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6); Brennan, Patti (NIH/NLM) [E] (b) (6)
Subject: RE: genome assemblies from Jesse Bloom

Pre-Decisional – Deliberative – Do Not Disclose

I conferred with OGC (b) (5)

(b) (5)

The GenBank Submissions Staff
Bethesda, Maryland USA

-Teresa

Teresa Zayas Cabán, PhD
Assistant Director for Policy Development
National Library of Medicine
National Institutes of Health

From: Yankie, Linda (NIH/NLM/NCBI) [E] (b) (6)
Sent: Monday, August 9, 2021 12:12 PM
To: Zayas Caban, Teresa (NIH/NLM) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Mizrachi, Ilene (NIH/NLM/NCBI) [E] (b) (6); Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6); Brennan, Patti (NIH/NLM) [E] (b) (6)
Subject: RE: genome assemblies from Jesse Bloom

*Linda Yankie, PhD
Staff Scientist*

Information Engineering Branch, NCBI/NLM/NIH

From: Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Sent: Monday, August 09, 2021 7:15 AM
To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Mizrachi, Ilene (NIH/NLM/NCBI) [E] (b) (6); Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6); Brennan, Patti (NIH/NLM) [E] (b) (6)
Cc: Yankie, Linda (NIH/NLM/NCBI) [E] (b) (6)
Subject: RE: genome assemblies from Jesse Bloom

Good morning all,

Am conferring with OGC on this but was wondering (b) (5)

-Teresa

Teresa Zayas Cabán, PhD
Assistant Director for Policy Development
National Library of Medicine
National Institutes of Health

From: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Sent: Friday, August 6, 2021 2:06 PM
To: Mizrachi, Ilene (NIH/NLM/NCBI) [E] (b) (6); Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6); Brennan, Patti (NIH/NLM) [E] (b) (6); Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Cc: Yankie, Linda (NIH/NLM/NCBI) [E] (b) (6)
Subject: RE: genome assemblies from Jesse Bloom

Thanks Ilene, this is a great start. Teresa, (b) (5)

From: Mizrachi, Ilene (NIH/NLM/NCBI) [E] (b) (6)
Sent: Friday, August 6, 2021 12:28 PM
To: Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Brennan, Patti (NIH/NLM) [E] (b) (6); Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Cc: Yankie, Linda (NIH/NLM/NCBI) [E] (b) (6)
Subject: RE: genome assemblies from Jesse Bloom

This is the reply that we would like to send to Bloom. Is it ok?

(b) (5)

(b) (5)

From: Mizrachi, Ilene (NIH/NLM/NCBI) [E]

Sent: Thursday, August 05, 2021 6:38 PM

To: Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Brennan, Patti (NIH/NLM) [E] (b) (6); Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)

Cc: Yankie, Linda (NIH/NLM/NCBI) [E] (b) (6)

Subject: RE: genome assemblies from Jesse Bloom

(b) (5)

Ilene

From: Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6)

Sent: Thursday, August 05, 2021 5:59 PM

To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Mizrachi, Ilene (NIH/NLM/NCBI) [E] (b) (6); Brennan, Patti (NIH/NLM) [E] (b) (6); Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Cc: Yankie, Linda (NIH/NLM/NCBI) [E] (b) (6)
Subject: RE: genome assemblies from Jesse Bloom

(b) (5), but defer to Ilene on that.

Kim D. Pruitt, Ph.D.
Chief, Information Engineering Branch, NCBI
National Library of Medicine | National Institutes of Health
Telework hours: 8:30-5:30

From: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Sent: Thursday, August 05, 2021 5:54 PM
To: Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6); Mizrachi, Ilene (NIH/NLM/NCBI) [E] (b) (6); Brennan, Patti (NIH/NLM) [E] (b) (6); Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Cc: Yankie, Linda (NIH/NLM/NCBI) [E] (b) (6)
Subject: RE: genome assemblies from Jesse Bloom

Thanks Kim. (b) (5)
(b) (5)
(b) (5)
(b) (5)

From: Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6)
Sent: Thursday, August 5, 2021 5:49 PM
To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Mizrachi, Ilene (NIH/NLM/NCBI) [E] (b) (6); Brennan, Patti (NIH/NLM) [E] (b) (6); Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Cc: Yankie, Linda (NIH/NLM/NCBI) [E] (b) (6)
Subject: RE: genome assemblies from Jesse Bloom

Was just about to send this reply –

(b) (5)

Options:

[Redacted] (b) (5)

Kim

Kim D. Pruitt, Ph.D.
Chief, Information Engineering Branch, NCBI
National Library of Medicine | National Institutes of Health
Telework hours: 8:30-5:30

From: Sherry, Steve (NIH/NLM/NCBI) [E] [Redacted] (b) (6)
Sent: Thursday, August 05, 2021 5:42 PM
To: Mizrachi, Ilene (NIH/NLM/NCBI) [E] [Redacted] (b) (6); Pruitt, Kim (NIH/NLM/NCBI) [E] [Redacted] (b) (6); Brennan, Patti (NIH/NLM) [E] [Redacted] (b) (6); Zayas Caban, Teresa (NIH/NLM) [E] <[Redacted] (b) (6)>
Cc: Yankie, Linda (NIH/NLM/NCBI) [E] [Redacted] (b) (6)>
Subject: RE: genome assemblies from Jesse Bloom

Looping in Patti and Teresa for awareness. [Redacted] (b) (5)
[Redacted]
[Redacted]
[Redacted]. Other recommendations?

Steve

From: Mizrachi, Ilene (NIH/NLM/NCBI) [E] [Redacted] (b) (6)
Sent: Thursday, August 5, 2021 5:35 PM
To: Pruitt, Kim (NIH/NLM/NCBI) [E] [Redacted] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] [Redacted] (b) (6)
Cc: Yankie, Linda (NIH/NLM/NCBI) [E] [Redacted] (b) (6)
Subject: genome assemblies from Jesse Bloom

Hi,

[Redacted] (b) (5)



Ilene

Ilene Karsch Mizrahi, PhD
GenBank Coordinator
Sequence Submission and Archives, Program Head
NCBI, NLM, NIH

(b) (6)



From: gb-admin@ncbi.nlm.nih.gov
Date: Wed, 11 Aug 2021 12:52:52 -0400 (Eastern Daylight Time)
To: (b) (6), jbloom@fredhutch.org, (b) (6)
Bcc: (b) (6)
Subject: GenBank Submissions grp 8164050
X-Mailer: Smart

Dear Dr. Bloom,

Thank you for your reply:

I assembled the consensus sequences from a dataset that was generated by Wuhan University, but then deleted from the SRA. So I did not generate the data myself, but wanted to somehow put it in a public sequence database. Is this allowed?
<https://www.biorxiv.org/content/10.1101/2021.06.18.449051v2>

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GenBank accepts data directly determined by the submitter per our submission guidelines outlined at https://www.ncbi.nlm.nih.gov/genbank/submit_types/. In some cases, sequence data not directly obtained by the submitter may be acceptable for the Third Party Annotation database (<https://www.insdc.org/documents/tpa-submission-guidelines>). However, the primary read data must be present in an INSDC database.

Unfortunately, we are unable to accept your submission since it does not meet the criteria for either GenBank or TPA.

The GenBank Submissions Staff
Bethesda, Maryland USA

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

From: Tuncer, Diane (NIH/NLM) [E]
Sent: Mon, 26 Jul 2021 11:54:02 -0400
To: Sherry, Steve (NIH/NLM/NCBI) [E];Pruitt, Kim (NIH/NLM/NCBI) [E]
Cc: Crutchman, Alise (NIH/NLM) [E]
Subject: FW: FYI - News report from China's Xinhua News Agency
Attachments: NLM SRA Deletion Media Responses 7.1.2021 New Responses.docx

Hi Steve and Kim,

We shared this news article with NIH OCPL too, and they [NIH OCPL] responded with the following information (see below). I'm also attaching the last set of QA (which we already sent to you last week).

(b) (5)

From: Tuncer, Diane (NIH/NLM) [E]
Sent: Friday, July 23, 2021 8:46 AM
To: Brennan, Patti (NIH/NLM) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E]
(b) (6); Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6)
Cc: Nurik, Jody (NIH/NLM) [E] (b) (6); Crutchman, Alise (NIH/NLM) [E]
(b) (6)
Subject: FYI - News report from China's Xinhua News Agency

Thought you would be interested in the following [news report](#) from China's major news agency, Xinhua, in response to Dr. Bloom's paper. In the article, China's deputy head of the National Health Commission provides an explanation for the events that led to the request. [See highlighted text below.](#)

Claim that Chinese researchers hid coronavirus data defies scientific ethics

Xinhua, July 23, 2021

Adjust font size: 

A staff member carries out testing at the inactivated COVID-19 vaccine quality inspection lab of Sinovac Life Sciences Co., Ltd. in Beijing, capital of China, Dec. 23, 2020. [Photo/Xinhua]

A U.S. researcher claiming that China hid coronavirus sequences to thwart the tracing of virus origin is against scientific ethics, a Chinese official said Thursday.

Last year, Chinese researchers published a research paper titled "Nanopore targeted sequencing for the accurate and comprehensive detection of coronavirus and other respiratory viruses" on the journal *Small*.

Jesse Bloom is a computational biologist and specialist in viral evolution at the Fred Hutchinson Cancer Research Center in Seattle. Last month, he said that the coronavirus sequences in the study had been removed from the Sequence Read Archive, an online database run by the U.S. National Institutes of Health (NIH), at the request of Chinese researchers.

Bloom said he was able to recover copies of the data stored on Google Cloud. "It therefore seems likely the sequences were deleted to obscure their existence " and "suggests a less than wholehearted effort to trace early spread of the epidemic," Bloom wrote in a preprint paper, not yet peer-reviewed by other scientists.

Speaking at a press conference on the novel coronavirus origin-tracing, Zeng Yixin, deputy head of the National Health Commission, said that China investigated the claim after it was reported.

The research paper is about a sequencing approach to help detect the coronavirus. According to Zeng, when the researchers submitted the paper last March, they needed to upload the sequencing results to prove their method.

On June 9, 2020, the journal sent the sample paper ready to be published to the researchers. They found that the uploading address where the sequencing data can be found was deleted during the review of the paper. Therefore, it was deemed unnecessary to keep their data in an NIH database. On June 16, 2020, the Chinese team emailed NIH to remove the data, and NIH removed the data at the request.

"The researcher has no need to hide or cover up and has no such subjective intention," Zeng said. Meanwhile, the researchers have uploaded the sequencing data, including 244 pieces of data from

61 samples, to the GSA database under China's National Genomics Data Center. The database is open to global users and anyone can make an inquiry.

Zeng added that the earliest sampling time of the virus samples is on Jan. 30, 2020, which has been some time since the beginning of the epidemic. The information and research value that these sample sequencing can provide is very limited in the coronavirus origin tracing.

Jesse Bloom did not get the confirmation from the Chinese researchers, did not understand the background of the data removal, and concocted the conspiracy theory claiming that it was a cover-up, Zeng said.

He noted that Bloom's conspiracy theory has a bad influence on international public opinion, slandered Chinese researchers and hurt them. "It is not only a departure from science but also a violation of scientific ethics."

During epidemics such as the COVID-19, the public pays attention to every word and action of scientists. Therefore, scientists should know their social responsibilities and not make arbitrary speculations, said Zeng, pointing out that Bloom's paper has been criticized by many scientists.

Diane Tuncer, MPH
Supervisory Writer/Editor
Office of Communications and Public Liaison
National Library of Medicine | National Institutes of Health
Mobile (b) (6)
(b) (6)



General Response That Had Been Provided to the Media:

Early in the pandemic, NIH and other federal agencies moved quickly to make COVID-19 open-access data and computational resources freely available to researchers. NIH's National Library of Medicine has a broad portfolio of open-access databases, including the Sequence Read Archive (SRA), the world's largest publicly available repository of high-throughput sequencing data. In the past year, SRA received approximately 2.4 million submissions of sequence data.

SRA is managed by NLM's National Center for Biotechnology (NCBI), which is the U.S. participating member of the International Nucleotide Sequence Database Collaboration (INSDC) since 1987. NCBI follows the INSDC [policies](#) and [guidelines for data submission and change requests](#), and collaborates with participating organizations on updating policies and guidelines as described in this 2018 [article](#). The guidelines describe the criteria for which submitting researchers can request a change in data status (for example, if the data have been corrupted) and actions taken if the criteria are met.

In March 2020, the SARS-CoV-2 sequences in question were submitted by a researcher at a China-based institution for posting in SRA. In June 2020, in response to a request by the same researcher, NCBI withdrew the sequences.

NCBI has initiated an independent review of SRA processes and standard operating procedures to determine whether the appropriate steps were taken to assess this withdrawal request. Withdrawal makes the data undiscoverable but does not erase it. Per the INSDC guidelines, NCBI retains withdrawn data for the scientific record and for disaster recovery. Pending outcome of the review, NCBI will work with INSDC to assign the data to the appropriate status.

The researcher from the China-based institution published relevant information about these sequences [by preprint in March, 2020](#) and in a [journal in June, 2020](#).

Will NLM/NCBI change its policy about data removal?

NLM/NCBI considers the policies and guidelines of the INSDC sound. NCBI has initiated an independent review of SRA processes and standard operating procedures to determine whether the appropriate steps were taken to assess this withdrawal request. Withdrawal makes the data undiscoverable but does not erase it. Per the INSDC guidelines, NCBI retains the data for the scientific record and for disaster recovery. Pending outcome of the review, NCBI will work with INSDC to assign the data to the appropriate status.

Can you say anything about whether NIH is doing any analysis or examination to look for any other SARS-CoV-2 sequence data that has been deleted from that database?

NLM/NCBI's analysis found that from January 2020 through June 2021 six institutions requested withdrawal of SARS-COV-2 submission packages through NLM/NCBI services. This included one requested by a researcher at a China-based institution and the rest from researchers at institutions from other countries, predominantly the U.S. In addition, five institutions requested withdrawal of sequence data through INSDC partners which were replicated within the SRA. NCBI has initiated an independent review of SRA processes and standard operating procedures to determine whether the appropriate steps were taken to assess this withdrawal request.

If the submitter has such rights, are the responses automatic, or reviewed? If reviewed, by whom?

Submitting institutions must contact NLM/NCBI to request that data be withdrawn. NLM/NCBI staff review the request against the INSDC guidelines. NCBI has initiated an independent review of SRA processes and standard operating procedures to determine whether the appropriate steps were taken to assess this withdrawal request.

Can you please make public the text of the delete request, so that I can see precisely how the submitter put it? What was the other database? What kind of update? Who signed the request?

(Reporters are referred to FOIA for this question. Also, NLM should consider posting the email in the FOIA library since it's been requested by three different requestors).

Is there a backup kept?

Yes. NCBI retains the data for the scientific record and for disaster recovery.

How common is it?

Over a one-year period from March 2020-2021, there were 2.4 million submissions made public through SRA of all types of sequence data (not just SARS-CoV-2) and posted to the SRA. 0.19% have been withdrawn.

What date was the request to withdraw the sequence data?

June 15, 2020

From: Zayas Caban, Teresa (NIH/NLM) [E]
Sent: Thu, 8 Jul 2021 17:18:35 -0400
To: Sherry, Steve (NIH/NLM/NCBI) [E]
Subject: RE: quick check: SRA next steps

Thanks I have it open.

-Teresa

Teresa Zayas Cabán, PhD
Assistant Director for Policy Development
National Library of Medicine
National Institutes of Health

From: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Sent: Thursday, July 8, 2021 5:18 PM
To: Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Subject: RE: quick check: SRA next steps

Patti just insisted that I share the document with you, her and FC right now, so it is in your inbox – encrypted. Please let me know if you cannot open it. (Patti couldn't but she says that happens to her sometimes.) (b) (5)

FOIA is just correspondence so hopefully review is minimal.

Steve

From: Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Sent: Thursday, July 8, 2021 5:02 PM
To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Subject: RE: quick check: SRA next steps

Well I didn't respond, did I? Yes that's perfect.

Why don't you send me times for Monday or Tuesday depending on when you think you'd be ready to connect again on this?

Teresa Zayas Cabán, PhD
Assistant Director for Policy Development
National Library of Medicine
National Institutes of Health

From: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Sent: Thursday, July 8, 2021 12:29 PM
To: Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Subject: RE: quick check: SRA next steps

Yes, [REDACTED] (b) (5)
Sound good?

steve

From: Zayas Caban, Teresa (NIH/NLM) [E] [REDACTED] (b) (6)
Sent: Thursday, July 8, 2021 12:15 PM
To: Sherry, Steve (NIH/NLM/NCBI) [E] [REDACTED] (b) (6)
Subject: RE: quick check: SRA next steps

Thanks Steve. And by ready I'm assuming that means ready to go to you, yes?

Should you and I connect early next week then? Just out of curiosity were you going to share with Patti prior to it moving to OD?

-Teresa

Teresa Zayas Cabán, PhD
Assistant Director for Policy Development
National Library of Medicine
National Institutes of Health

From: Sherry, Steve (NIH/NLM/NCBI) [E] [REDACTED] (b) (6)
Sent: Thursday, July 8, 2021 12:14 PM
To: Zayas Caban, Teresa (NIH/NLM) [E] [REDACTED] (b) (6)
Subject: RE: quick check: SRA next steps

Update on FOIA status. I just spoke to Dennis and he said the FOIA should be ready by COB today. The delay has been in [REDACTED] (b) (5)

[REDACTED]
[REDACTED] Dynamics does not make the search straightforward.

From: Zayas Caban, Teresa (NIH/NLM) [E] [REDACTED] (b) (6)
Sent: Wednesday, July 7, 2021 4:52 PM
To: Sherry, Steve (NIH/NLM/NCBI) [E] [REDACTED] (b) (6)
Subject: RE: quick check: SRA next steps

Sounds good will wait to hear. And I'm happy to join whatever conversation is being planned regarding the proposal

I'm also beginning to wonder if we should have a standing meeting, just give it some thought

-Teresa

Teresa Zayas Cabán, PhD
Assistant Director for Policy Development
National Library of Medicine
National Institutes of Health

From: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Sent: Wednesday, July 7, 2021 4:51 PM
To: Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Subject: RE: quick check: SRA next steps

Yes, that is what I was thinking as well. Let's talk when the FOIA material is ready.

I am also about to read you into a new issue – (b) (5)
(b) (5)
(b) (5), I think you may want (b) (5)
(b) (5)
(b) (5) this is not just him trying to direct work for NCBI.

From: Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Sent: Wednesday, July 7, 2021 4:48 PM
To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Subject: RE: quick check: SRA next steps

Thanks for this, I know you're swamped – should we try to chat after you have received the material and/or had a chance to review?

-Teresa

Teresa Zayas Cabán, PhD
Assistant Director for Policy Development
National Library of Medicine
National Institutes of Health

From: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Sent: Wednesday, July 7, 2021 4:47 PM
To: Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Subject: RE: quick check: SRA next steps

Hi Teresa,

(b) (5) still working (b) (5)
(b) (5)
(b) (5) I am expecting (b) (5)

Steve

From: Zayas Caban, Teresa (NIH/NLM) [E] (b) (6)
Sent: Wednesday, July 7, 2021 4:00 PM
To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Subject: quick check: SRA next steps

Steve,

Patti mentioned there was an update re: FOIA requests, let me know if we should connect tomorrow prior to [REDACTED] (b) (5)

Thanks!

-Teresa

Teresa Zayas Cabán, PhD
Assistant Director for Policy Development
National Library of Medicine
National Institutes of Health

Email: [REDACTED] (b) (6)

Phone: [REDACTED] (b) (6)

From: Benson, Dennis (NIH/NLM/NCBI) [E]
Sent: Thu, 8 Jul 2021 16:25:12 -0400
To: Sherry, Steve (NIH/NLM/NCBI) [E]
Cc: Coleman, Janet (NIH/NLM/NCBI) [C]
Subject: Proposed response to FOIA request 56587 (Jon Cohen, Science)
Attachments: 56587 FOIA request 07-08-21.docx

Hi Steve – Janet compiled all the e-mail correspondence related to BioProject PRJNA612766 which was the project Jesse Bloom referred to in his paper. We reviewed the sequence and the contents of all the correspondence which was provided by Eric and Ilene.

BioProject PRJNA637497 was also mentioned in the correspondence associated with PRJNA612766 and therefore falls within the scope of Request 56597 from Jon Cohen, Science Magazine: "email correspondence with researche(r)s who requested the following data removed from the NCBI SRA Database".

Please supply me with the e-mail correspondence with researches who requested the following data removed from the NCBI SRA Database, which Jesse Bloom has described in this preprint: <https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1>

The FOIA Office is in negotiations with the other six requesters to determine if they will be satisfied in limiting their requests to the same scope as the Cohen request.

The attachment contains no redactions. Redactions will be decided by the NHLBI FOIA Office in consultation with the NIH FOIA Office.

The FOIA Office had no objections to sharing the unredacted version of this response with Dr. Brennan and Dr. Collins. Also, they will be both be involved in clearing the final response before it is sent to the requestor.

Let me know if you have any questions.

Per Patti's request we can share this preliminary response with Diane Tuncer and Tara Mowery.

Dennis

bioprojecthelp at ncbi.nlm.nih.gov
Mon Mar 16 06:19:45 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your submission:

SubmissionID: SUB7147304
BioProject ID: PRJNA612766
Title:

has been successfully registered with the BioProject database. After review by the database staff, your project information will be accessible with the following link, usually within a few days of the release date that you set (or the release of linked data, whichever is first):

<http://www.ncbi.nlm.nih.gov/bioproject/612766>

Please use the BioProject ID PRJNA612766 with your correspondence and your data submissions.

Send questions to bioprojecthelp at ncbi.nlm.nih.gov, and include the BioProject ID and organism name.

Regards,

NCBI BioProject Submissions Staff
Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

bioprojecthelp at ncbi.nlm.nih.gov (for BioProject questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

biosamplehelp at ncbi.nlm.nih.gov
Mon Mar 16 06:30:03 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your submission has been successfully registered with the BioSample database:

Temporary SubmissionID: SUB7147304
Release date: as soon as processing is complete

Attached is a list of the sample names you submitted.

Database staff will review your submission within the next few days and will contact you if problems are identified.

Once processing is complete, you will receive another email with assigned accession numbers.

Send questions and update requests to biosamplehelp at ncbi.nlm.nih.gov.

Regards,

NCBI BioSample Submissions Staff
Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

biosamplehelp at ncbi.nlm.nih.gov (for BioSample questions/replies) info at
ncbi.nlm.nih.gov (for general questions regarding NCBI)

----- next part -----

Object IDs and corresponding URLs:

14381198: <https://www.ncbi.nlm.nih.gov/sra/14381198>
14381199: <https://www.ncbi.nlm.nih.gov/sra/14381199>
14381200: <https://www.ncbi.nlm.nih.gov/sra/14381200>
14381201: <https://www.ncbi.nlm.nih.gov/sra/14381201>
14381202: <https://www.ncbi.nlm.nih.gov/sra/14381202>
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14381311: <https://www.ncbi.nlm.nih.gov/sra/14381311>

----- next part -----

| Sample Name | SPUID | Organism | Tax ID | Isolate |
|-------------|-----------|---|---------|---------|
| A12-10min | A12-10min | Severe acute respiratory syndrome coronavirus 2 | | |
| 2697049 | A12-10min | | | |
| A12-4h | A12-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A12-4h |
| A1-10min | A1-10min | Severe acute respiratory syndrome coronavirus 2 | | |
| 2697049 | A1-10min | | | |
| A1-4h | A1-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A1-4h |
| A2-10min | A2-10min | Severe acute respiratory syndrome coronavirus 2 | | |
| 2697049 | A2-10min | | | |
| A2-4h | A2-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A2-4h |
| A3-10min | A3-10min | Severe acute respiratory syndrome coronavirus 2 | | |
| 2697049 | A3-10min | | | |
| A3-4h | A3-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A3-4h |
| A4-10min | A4-10min | Severe acute respiratory syndrome coronavirus 2 | | |
| 2697049 | A4-10min | | | |
| A4-4h | A4-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | A4-4h |
| A5-10min | A5-10min | Severe acute respiratory syndrome coronavirus 2 | | |
| 2697049 | A5-10min | | | |

A5-4h A5-4h Severe acute respiratory syndrome coronavirus 2 2697049 A5-4h
A6-10min A6-10min Severe acute respiratory syndrome coronavirus 2
2697049 A6-10min
A6-4h A6-4h Severe acute respiratory syndrome coronavirus 2 2697049 A6-4h
A7-10min A7-10min Severe acute respiratory syndrome coronavirus 2
2697049 A7-10min
A7-4h A7-4h Severe acute respiratory syndrome coronavirus 2 2697049 A7-4h
A8-10min A8-10min Severe acute respiratory syndrome coronavirus 2
2697049 A8-10min
A8-4h A8-4h Severe acute respiratory syndrome coronavirus 2 2697049 A8-4h
A9-10min A9-10min Severe acute respiratory syndrome coronavirus 2
2697049 A9-10min
A9-4h A9-4h Severe acute respiratory syndrome coronavirus 2 2697049 A9-4h
B4-10min B4-10min Severe acute respiratory syndrome coronavirus 2
2697049 B4-10min
B4-4h B4-4h Severe acute respiratory syndrome coronavirus 2 2697049 B4-4h
C11-10min C11-10min Severe acute respiratory syndrome coronavirus 2
2697049 C11-10min
C11-4h C11-4h Severe acute respiratory syndrome coronavirus 2 2697049 C11-4h
C1-10min C1-10min Severe acute respiratory syndrome coronavirus 2
2697049 C1-10min
C1-4h C1-4h Severe acute respiratory syndrome coronavirus 2 2697049 C1-4h
C2-10min C2-10min Severe acute respiratory syndrome coronavirus 2
2697049 C2-10min
C2-4h C2-4h Severe acute respiratory syndrome coronavirus 2 2697049 C2-4h
D10-10min D10-10min Severe acute respiratory syndrome coronavirus 2
2697049 D10-10min
D10-4h D10-4h Severe acute respiratory syndrome coronavirus 2 2697049 D10-4h
D12-10min D12-10min Severe acute respiratory syndrome coronavirus 2
2697049 D12-10min
D12-4h D12-4h Severe acute respiratory syndrome coronavirus 2 2697049 D12-4h
D2-10min D2-10min Severe acute respiratory syndrome coronavirus 2
2697049 D2-10min
D2-4h D2-4h Severe acute respiratory syndrome coronavirus 2 2697049 D2-4h
E1-10min E1-10min Severe acute respiratory syndrome coronavirus 2
2697049 E1-10min
E1-4h E1-4h Severe acute respiratory syndrome coronavirus 2 2697049 E1-4h
E5-10min E5-10min Severe acute respiratory syndrome coronavirus 2
2697049 E5-10min
E5-4h E5-4h Severe acute respiratory syndrome coronavirus 2 2697049 E5-4h
F12-10min F12-10min Severe acute respiratory syndrome coronavirus 2
2697049 F12-10min

F12-4h F12-4h Severe acute respiratory syndrome coronavirus 2 2697049 F12-4h
F5-10min F5-10min Severe acute respiratory syndrome coronavirus 2
2697049 F5-10min
F5-4h F5-4h Severe acute respiratory syndrome coronavirus 2 2697049 F5-4h
G1-10min G1-10min Severe acute respiratory syndrome coronavirus 2
2697049 G1-10min
G1-4h G1-4h Severe acute respiratory syndrome coronavirus 2 2697049 G1-4h
H12-10min H12-10min Severe acute respiratory syndrome coronavirus 2
2697049 H12-10min
H12-4h H12-4h Severe acute respiratory syndrome coronavirus 2 2697049 H12-4h
H9-10min H9-10min Severe acute respiratory syndrome coronavirus 2
2697049 H9-10min
H9-4h H9-4h Severe acute respiratory syndrome coronavirus 2 2697049 H9-4h
NC1-10min NC1-10min Severe acute respiratory syndrome coronavirus 2
2697049 NC1-10min
NC1-4h NC1-4h Severe acute respiratory syndrome coronavirus 2 2697049 NC1-4h
PC1-10min PC1-10min Severe acute respiratory syndrome coronavirus 2
2697049 PC1-10min
PC1-4h PC1-4h Severe acute respiratory syndrome coronavirus 2 2697049 PC1-4h
A10-10min A10-10min Severe acute respiratory syndrome coronavirus 2
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A10-4h A10-4h Severe acute respiratory syndrome coronavirus 2 2697049 A10-4h
A11-10min A11-10min Severe acute respiratory syndrome coronavirus 2
2697049 A11-10min
A11-4h A11-4h Severe acute respiratory syndrome coronavirus 2 2697049 A11-4h
B1-10min B1-10min Severe acute respiratory syndrome coronavirus 2
2697049 B1-10min
B1-4h B1-4h Severe acute respiratory syndrome coronavirus 2 2697049 B1-4h
B2-10min B2-10min Severe acute respiratory syndrome coronavirus 2
2697049 B2-10min
B2-4h B2-4h Severe acute respiratory syndrome coronavirus 2 2697049 B2-4h
B3-10min B3-10min Severe acute respiratory syndrome coronavirus 2
2697049 B3-10min
B3-4h B3-4h Severe acute respiratory syndrome coronavirus 2 2697049 B3-4h
B5-4h B5-4h Severe acute respiratory syndrome coronavirus 2 2697049 B5-4h
B9-10min B9-10min Severe acute respiratory syndrome coronavirus 2
2697049 B9-10min
B9-4h B9-4h Severe acute respiratory syndrome coronavirus 2 2697049 B9-4h
C12-10min C12-10min Severe acute respiratory syndrome coronavirus 2
2697049 C12-10min
C12-4h C12-4h Severe acute respiratory syndrome coronavirus 2 2697049 C12-4h

C9-10min C9-10min Severe acute respiratory syndrome coronavirus 2
2697049 C9-10min
C9-4h C9-4h Severe acute respiratory syndrome coronavirus 2 2697049 C9-
4h
D11-10min D11-10min Severe acute respiratory syndrome coronavirus 2
2697049 D11-10min
D11-4h D11-4h Severe acute respiratory syndrome coronavirus 2 2697049 D11-
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D9-10min D9-10min Severe acute respiratory syndrome coronavirus 2
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D9-4h D9-4h Severe acute respiratory syndrome coronavirus 2 2697049 D9-
4h
E11-10min E11-10min Severe acute respiratory syndrome coronavirus 2
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E11-4h E11-4h Severe acute respiratory syndrome coronavirus 2 2697049 E11-
4h
E12-10min E12-10min Severe acute respiratory syndrome coronavirus 2
2697049 E12-10min
E12-4h E12-4h Severe acute respiratory syndrome coronavirus 2 2697049 E12-
4h
E3-10min E3-10min Severe acute respiratory syndrome coronavirus 2
2697049 E3-10min
E3-4h E3-4h Severe acute respiratory syndrome coronavirus 2 2697049 E3-
4h
E6-10min E6-10min Severe acute respiratory syndrome coronavirus 2
2697049 E6-10min
E6-4h E6-4h Severe acute respiratory syndrome coronavirus 2 2697049 E6-
4h
F11-10min F11-10min Severe acute respiratory syndrome coronavirus 2
2697049 F11-10min
F11-4h F11-4h Severe acute respiratory syndrome coronavirus 2 2697049 F11-
4h
F8-10min F8-10min Severe acute respiratory syndrome coronavirus 2
2697049 F8-10min
F8-4h F8-4h Severe acute respiratory syndrome coronavirus 2 2697049 F8-
4h
G11-10min G11-10min Severe acute respiratory syndrome coronavirus 2
2697049 G11-10min
G11-4h G11-4h Severe acute respiratory syndrome coronavirus 2 2697049 G11-
4h
G12-10min G12-10min Severe acute respiratory syndrome coronavirus 2
2697049 G12-10min
G12-4h G12-4h Severe acute respiratory syndrome coronavirus 2 2697049 G12-
4h
G6-10min G6-10min Severe acute respiratory syndrome coronavirus 2
2697049 G6-10min
G6-4h G6-4h Severe acute respiratory syndrome coronavirus 2 2697049 G6-
4h
H3-10min H3-10min Severe acute respiratory syndrome coronavirus 2
2697049 H3-10min
H3-4h H3-4h Severe acute respiratory syndrome coronavirus 2 2697049 H3-
4h
NC2-4h NC2-4h Severe acute respiratory syndrome coronavirus 2 2697049 NC2-
4h
PC2-10min PC2-10min Severe acute respiratory syndrome coronavirus 2
2697049 PC2-10min

PC2-4h PC2-4h Severe acute respiratory syndrome coronavirus 2 2697049 PC2-4h
R01-10min R01-10min Severe acute respiratory syndrome coronavirus 2
2697049 R01-10min
R01-4h R01-4h Severe acute respiratory syndrome coronavirus 2 2697049 R01-4h
R02-10min R02-10min Severe acute respiratory syndrome coronavirus 2
2697049 R02-10min
R02-4h R02-4h Severe acute respiratory syndrome coronavirus 2 2697049 R02-4h
R03-10min R03-10min Severe acute respiratory syndrome coronavirus 2
2697049 R03-10min
R03-4h R03-4h Severe acute respiratory syndrome coronavirus 2 2697049 R03-4h
R04-4h R04-4h Severe acute respiratory syndrome coronavirus 2 2697049 R04-4h
R05-10min R05-10min Severe acute respiratory syndrome coronavirus 2
2697049 R05-10min
R05-4h R05-4h Severe acute respiratory syndrome coronavirus 2 2697049 R05-4h
R06-10min R06-10min Severe acute respiratory syndrome coronavirus 2
2697049 R06-10min
R06-4h R06-4h Severe acute respiratory syndrome coronavirus 2 2697049 R06-4h
R07-10min R07-10min Severe acute respiratory syndrome coronavirus 2
2697049 R07-10min
R07-4h R07-4h Severe acute respiratory syndrome coronavirus 2 2697049 R07-4h
R08-10min R08-10min Severe acute respiratory syndrome coronavirus 2
2697049 R08-10min
R08-4h R08-4h Severe acute respiratory syndrome coronavirus 2 2697049 R08-4h
R09-10min R09-10min Severe acute respiratory syndrome coronavirus 2
2697049 R09-10min
R09-4h R09-4h Severe acute respiratory syndrome coronavirus 2 2697049 R09-4h
R10-10min R10-10min Severe acute respiratory syndrome coronavirus 2
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R10-4h R10-4h Severe acute respiratory syndrome coronavirus 2 2697049 R10-4h
R11-10min R11-10min Severe acute respiratory syndrome coronavirus 2
2697049 R11-10min
R11-4h R11-4h Severe acute respiratory syndrome coronavirus 2 2697049 R11-4h
R12-10min R12-10min Severe acute respiratory syndrome coronavirus 2
2697049 R12-10min
R12-4h R12-4h Severe acute respiratory syndrome coronavirus 2 2697049 R12-4h
R13-10min R13-10min Severe acute respiratory syndrome coronavirus 2
2697049 R13-10min
R13-4h R13-4h Severe acute respiratory syndrome coronavirus 2 2697049 R13-4h
R14-10min R14-10min Severe acute respiratory syndrome coronavirus 2
2697049 R14-10min
R14-4h R14-4h Severe acute respiratory syndrome coronavirus 2 2697049 R14-4h

R15-10min R15-10min Severe acute respiratory syndrome coronavirus 2
2697049 R15-10min
R15-4h R15-4h Severe acute respiratory syndrome coronavirus 2 2697049 R15-
4h
R16-10min R16-10min Severe acute respiratory syndrome coronavirus 2
2697049 R16-10min
R16-4h R16-4h Severe acute respiratory syndrome coronavirus 2 2697049 R16-
4h

biosamplehelp at ncbi.nlm.nih.gov
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| Accession ID | Sample Name | SPUID | Organism | Tax |
|--------------|-------------|-------|------------|-----|
| | Isolate | | BioProject | |

| | | | |
|---------------|-----------|-----------|-----------------------------------|
| SAMN14381071 | A12-10min | A12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A12-10min | PRJNA612766 |
| SAMN14381072 | A12-4h | A12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A12-4h | PRJNA612766 |
| SAMN14381073 | A1-10min | A1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A1-10min | PRJNA612766 |
| SAMN14381074 | A1-4h | A1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A1-4h | PRJNA612766 |
| SAMN14381075 | A2-10min | A2-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A2-10min | PRJNA612766 |
| SAMN14381076 | A2-4h | A2-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A2-4h | PRJNA612766 |
| SAMN14381077 | A3-10min | A3-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A3-10min | PRJNA612766 |
| SAMN14381078 | A3-4h | A3-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A3-4h | PRJNA612766 |
| SAMN14381079 | A4-10min | A4-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A4-10min | PRJNA612766 |
| SAMN14381080 | A4-4h | A4-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A4-4h | PRJNA612766 |
| SAMN14381081 | A5-10min | A5-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A5-10min | PRJNA612766 |
| SAMN14381082 | A5-4h | A5-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A5-4h | PRJNA612766 |
| SAMN14381083 | A6-10min | A6-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A6-10min | PRJNA612766 |
| SAMN14381084 | A6-4h | A6-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A6-4h | PRJNA612766 |
| SAMN14381085 | A7-10min | A7-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A7-10min | PRJNA612766 |
| SAMN14381086 | A7-4h | A7-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A7-4h | PRJNA612766 |
| SAMN14381087 | A8-10min | A8-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A8-10min | PRJNA612766 |
| SAMN14381088 | A8-4h | A8-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A8-4h | PRJNA612766 |
| SAMN14381089 | A9-10min | A9-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A9-10min | PRJNA612766 |
| SAMN14381090 | A9-4h | A9-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A9-4h | PRJNA612766 |
| SAMN14381091 | B4-10min | B4-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B4-10min | PRJNA612766 |
| SAMN14381092 | B4-4h | B4-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B4-4h | PRJNA612766 |
| SAMN14381093 | C11-10min | C11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C11-10min | PRJNA612766 |
| SAMN14381094 | C11-4h | C11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C11-4h | PRJNA612766 |
| SAMN14381095 | C1-10min | C1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C1-10min | PRJNA612766 |

| | | | |
|---------------|-----------|-----------|-----------------------------------|
| SAMN14381096 | C1-4h | C1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C1-4h | PRJNA612766 |
| SAMN14381097 | C2-10min | C2-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C2-10min | PRJNA612766 |
| SAMN14381098 | C2-4h | C2-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C2-4h | PRJNA612766 |
| SAMN14381099 | D10-10min | D10-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D10-10min | PRJNA612766 |
| SAMN14381100 | D10-4h | D10-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D10-4h | PRJNA612766 |
| SAMN14381101 | D12-10min | D12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D12-10min | PRJNA612766 |
| SAMN14381102 | D12-4h | D12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D12-4h | PRJNA612766 |
| SAMN14381103 | D2-10min | D2-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D2-10min | PRJNA612766 |
| SAMN14381104 | D2-4h | D2-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D2-4h | PRJNA612766 |
| SAMN14381105 | E1-10min | E1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E1-10min | PRJNA612766 |
| SAMN14381106 | E1-4h | E1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E1-4h | PRJNA612766 |
| SAMN14381107 | E5-10min | E5-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E5-10min | PRJNA612766 |
| SAMN14381108 | E5-4h | E5-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E5-4h | PRJNA612766 |
| SAMN14381109 | F12-10min | F12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F12-10min | PRJNA612766 |
| SAMN14381110 | F12-4h | F12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F12-4h | PRJNA612766 |
| SAMN14381111 | F5-10min | F5-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F5-10min | PRJNA612766 |
| SAMN14381112 | F5-4h | F5-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F5-4h | PRJNA612766 |
| SAMN14381113 | G1-10min | G1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G1-10min | PRJNA612766 |
| SAMN14381114 | G1-4h | G1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G1-4h | PRJNA612766 |
| SAMN14381115 | H12-10min | H12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | H12-10min | PRJNA612766 |
| SAMN14381116 | H12-4h | H12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | H12-4h | PRJNA612766 |
| SAMN14381117 | H9-10min | H9-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | H9-10min | PRJNA612766 |
| SAMN14381118 | H9-4h | H9-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | H9-4h | PRJNA612766 |
| SAMN14381119 | NC1-10min | NC1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | NC1-10min | PRJNA612766 |
| SAMN14381120 | NC1-4h | NC1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | NC1-4h | PRJNA612766 |

| | | | |
|---------------|-----------|-----------|-----------------------------------|
| SAMN14381121 | PC1-10min | PC1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | PC1-10min | PRJNA612766 |
| SAMN14381122 | PC1-4h | PC1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | PC1-4h | PRJNA612766 |
| SAMN14381123 | A10-10min | A10-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A10-10min | PRJNA612766 |
| SAMN14381124 | A10-4h | A10-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A10-4h | PRJNA612766 |
| SAMN14381125 | A11-10min | A11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A11-10min | PRJNA612766 |
| SAMN14381126 | A11-4h | A11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | A11-4h | PRJNA612766 |
| SAMN14381127 | B1-10min | B1-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B1-10min | PRJNA612766 |
| SAMN14381128 | B1-4h | B1-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B1-4h | PRJNA612766 |
| SAMN14381129 | B2-10min | B2-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B2-10min | PRJNA612766 |
| SAMN14381130 | B2-4h | B2-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B2-4h | PRJNA612766 |
| SAMN14381131 | B3-10min | B3-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B3-10min | PRJNA612766 |
| SAMN14381132 | B3-4h | B3-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B3-4h | PRJNA612766 |
| SAMN14381133 | B5-4h | B5-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B5-4h | PRJNA612766 |
| SAMN14381134 | B9-10min | B9-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B9-10min | PRJNA612766 |
| SAMN14381135 | B9-4h | B9-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | B9-4h | PRJNA612766 |
| SAMN14381136 | C12-10min | C12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C12-10min | PRJNA612766 |
| SAMN14381137 | C12-4h | C12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C12-4h | PRJNA612766 |
| SAMN14381138 | C9-10min | C9-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C9-10min | PRJNA612766 |
| SAMN14381139 | C9-4h | C9-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | C9-4h | PRJNA612766 |
| SAMN14381140 | D11-10min | D11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D11-10min | PRJNA612766 |
| SAMN14381141 | D11-4h | D11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D11-4h | PRJNA612766 |
| SAMN14381142 | D9-10min | D9-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D9-10min | PRJNA612766 |
| SAMN14381143 | D9-4h | D9-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | D9-4h | PRJNA612766 |
| SAMN14381144 | E11-10min | E11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E11-10min | PRJNA612766 |
| SAMN14381145 | E11-4h | E11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E11-4h | PRJNA612766 |

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| SAMN14381146 | E12-10min | E12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E12-10min | PRJNA612766 |
| SAMN14381147 | E12-4h | E12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E12-4h | PRJNA612766 |
| SAMN14381148 | E3-10min | E3-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E3-10min | PRJNA612766 |
| SAMN14381149 | E3-4h | E3-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E3-4h | PRJNA612766 |
| SAMN14381150 | E6-10min | E6-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E6-10min | PRJNA612766 |
| SAMN14381151 | E6-4h | E6-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | E6-4h | PRJNA612766 |
| SAMN14381152 | F11-10min | F11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F11-10min | PRJNA612766 |
| SAMN14381153 | F11-4h | F11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F11-4h | PRJNA612766 |
| SAMN14381154 | F8-10min | F8-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F8-10min | PRJNA612766 |
| SAMN14381155 | F8-4h | F8-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | F8-4h | PRJNA612766 |
| SAMN14381156 | G11-10min | G11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G11-10min | PRJNA612766 |
| SAMN14381157 | G11-4h | G11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G11-4h | PRJNA612766 |
| SAMN14381158 | G12-10min | G12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G12-10min | PRJNA612766 |
| SAMN14381159 | G12-4h | G12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G12-4h | PRJNA612766 |
| SAMN14381160 | G6-10min | G6-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G6-10min | PRJNA612766 |
| SAMN14381161 | G6-4h | G6-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | G6-4h | PRJNA612766 |
| SAMN14381162 | H3-10min | H3-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | H3-10min | PRJNA612766 |
| SAMN14381163 | H3-4h | H3-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | H3-4h | PRJNA612766 |
| SAMN14381164 | NC2-4h | NC2-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | NC2-4h | PRJNA612766 |
| SAMN14381165 | PC2-10min | PC2-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | PC2-10min | PRJNA612766 |
| SAMN14381166 | PC2-4h | PC2-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | PC2-4h | PRJNA612766 |
| SAMN14381167 | R01-10min | R01-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R01-10min | PRJNA612766 |
| SAMN14381168 | R01-4h | R01-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R01-4h | PRJNA612766 |
| SAMN14381169 | R02-10min | R02-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R02-10min | PRJNA612766 |
| SAMN14381170 | R02-4h | R02-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R02-4h | PRJNA612766 |

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| SAMN14381171 | R03-10min | R03-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R03-10min | PRJNA612766 |
| SAMN14381172 | R03-4h | R03-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R03-4h | PRJNA612766 |
| SAMN14381173 | R04-4h | R04-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R04-4h | PRJNA612766 |
| SAMN14381174 | R05-10min | R05-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R05-10min | PRJNA612766 |
| SAMN14381175 | R05-4h | R05-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R05-4h | PRJNA612766 |
| SAMN14381176 | R06-10min | R06-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R06-10min | PRJNA612766 |
| SAMN14381177 | R06-4h | R06-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R06-4h | PRJNA612766 |
| SAMN14381178 | R07-10min | R07-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R07-10min | PRJNA612766 |
| SAMN14381179 | R07-4h | R07-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R07-4h | PRJNA612766 |
| SAMN14381180 | R08-10min | R08-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R08-10min | PRJNA612766 |
| SAMN14381181 | R08-4h | R08-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R08-4h | PRJNA612766 |
| SAMN14381182 | R09-10min | R09-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R09-10min | PRJNA612766 |
| SAMN14381183 | R09-4h | R09-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R09-4h | PRJNA612766 |
| SAMN14381184 | R10-10min | R10-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R10-10min | PRJNA612766 |
| SAMN14381185 | R10-4h | R10-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R10-4h | PRJNA612766 |
| SAMN14381186 | R11-10min | R11-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R11-10min | PRJNA612766 |
| SAMN14381187 | R11-4h | R11-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R11-4h | PRJNA612766 |
| SAMN14381188 | R12-10min | R12-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R12-10min | PRJNA612766 |
| SAMN14381189 | R12-4h | R12-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R12-4h | PRJNA612766 |
| SAMN14381190 | R13-10min | R13-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R13-10min | PRJNA612766 |
| SAMN14381191 | R13-4h | R13-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R13-4h | PRJNA612766 |
| SAMN14381192 | R14-10min | R14-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R14-10min | PRJNA612766 |
| SAMN14381193 | R14-4h | R14-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R14-4h | PRJNA612766 |
| SAMN14381194 | R15-10min | R15-10min | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R15-10min | PRJNA612766 |
| SAMN14381195 | R15-4h | R15-4h | Severe acute respiratory syndrome |
| coronavirus 2 | 2697049 | R15-4h | PRJNA612766 |

SAMN14381196 R16-10min R16-10min Severe acute respiratory syndrome
 coronavirus 2 2697049 R16-10min PRJNA612766
 SAMN14381197 R16-4h R16-4h Severe acute respiratory syndrome
 coronavirus 2 2697049 R16-4h PRJNA612766
 SAMN14381198 0cp-replicate01-2h 0cp-replicate01-2h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate01-
 2h PRJNA612766
 SAMN14381199 0cp-replicate01-4h 0cp-replicate01-4h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate01-
 4h PRJNA612766
 SAMN14381200 0cp-replicate02-30min 0cp-replicate02-30min Severe
 acute respiratory syndrome coronavirus 2 2697049 0cp-replicate02-
 30min PRJNA612766
 SAMN14381201 0cp-replicate02-1h 0cp-replicate02-1h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate02-
 1h PRJNA612766
 SAMN14381202 0cp-replicate02-2h 0cp-replicate02-2h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate02-
 2h PRJNA612766
 SAMN14381203 0cp-replicate02-4h 0cp-replicate02-4h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate02-
 4h PRJNA612766
 SAMN14381204 0cp-replicate03-30min 0cp-replicate03-30min Severe
 acute respiratory syndrome coronavirus 2 2697049 0cp-replicate03-
 30min PRJNA612766
 SAMN14381205 0cp-replicate03-1h 0cp-replicate03-1h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate03-
 1h PRJNA612766
 SAMN14381206 0cp-replicate03-2h 0cp-replicate03-2h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate03-
 2h PRJNA612766
 SAMN14381207 0cp-replicate03-4h 0cp-replicate03-4h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate03-
 4h PRJNA612766
 SAMN14381208 0cp-replicate04-1h 0cp-replicate04-1h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate04-
 1h PRJNA612766
 SAMN14381209 0cp-replicate04-2h 0cp-replicate04-2h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate04-
 2h PRJNA612766
 SAMN14381210 0cp-replicate04-4h 0cp-replicate04-4h Severe acute
 respiratory syndrome coronavirus 2 2697049 0cp-replicate04-
 4h PRJNA612766
 SAMN14381211 10cp-replicate01-10min 10cp-replicate01-10min Severe
 acute respiratory syndrome coronavirus 2 2697049 10cp-replicate01-
 10min PRJNA612766
 SAMN14381212 10cp-replicate01-30min 10cp-replicate01-30min Severe
 acute respiratory syndrome coronavirus 2 2697049 10cp-replicate01-
 30min PRJNA612766
 SAMN14381213 10cp-replicate01-1h 10cp-replicate01-1h Severe acute
 respiratory syndrome coronavirus 2 2697049 10cp-replicate01-
 1h PRJNA612766

SAMN14381214 10cp-replicate01-2h 10cp-replicate01-2h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate01-
2h PRJNA612766

SAMN14381215 10cp-replicate01-4h 10cp-replicate01-4h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate01-
4h PRJNA612766

SAMN14381216 10cp-replicate02-10min 10cp-replicate02-10min Severe
acute respiratory syndrome coronavirus 2 2697049 10cp-replicate02-
10min PRJNA612766

SAMN14381217 10cp-replicate02-30min 10cp-replicate02-30min Severe
acute respiratory syndrome coronavirus 2 2697049 10cp-replicate02-
30min PRJNA612766

SAMN14381218 10cp-replicate02-1h 10cp-replicate02-1h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate02-
1h PRJNA612766

SAMN14381219 10cp-replicate02-2h 10cp-replicate02-2h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate02-
2h PRJNA612766

SAMN14381220 10cp-replicate02-4h 10cp-replicate02-4h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate02-
4h PRJNA612766

SAMN14381221 10cp-replicate03-10min 10cp-replicate03-10min Severe
acute respiratory syndrome coronavirus 2 2697049 10cp-replicate03-
10min PRJNA612766

SAMN14381222 10cp-replicate03-30min 10cp-replicate03-30min Severe
acute respiratory syndrome coronavirus 2 2697049 10cp-replicate03-
30min PRJNA612766

SAMN14381223 10cp-replicate03-1h 10cp-replicate03-1h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate03-
1h PRJNA612766

SAMN14381224 10cp-replicate03-2h 10cp-replicate03-2h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate03-
2h PRJNA612766

SAMN14381225 10cp-replicate03-4h 10cp-replicate03-4h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate03-
4h PRJNA612766

SAMN14381226 10cp-replicate04-10min 10cp-replicate04-10min Severe
acute respiratory syndrome coronavirus 2 2697049 10cp-replicate04-
10min PRJNA612766

SAMN14381227 10cp-replicate04-30min 10cp-replicate04-30min Severe
acute respiratory syndrome coronavirus 2 2697049 10cp-replicate04-
30min PRJNA612766

SAMN14381228 10cp-replicate04-1h 10cp-replicate04-1h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate04-
1h PRJNA612766

SAMN14381229 10cp-replicate04-2h 10cp-replicate04-2h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate04-
2h PRJNA612766

SAMN14381230 10cp-replicate04-4h 10cp-replicate04-4h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate04-
4h PRJNA612766

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| SAMN14381231 | 100cp-replicate01-10min | 100cp-replicate01-10min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate01-10min | PRJNA612766 |
| SAMN14381232 | 100cp-replicate01-30min | 100cp-replicate01-30min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate01-30min | PRJNA612766 |
| SAMN14381233 | 100cp-replicate01-1h | 100cp-replicate01-1h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate01-1h | PRJNA612766 |
| SAMN14381234 | 100cp-replicate01-2h | 100cp-replicate01-2h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate01-2h | PRJNA612766 |
| SAMN14381235 | 100cp-replicate01-4h | 100cp-replicate01-4h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate01-4h | PRJNA612766 |
| SAMN14381236 | 100cp-replicate02-10min | 100cp-replicate02-10min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate02-10min | PRJNA612766 |
| SAMN14381237 | 100cp-replicate02-30min | 100cp-replicate02-30min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate02-30min | PRJNA612766 |
| SAMN14381238 | 100cp-replicate02-1h | 100cp-replicate02-1h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate02-1h | PRJNA612766 |
| SAMN14381239 | 100cp-replicate02-2h | 100cp-replicate02-2h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate02-2h | PRJNA612766 |
| SAMN14381240 | 100cp-replicate02-4h | 100cp-replicate02-4h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate02-4h | PRJNA612766 |
| SAMN14381241 | 100cp-replicate03-10min | 100cp-replicate03-10min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate03-10min | PRJNA612766 |
| SAMN14381242 | 100cp-replicate03-30min | 100cp-replicate03-30min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate03-30min | PRJNA612766 |
| SAMN14381243 | 100cp-replicate03-1h | 100cp-replicate03-1h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate03-1h | PRJNA612766 |
| SAMN14381244 | 100cp-replicate03-2h | 100cp-replicate03-2h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate03-2h | PRJNA612766 |
| SAMN14381245 | 100cp-replicate03-4h | 100cp-replicate03-4h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate03-4h | PRJNA612766 |
| SAMN14381246 | 100cp-replicate04-30min | 100cp-replicate04-30min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate04-30min | PRJNA612766 |
| SAMN14381247 | 100cp-replicate04-1h | 100cp-replicate04-1h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate04-1h | PRJNA612766 |

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|--------------|-------------------------|-------------------------|---|---------|-------------------------|-------------|
| SAMN14381248 | 100cp-replicate04-2h | 100cp-replicate04-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate04-2h | PRJNA612766 |
| SAMN14381249 | 100cp-replicate04-4h | 100cp-replicate04-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 100cp-replicate04-4h | PRJNA612766 |
| SAMN14381250 | 500cp-replicate01-10min | 500cp-replicate01-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate01-10min | PRJNA612766 |
| SAMN14381251 | 500cp-replicate01-30min | 500cp-replicate01-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate01-30min | PRJNA612766 |
| SAMN14381252 | 500cp-replicate01-1h | 500cp-replicate01-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate01-1h | PRJNA612766 |
| SAMN14381253 | 500cp-replicate01-2h | 500cp-replicate01-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate01-2h | PRJNA612766 |
| SAMN14381254 | 500cp-replicate01-4h | 500cp-replicate01-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate01-4h | PRJNA612766 |
| SAMN14381255 | 500cp-replicate02-10min | 500cp-replicate02-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate02-10min | PRJNA612766 |
| SAMN14381256 | 500cp-replicate02-30min | 500cp-replicate02-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate02-30min | PRJNA612766 |
| SAMN14381257 | 500cp-replicate02-1h | 500cp-replicate02-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate02-1h | PRJNA612766 |
| SAMN14381258 | 500cp-replicate02-2h | 500cp-replicate02-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate02-2h | PRJNA612766 |
| SAMN14381259 | 500cp-replicate02-4h | 500cp-replicate02-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate02-4h | PRJNA612766 |
| SAMN14381260 | 500cp-replicate03-10min | 500cp-replicate03-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate03-10min | PRJNA612766 |
| SAMN14381261 | 500cp-replicate03-30min | 500cp-replicate03-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate03-30min | PRJNA612766 |
| SAMN14381262 | 500cp-replicate03-1h | 500cp-replicate03-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate03-1h | PRJNA612766 |
| SAMN14381263 | 500cp-replicate03-2h | 500cp-replicate03-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate03-2h | PRJNA612766 |
| SAMN14381264 | 500cp-replicate03-4h | 500cp-replicate03-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate03-4h | PRJNA612766 |

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| SAMN14381265 | 500cp-replicate04-10min | 500cp-replicate04-10min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-10min | PRJNA612766 |
| SAMN14381266 | 500cp-replicate04-30min | 500cp-replicate04-30min | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-30min | PRJNA612766 |
| SAMN14381267 | 500cp-replicate04-1h | 500cp-replicate04-1h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-1h | PRJNA612766 |
| SAMN14381268 | 500cp-replicate04-2h | 500cp-replicate04-2h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-2h | PRJNA612766 |
| SAMN14381269 | 500cp-replicate04-4h | 500cp-replicate04-4h | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 500cp-replicate04-4h | PRJNA612766 |
| SAMN14381270 | 1000cp-replicate01-10min | 1000cp-replicate01-10min | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-10min | PRJNA612766 |
| SAMN14381271 | 1000cp-replicate01-30min | 1000cp-replicate01-30min | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-30min | PRJNA612766 |
| SAMN14381272 | 1000cp-replicate01-1h | 1000cp-replicate01-1h | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-1h | PRJNA612766 |
| SAMN14381273 | 1000cp-replicate01-2h | 1000cp-replicate01-2h | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-2h | PRJNA612766 |
| SAMN14381274 | 1000cp-replicate01-4h | 1000cp-replicate01-4h | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-4h | PRJNA612766 |
| SAMN14381275 | 1000cp-replicate02-10min | 1000cp-replicate02-10min | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate02-10min | PRJNA612766 |
| SAMN14381276 | 1000cp-replicate02-30min | 1000cp-replicate02-30min | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate02-30min | PRJNA612766 |
| SAMN14381277 | 1000cp-replicate02-1h | 1000cp-replicate02-1h | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate02-1h | PRJNA612766 |
| SAMN14381278 | 1000cp-replicate02-2h | 1000cp-replicate02-2h | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate02-2h | PRJNA612766 |
| SAMN14381279 | 1000cp-replicate02-4h | 1000cp-replicate02-4h | Severe |
| acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate02-4h | PRJNA612766 |
| SAMN14381280 | 1000cp-replicate03-10min | 1000cp-replicate03-10min | Severe acute |
| respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate03-10min | PRJNA612766 |
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2 2697049 R02-4h PRJNA612766
SAMN14381171 R03-10min R03-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R03-10min PRJNA612766
SAMN14381172 R03-4h R03-4h Severe acute respiratory syndrome coronavirus
2 2697049 R03-4h PRJNA612766

SAMN14381173 R04-4h R04-4h Severe acute respiratory syndrome coronavirus
2 2697049 R04-4h PRJNA612766
SAMN14381174 R05-10min R05-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R05-10min PRJNA612766
SAMN14381175 R05-4h R05-4h Severe acute respiratory syndrome coronavirus
2 2697049 R05-4h PRJNA612766
SAMN14381176 R06-10min R06-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R06-10min PRJNA612766
SAMN14381177 R06-4h R06-4h Severe acute respiratory syndrome coronavirus
2 2697049 R06-4h PRJNA612766
SAMN14381178 R07-10min R07-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R07-10min PRJNA612766
SAMN14381179 R07-4h R07-4h Severe acute respiratory syndrome coronavirus
2 2697049 R07-4h PRJNA612766
SAMN14381180 R08-10min R08-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R08-10min PRJNA612766
SAMN14381181 R08-4h R08-4h Severe acute respiratory syndrome coronavirus
2 2697049 R08-4h PRJNA612766
SAMN14381182 R09-10min R09-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R09-10min PRJNA612766
SAMN14381183 R09-4h R09-4h Severe acute respiratory syndrome coronavirus
2 2697049 R09-4h PRJNA612766
SAMN14381184 R10-10min R10-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R10-10min PRJNA612766
SAMN14381185 R10-4h R10-4h Severe acute respiratory syndrome coronavirus
2 2697049 R10-4h PRJNA612766
SAMN14381186 R11-10min R11-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R11-10min PRJNA612766
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2 2697049 R11-4h PRJNA612766
SAMN14381188 R12-10min R12-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R12-10min PRJNA612766
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2 2697049 R12-4h PRJNA612766
SAMN14381190 R13-10min R13-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R13-10min PRJNA612766
SAMN14381191 R13-4h R13-4h Severe acute respiratory syndrome coronavirus
2 2697049 R13-4h PRJNA612766
SAMN14381192 R14-10min R14-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R14-10min PRJNA612766
SAMN14381193 R14-4h R14-4h Severe acute respiratory syndrome coronavirus
2 2697049 R14-4h PRJNA612766
SAMN14381194 R15-10min R15-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R15-10min PRJNA612766
SAMN14381195 R15-4h R15-4h Severe acute respiratory syndrome coronavirus
2 2697049 R15-4h PRJNA612766
SAMN14381196 R16-10min R16-10min Severe acute respiratory syndrome
coronavirus 2 2697049 R16-10min PRJNA612766
SAMN14381197 R16-4h R16-4h Severe acute respiratory syndrome coronavirus
2 2697049 R16-4h PRJNA612766
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respiratory syndrome coronavirus 2 2697049 0cp-replicate01-2h PRJNA612766
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respiratory syndrome coronavirus 2 2697049 0cp-replicate01-4h PRJNA612766
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SAMN14381201 0cp-replicate02-1h 0cp-replicate02-1h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate02-1h PRJNA612766
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respiratory syndrome coronavirus 2 2697049 0cp-replicate02-2h PRJNA612766
SAMN14381203 0cp-replicate02-4h 0cp-replicate02-4h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate02-4h PRJNA612766
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respiratory syndrome coronavirus 2 2697049 0cp-replicate03-30min PRJNA612766
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respiratory syndrome coronavirus 2 2697049 0cp-replicate03-1h PRJNA612766
SAMN14381206 0cp-replicate03-2h 0cp-replicate03-2h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate03-2h PRJNA612766
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respiratory syndrome coronavirus 2 2697049 0cp-replicate03-4h PRJNA612766
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respiratory syndrome coronavirus 2 2697049 0cp-replicate04-2h PRJNA612766
SAMN14381210 0cp-replicate04-4h 0cp-replicate04-4h Severe acute
respiratory syndrome coronavirus 2 2697049 0cp-replicate04-4h PRJNA612766
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respiratory syndrome coronavirus 2 2697049 10cp-replicate01-10min PRJNA612766
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respiratory syndrome coronavirus 2 2697049 10cp-replicate01-30min PRJNA612766
SAMN14381213 10cp-replicate01-1h 10cp-replicate01-1h Severe acute
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SAMN14381217 10cp-replicate02-30min 10cp-replicate02-30min Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate02-30min PRJNA612766
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respiratory syndrome coronavirus 2 2697049 10cp-replicate03-10min PRJNA612766
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SAMN14381223 10cp-replicate03-1h 10cp-replicate03-1h Severe acute
respiratory syndrome coronavirus 2 2697049 10cp-replicate03-1h PRJNA612766
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respiratory syndrome coronavirus 2 2697049 10cp-replicate03-2h PRJNA612766
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respiratory syndrome coronavirus 2 2697049 10cp-replicate03-4h PRJNA612766
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respiratory syndrome coronavirus 2 2697049 10cp-replicate04-10min PRJNA612766
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respiratory syndrome coronavirus 2 2697049 10cp-replicate04-1h PRJNA612766

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| SAMN14381274 | 1000cp-replicate01-4h | 1000cp-replicate01-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 1000cp-replicate01-4h | PRJNA612766 |
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| SAMN14381292 | 3000cp-replicate01-1h | 3000cp-replicate01-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate01-1h | PRJNA612766 |
| SAMN14381293 | 3000cp-replicate01-2h | 3000cp-replicate01-2h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate01-2h | PRJNA612766 |
| SAMN14381294 | 3000cp-replicate01-4h | 3000cp-replicate01-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate01-4h | PRJNA612766 |
| SAMN14381295 | 3000cp-replicate02-10min | 3000cp-replicate02-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate02-10min | PRJNA612766 |
| SAMN14381296 | 3000cp-replicate02-30min | 3000cp-replicate02-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate02-30min | PRJNA612766 |
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| SAMN14381301 | 3000cp-replicate03-30min | 3000cp-replicate03-30min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate03-30min | PRJNA612766 |
| SAMN14381302 | 3000cp-replicate03-1h | 3000cp-replicate03-1h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate03-1h | PRJNA612766 |
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| SAMN14381304 | 3000cp-replicate03-4h | 3000cp-replicate03-4h | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate03-4h | PRJNA612766 |
| SAMN14381305 | 3000cp-replicate04-10min | 3000cp-replicate04-10min | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 3000cp-replicate04-10min | PRJNA612766 |

SAMN14381306 3000cp-replicate04-30min 3000cp-replicate04-30min Severe acute respiratory syndrome coronavirus 2 2697049 3000cp-replicate04-30min PRJNA612766
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SAMN14381311 respiratory viruses-2h respiratory viruses-2h Severe acute respiratory syndrome coronavirus 2 2697049 respiratory viruses-2h PRJNA612766

sra at ncbi.nlm.nih.gov
Tue Mar 17 07:44:44 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your recent submission to SRA database has been successfully processed and will be released on the date specified.

Please reference PRJNA612766 in your publication. This BioProject accession number is provided above in lieu of SRP and should be used in your publication as it will allow better searching in Entrez.

SRA accession: PRJNA612766
Temporary Submission ID: SUB7147304
Release date: 2020-03-17

Your SRA records will be accessible with the following link after the indicated release date:

<https://www.ncbi.nlm.nih.gov/sra/PRJNA612766>

Send questions and update requests to sra at ncbi.nlm.nih.gov; include the SRA accession PRJNA612766 in any correspondence.

Regards,

NCBI SRA Submissions Staff
Bethesda, Maryland USA

----- next part -----

Object IDs and corresponding URLs:

RUN:13817617: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817617>
RUN:13817616: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817616>
RUN:13817615: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817615>
RUN:13817614: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817614>
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RUN:13817557: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817557>
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RUN:13817551: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817551>
RUN:13817549: <https://www.ncbi.nlm.nih.gov/sra/RUN:13817549>

From: (b) (6)
Received: Wed Mar 18 2020 06:01:21 GMT-0400 (Eastern Daylight Time)
To: NLM/NCBI List sra; SRA Support;
Subject: Re: SRA submission SUB7147304, "Nanopore targeted sequencing for SARS-CoV-2 and other respiratory viruses, Mar 13 '20"

Dear Staff,

Thank you for informing my submission state.

Now, I can search PRJNA612766 in BioProject, but why I can't download the raw data (.fastq file) which I uploaded in the submission. Hasn't the raw data been released yet?

Regards,

(b) (6)

(b) (6)

From: [sra](#)
Date: 2020-03-17 19:44
To: (b) (6)
Subject: SRA submission SUB7147304, "Nanopore targeted sequencing for SARS-CoV-2 and other respiratory viruses, Mar 13 '20"
Dear (b) (6)

This is an automatic acknowledgment that your recent submission to SRA database has been successfully processed and will be released on the date specified.

Please reference PRJNA612766 in your publication. This BioProject accession number is provided above in lieu of SRP and should be used in your publication as it will allow better searching in Entrez.

SRA accession: PRJNA612766
Temporary Submission ID: SUB7147304
Release date: 2020-03-17

Your SRA records will be accessible with the following link after the indicated release date:
<https://www.ncbi.nlm.nih.gov/sra/PRJNA612766>

Send questions and update requests to sra@ncbi.nlm.nih.gov; include the SRA accession PRJNA612766 in any correspondence.

Regards,

NCBI SRA Submissions Staff
Bethesda, Maryland USA

From: NLM Support <nlm-support@nlm.nih.gov>;
Received: Wed Mar 18 2020 10:28:22 GMT-0400 (Eastern Daylight Time)
To: (b) (6);
Subject: case #CAS-507212-JOB4H5: Re: SRA submission SUB7147304, "Nanopore targeted...
TRACKING:000393000005604

The raw data is public, but Entrez indexing is currently delayed. In the meantime, the data is listed publicly at the SRA Run Selector:

<https://www.ncbi.nlm.nih.gov/Traces/study/?acc=PRJNA612766>

And the accessions listed here can be used to download the sequences via the SRA toolkit.

Cheers,

(b) (6)
SRA Curator

----- Original Message -----

From: (b) (6);
Received: Wed Mar 18 2020 06:01:21 GMT-0400 (Eastern Daylight Time)
To: NLM/NCBI List sra; SRA Support;
Subject: Re: SRA submission SUB7147304, "Nanopore targeted sequencing for SARS-CoV-2 and other respiratory viruses, Mar 13 '20"

Dear Staff,

Thank you for informing my submission state.

Now, I can search PRJNA612766 in BioProject, but why I can't download the raw data (.fastq file) which I uploaded in the submission. Hasn't the raw data been released yet?

Regards,

(b) (6)

(b) (6)

From: [sra](#)

Date: 2020-03-17 19:44

To: (b) (6)

Subject: SRA submission SUB7147304, "Nanopore targeted sequencing for SARS-CoV-2 and other respiratory viruses, Mar 13 '20"

Dear (b) (6)

This is an automatic acknowledgment that your recent submission to SRA database has been successfully processed and will be released on the date specified.

Please reference PRJNA612766 in your publication. This BioProject accession number is provided above in lieu of SRP and should be used in your publication as it will allow better searching in Entrez.

SRA accession: PRJNA612766

Temporary Submission ID: SUB7147304

Release date: 2020-03-17

Your SRA records will be accessible with the following link after the indicated release date:

<https://www.ncbi.nlm.nih.gov/sra/PRJNA612766>

Send questions and update requests to sra@ncbi.nlm.nih.gov; include the SRA accession PRJNA612766 in any correspondence.

Regards,

NCBI SRA Submissions Staff
Bethesda, Maryland USA

bioprojecthelp at ncbi.nlm.nih.gov

Fri Jun 5 08:01:17 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your submission:

SubmissionID: SUB7554642

BioProject ID: PRJNA637497

Title:

has been successfully registered with the BioProject database. After review by the database staff, your project information will be accessible with the following link, usually within a few days of the release date that you set (or the release of linked data, whichever is first):

<http://www.ncbi.nlm.nih.gov/bioproject/637497>

Please use the BioProject ID PRJNA637497 with your correspondence and your data submissions.

Send questions to bioprojecthelp at ncbi.nlm.nih.gov, and include the BioProject ID and organism name.

Regards,

NCBI BioProject Submissions Staff
Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

bioprojecthelp at ncbi.nlm.nih.gov (for BioProject questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

biosamplehelp at ncbi.nlm.nih.gov

Fri Jun 5 08:10:02 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your recent submission to the BioSample database has been successfully processed and will be released on the date specified.

BioSample accession: SAMN15143806
Temporary SubmissionID: SUB7554642
Release date: as soon as processing is complete

A submission summary and the links by which your BioSample records will be accessible are appended and attached.

Please reference BioSample accession SAMN15143806 when making corresponding sequence data submissions.

Send questions and update requests to biosamplehelp at ncbi.nlm.nih.gov; include the BioSample accession SAMN15143806 in any correspondence.

Regards,

NCBI BioSample Submissions Staff
Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

biosamplehelp at ncbi.nlm.nih.gov (for BioSample questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

| Accession | Sample Name | SPUID | Organism | Tax ID | Isolate |
|--------------|-------------|--------|---|---------|---------|
| SAMN15143806 | tmp_75 | tmp_75 | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 75 |

<https://www.ncbi.nlm.nih.gov/biosample/15143806>

----- next part -----

| Accession | Sample Name | SPUID | Organism | Tax ID | Isolate |
|--------------|-------------|--------|---|---------|---------|
| SAMN15143806 | tmp_75 | tmp_75 | Severe acute respiratory syndrome coronavirus 2 | 2697049 | 75 |

sra at ncbi.nlm.nih.gov
Fri Jun 5 08:20:05 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your recent submission to SRA database has been successfully processed and will be released on the date specified.

Please reference PRJNA637497 in your publication. This BioProject accession number is provided above in lieu of SRP and should be used in your publication as it will allow better searching in Entrez.

SRA accession: PRJNA637497
Temporary Submission ID: SUB7554642
Release date: 2020-06-05

Your SRA records will be accessible with the following link after the indicated release date:
<https://www.ncbi.nlm.nih.gov/sra/PRJNA637497>

Send questions and update requests to sra at ncbi.nlm.nih.gov; include the SRA accession PRJNA637497 in any correspondence.

Regards,

NCBI SRA Submissions Staff
Bethesda, Maryland USA

From: (b) (6)
Received: Fri Jun 05 2020 21:45:04 GMT-0400 (Eastern Daylight Time)
To: Bioproject Support <bioprojecthelp@ncbi.nlm.nih.gov>;
Subject: retract BioProject

Dear Mr/Ms,

I want to retract a submission, and the BioProject ID is PRJNA637497.
I'm sorry for my wrong submitting. Thank you for your help.

Regards



bioprojecthelp at ncbi.nlm.nih.gov
Sat Jun 6 06:20:26 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your submission:

SubmissionID: SUB7554642
BioProject ID: PRJNA637497
Title:
Locus tag prefix:
None (SAMN15143806)

has been updated, eg by the linkage of one or more BioSamples. The locus_tag prefixes for each linked BioSample are included in the locustagprefix.txt file that can be accessed from this BioProject in the submission portal:

<https://submit.ncbi.nlm.nih.gov/subs/bioproject/SUB7554642/overview>

In addition, you can view the locustagprefix.txt files for all of your BioProjects from the BioProject submission page,

[https://submit.ncbi.nlm.nih.gov/subs/bioproject/.](https://submit.ncbi.nlm.nih.gov/subs/bioproject/)

Please use the BioProject ID PRJNA637497 with your correspondence and your data submissions.
Use the registered locus tag prefix when you include annotation in your submission.

Send questions to bioprojecthelp at ncbi.nlm.nih.gov, and include the BioProject ID and organism name.

Regards,

NCBI BioProject Submissions Staff
Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

bioprojecthelp at ncbi.nlm.nih.gov (for BioProject questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

----- next part -----

A non-text attachment was scrubbed...

Name: locus_tag_prefixes.csv

Type: text/csv

Size: 51 bytes

Desc: not available

URL: <<http://www.ncbi.nlm.nih.gov/mailman/pipermail/sp-mail/attachments/20200606/7379b3ea/attachment-0001.csv>>

From: NLM Support <nlm-support@nlm.nih.gov>;

Received: Mon Jun 08 2020 13:36:22 GMT-0400 (Eastern Daylight Time)

To: (b) (6)

Subject: Re: case #CAS-550133-G8S8X0: retract BioProject TRACKING:00030000004630

Dear (b) (6)

Thank you for your email. We prefer to edit an existing BioProject or change its status to "replaced by" a new BioProject, rather than delete. If you submitted another BioProject to replace this one, please provide the BioProject ID for that project and we will set the status of this project to "replaced by" the desired one.

We have implemented a new capability that allows submitters to view the current content of a BioProject and make minor edits, including updating the title and description, and changing the release date. Please go to the submission portal and click on "Manage Data" where you can access your BioProject. Click on the BioProject accession in the left ("Accession") column and you will have the opportunity to make the desired change. The updates will be processed automatically and the page should refresh with the edited information within a few minutes (typically seconds). You will then be able to make additional changes, if needed.

If you need to make changes in other fields, please email the desired changes and we will edit for you. If you do not plan to use this BioProject or submit a replacement, we can delete it.

If you have other comments or questions, please reply to bioprojecthelp@ncbi.nlm.nih.gov.

Best regards,

(b) (6)

BioProject Curation Staff

* PLEASE DO NOT MODIFY THE SUBJECT LINE OF THIS EMAIL WHEN RESPONDING TO ENSURE CORRECT TRACKING

*

Case Information:

Case #: CAS-550133-G8S8X0

Customer Name: (b) (6)

Customer Email: (b) (6)

Case Created: 2020-06-06T01:45:32Z

Summary: retract BioProject

Details:

Dear Mr/Ms,

I want to retract a submission, and the BioProject ID is PRJNA637497. I'm sorry for my wrong submitting. Thank you for your help.

Regards

(b) (6)

From: (b) (6)

Received: Mon Jun 15 2020 23:10:41 GMT-0400 (Eastern Daylight Time)

To: NLM/NCBI List sra <sra@ncbi.nlm.nih.gov>; SRA Support <sra@ncbi.nlm.nih.gov>;

Subject: Re: SUB7554642/subs/sra/SUB7554642/overview

Dear Mr/Ms,

Recently, I found that it's hard to visit my submitted SRA data, and it would also be very difficult for me to update the data. I have submitted an updated version of this SRA data to another website, so I want to withdraw the old one at NCBI in order to avoid the data version issue. The Submission ID is SUB7147304. I would appreciate your help.

Best regard,

(b) (6)

From: NLM Support <nlm-support@nlm.nih.gov>;

Received: Tue Jun 16 2020 09:00:09 GMT-0400 (Eastern Daylight Time)

To: (b) (6)

Subject: Re: case #CAS-555084-Z9T9P7: Re: SUB7554642/subs/sra/SUB7554642/overview
TRACKING:00041400006890

Dear (b) (6)

Do you want to withdraw all SRA objects created in your account?
here are 2 submissions SUB7554642 and SUB7147304.
Also, bioprojects and biosamples whould be withdrawn as well, right?

Best regards,

(b) (6)

If you have any questions or concerns regarding your **SRA** submission please don't
hesitate to contact sra@ncbi.nlm.nih.gov (applies to new
questions). We *normally* respond *within 2 business days*.

(b) (6)

The NCBI SRA database submission staff

* PLEASE DO NOT MODIFY THE SUBJECT LINE OF THIS EMAIL WHEN RESPONDING TO ENSURE CORRECT TRACKING
*

Case Information:

Case #: CAS-555084-Z9T9P7

Customer Name: (b) (6)

Customer Email: (b) (6)

Case Created: 2020-06-16T03:11:52Z

Summary: Re: SUB7554642/subs/sra/SUB7554642/overview

Details:

Dear Mr/Ms,

Recently, I found that it's hard to visit my submitted SRA data, and
it would also be very difficult for me to update the data. I have submitted an updated version of this SRA
data to another website, so I want to withdraw the old one at NCBI in order to avoid the data version
issue. The Submission ID is SUB7147304. I would appreciate your help.

Best regard,

(b) (6)

From: (b) (6)
Received: Tue Jun 16 2020 20:48:44 GMT-0400 (Eastern Daylight Time)
To: nlm-support@nlm.nih.gov <nlm-support@nlm.nih.gov>; NLM Support <nlm-support@nlm.nih.gov>; Triage Team <nlm-support@nlm.nih.gov>;
Subject: Re: Re: case #CAS-555084-Z9T9P7: Re: SUB7554642/subs/sra/SUB7554642/overview
TRACKING:000414000006890

Dear (b) (6)

Thanks for your replay. Yes, I want to withdraw both 2 submissions SUB7554642 and SUB7147304. The Bioprojects, Biosamples and all SRA objects should be withdrawn as well.

Best regards,

(b) (6)

(b) (6)

From: [NLM Support](#)
Date: 2020-06-16 21:00
To: (b) (6)
Subject: Re: case #CAS-555084-Z9T9P7: Re: SUB7554642/subs/sra/SUB7554642/overview
TRACKING:000414000006890
Dear (b) (6)

Do you want to withdraw all SRA objects created in your account?
here are 2 submissions SUB7554642 and SUB7147304.
Also, bioprojects and biosamples whould be withdrawn as well, right?

Best regards,

(b) (6)

If you have any questions or concerns regarding your **SRA** submission please don't hesitate to contact sra@ncbi.nlm.nih.gov (applies to new questions). We *normally* respond *within 2 business days*.

(b) (6)

The NCBI SRA database submission staff

* PLEASE DO NOT MODIFY THE SUBJECT LINE OF THIS EMAIL WHEN RESPONDING TO ENSURE CORRECT TRACKING
*

Case Information:
Case #: CAS-555084-Z9T9P7

Customer Name: (b) (6)
Customer Email: (b) (6)
Case Created: 2020-06-16T03:11:52Z

Summary: Re: SUB7554642/subs/sra/SUB7554642/overview

Details:

Dear Mr/Ms,

Recently, I found that it's hard to visit my submitted SRA data, and it would also be very difficult for me to update the data. I have submitted an updated version of this SRA data to another website, so I want to withdraw the old one at NCBI in order to avoid the data version issue. The Submission ID is SUB7147304. I would appreciate your help.

Best regard,

(b) (6)

From: NLM Support <nlm-support@nlm.nih.gov>;
Received: Wed Jun 17 2020 12:58:07 GMT-0400 (Eastern Daylight Time)
To: (b) (6)
Subject: Re: Re: case #CAS-555084-Z9T9P7: Re: SUB7554642/subs/sra/SUB7554642/overview
TRACKING:000414000006890

Hi (b) (6)

I had withdrawn everything.

Best regards,

(b) (6)

If you have any questions or concerns regarding your **SRA** submission please don't hesitate to contact sra@ncbi.nlm.nih.gov (applies to new questions). We *normally* respond *within 2 business days*.

(b) (6)

The NCBI SRA database submission staff

----- Original Message -----

From: (b) (6)

Received: Tue Jun 16 2020 20:48:44 GMT-0400 (Eastern Daylight Time)
To: nlm-support@nlm.nih.gov; Inbound - NLM Support; Triage Team;
Subject: Re: Re: case #CAS-555084-Z9T9P7: Re: SUB7554642/subs/sra/SUB7554642/overview
TRACKING:000414000006890

Dear (b) (6)

Thanks for your replay. Yes, I want to withdraw both 2 submissions SUB7554642 and SUB7147304. The Bioprojects, Biosamples and all SRA objects should be withdrawn as well.

Best regards,

(b) (6)

(b) (6)

From: [NLM Support](#)
Date: 2020-06-16 21:00
To: (b) (6)
Subject: Re: case #CAS-555084-Z9T9P7: Re: SUB7554642/subs/sra/SUB7554642/overview
TRACKING:000414000006890
Dear (b) (6)

Do you want to withdraw all SRA objects created in your account?
here are 2 submissions SUB7554642 and SUB7147304.
Also, bioprojects and biosamples whould be withdrawn as well, right?

Best regards,

(b) (6)

If you have any questions or concerns regarding your **SRA** submission please don't hesitate to contact sra@ncbi.nlm.nih.gov (applies to new questions). *We normally respond within 2 business days.*

(b) (6)

The NCBI SRA database submission staff

* PLEASE DO NOT MODIFY THE SUBJECT LINE OF THIS EMAIL WHEN RESPONDING TO ENSURE CORRECT TRACKING
*

Case Information:
Case #: CAS-555084-Z9T9P7
Customer Name: (b) (6)
Customer Email: (b) (6)

Case Created: 2020-06-16T03:11:52Z

Summary: Re: SUB7554642/subs/sra/SUB7554642/overview

Details:

Dear Mr/Ms,

Recently, I found that it's hard to visit my submitted SRA data, and it would also be very difficult for me to update the data. I have submitted an updated version of this SRA data to another website, so I want to withdraw the old one at NCBI in order to avoid the data version issue. The Submission ID is SUB7147304. I would appreciate your help.

Best regard,

(b) (6)

bioprojecthelp at ncbi.nlm.nih.gov
Wed Jun 17 14:40:20 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your submission:

SubmissionID: SUB7554642
BioProject ID: PRJNA637497
Title:
Locus tag prefix:
None (SAMN15143806)

has been updated, eg by the linkage of one or more BioSamples. The locus_tag prefixes for each linked BioSample are included in the locustagprefix.txt file that can be accessed from this BioProject in the submission portal:

<https://submit.ncbi.nlm.nih.gov/subs/bioproject/SUB7554642/overview>

In addition, you can view the locustagprefix.txt files for all of your BioProjects from the BioProject submission page,

<https://submit.ncbi.nlm.nih.gov/subs/bioproject/>.

Please use the BioProject ID PRJNA637497 with your correspondence and your data submissions.

Use the registered locus tag prefix when you include annotation in your submission.

Send questions to bioprojecthelp at ncbi.nlm.nih.gov, and include the BioProject ID and organism name.

Regards,

NCBI BioProject Submissions Staff
Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

bioprojecthelp at ncbi.nlm.nih.gov (for BioProject questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

----- next part -----

A non-text attachment was scrubbed...

Name: locus_tag_prefixes.csv

Type: text/csv

Size: 51 bytes

Desc: not available

URL: <<http://www.ncbi.nlm.nih.gov/mailman/pipermail/sp-mail/attachments/20200617/763bf2f8/attachment-0001.csv>>

bioprojecthelp at ncbi.nlm.nih.gov

Wed Jun 17 14:40:23 EDT 2020

Dear (b) (6)

This is an automatic acknowledgment that your submission:

SubmissionID: SUB7147304

BioProject ID: PRJNA612766

Title:

Locus tag prefixes:

None (SAMN14381071)

None (SAMN14381072)

has been updated, eg by the linkage of one or more BioSamples. The locus_tag prefixes for

each linked BioSample are included in the locustagprefix.txt file that can accessed

from this BioProject in the submission portal:

<https://submit.ncbi.nlm.nih.gov/subs/bioproject/SUB7147304/overview>

In addition, you can view the locustagprefix.txt files for all of your BioProjects from the BioProject submission page,

<https://submit.ncbi.nlm.nih.gov/subs/bioproject/>.

Please use the BioProject ID PRJNA612766 with your correspondence and your data submissions.

Use the registered locus tag prefixes when you include annotation in your submission.

Send questions to bioprojecthelp at ncbi.nlm.nih.gov, and include the BioProject ID and organism name.

Regards,

NCBI BioProject Submissions Staff

Bethesda, Maryland USA

(301) 496-2475

(301) 480-2918 (Fax)

bioprojecthelp at ncbi.nlm.nih.gov (for BioProject questions/replies)

info at ncbi.nlm.nih.gov (for general questions regarding NCBI)

----- next part -----

A non-text attachment was scrubbed...

Name: locus_tag_prefixes.csv

Type: text/csv

Size: 65 bytes

Desc: not available

URL: <<http://www.ncbi.nlm.nih.gov/mailman/pipermail/sp-mail/attachments/20200617/29ac3592/attachment-0001.csv>>

From: Huerta, Mike (NIH/NLM) [E]
Sent: Wed, 30 Jun 2021 14:00:50 -0400
To: Sherry, Steve (NIH/NLM/NCBI) [E]
Subject: RE: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, 56602, 56616

Not a problem!

From: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Sent: Wednesday, June 30, 2021 1:58 PM
To: Huerta, Mike (NIH/NLM) [E] (b) (6)
Subject: RE: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, 56602, 56616

Eeek. Just saw this note – working my inbox in reverse order as you can tell....

Sorry for the extra bandwidth.

steve

From: Mowery, Tara (NIH/NLM) [E] (b) (6)
Sent: Wednesday, June 30, 2021 11:13 AM
To: Huerta, Mike (NIH/NLM) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Cc: Nurik, Jody (NIH/NLM) [E] (b) (6); Tuncer, Diane (NIH/NLM) [E] (b) (6); Lemon, Alison (NIH/NLM) [E] (b) (6)
Subject: RE: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, 56602, 56616

We received all of these requests from NHLBI's FOIA Service Center.

Tara Mowery
Office of Communications and Public Liaison
National Library of Medicine
National Institutes of Health
8600 Rockville Pike
Lister Hill Building (#38A), Room 127
Bethesda, MD 20894

(b) (6) (Direct)
(b) (6) (Main)
(b) (6) (Cell)
(b) (6)

From: Huerta, Mike (NIH/NLM) [E] (b) (6)
Sent: Wednesday, June 30, 2021 11:05 AM
To: Mowery, Tara (NIH/NLM) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)

Cc: Nurik, Jody (NIH/NLM) [E] (b) (6); Tuncer, Diane (NIH/NLM) [E] (b) (6); Lemon, Alison (NIH/NLM) [E] (b) (6)
Subject: RE: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, 56602, 56616

Thanks, Tara – I am including Steve so he knows he **need not** also send me the FOIAs. My understanding is that these have also been sent to NHLBI for them to process; is that correct?

From: Mowery, Tara (NIH/NLM) [E] (b) (6)
Sent: Wednesday, June 30, 2021 11:01 AM
To: Huerta, Mike (NIH/NLM) [E] (b) (6)
Cc: Nurik, Jody (NIH/NLM) [E] (b) (6); Tuncer, Diane (NIH/NLM) [E] (b) (6); Lemon, Alison (NIH/NLM) [E] (b) (6)
Subject: FW: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, 56602, 56616

Good Morning Mike,
There are currently 7 FOIA requests (attached) and all have been sent to Steve Sherry.
Thank you,
Tara

Tara Mowery
Office of Communications and Public Liaison
National Library of Medicine
National Institutes of Health
8600 Rockville Pike
Lister Hill Building (#38A), Room 127
Bethesda, MD 20894

(b) (6) (Direct)
(b) (6) (Main)
(b) (6) (Cell)
(b) (6)

From: Meadows, Nikki (NIH/NHLBI) [C] (b) (6)
Sent: Tuesday, June 29, 2021 2:55 PM
To: Mowery, Tara (NIH/NLM) [E] (b) (6)
Cc: Danielson, Todd (NIH/NLM) [E] (b) (6); Manheim, Marianne (NIH/NHLBI) [E] (b) (6); Ma, Dongying (NIH/NHLBI) [C] (b) (6); Nguyen, Pam (NIH/NLM) [E] (b) (6); Nurik, Jody (NIH/NLM) [E] (b) (6); Tuncer, Diane (NIH/NLM) [E] (b) (6); Lemon, Alison (NIH/NLM) [E] (b) (6)>
Subject: RE: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, and 56602

Hi Tara,

We had another request sent over to us this morning. Please see attached.

Thanks,

Nikki

Nikki Meadows [C], PhD

Policy Analyst

Freedom of Information and Privacy Act Branch/FOIA Service Center

National Heart, Lung and Blood Institute (NHLBI), NIH

Kelly Government Solutions

(b) (6)

Rockledge I, 4th Floor, MSC 7957

T: (b) (6)

From: Mowery, Tara (NIH/NLM) [E] (b) (6)

Sent: Monday, June 28, 2021 4:19 PM

To: Meadows, Nikki (NIH/NHLBI) [C] (b) (6)

Cc: Danielson, Todd (NIH/NLM) [E] (b) (6); Manheim, Marianne (NIH/NHLBI) [E]

(b) (6); Ma, Dongying (NIH/NHLBI) [C] (b) (6); Nguyen, Pam

(NIH/NLM) [E] (b) (6); Nurik, Jody (NIH/NLM) [E] (b) (6); Tuncer,

Diane (NIH/NLM) [E] (b) (6); Lemon, Alison (NIH/NLM) [E] (b) (6)

Subject: RE: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, and 56602

Good Afternoon Nikki,

We have forwarded this email on to NLM Senior Staff.

Please keep us informed on the deadlines.

Thank you,

Tara

Tara Mowery

Office of Communications and Public Liaison

National Library of Medicine

National Institutes of Health

8600 Rockville Pike

Lister Hill Building (#38A), Room 127

Bethesda, MD 20894

(b) (6) (Direct)

(b) (6) (Main)

(b) (6) (Cell)

(b) (6)

From: Meadows, Nikki (NIH/NHLBI) [C] (b) (6)

Sent: Monday, June 28, 2021 1:55 PM

To: Mowery, Tara (NIH/NLM) [E] (b) (6); Nguyen, Pam (NIH/NLM) [E]

(b) (6)

Cc: Danielson, Todd (NIH/NLM) [E] (b) (6); Manheim, Marianne (NIH/NHLBI) [E]

(b) (6); Ma, Dongying (NIH/NHLBI) [C] (b) (6)

Subject: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, and 56602

Hi NLM team,

We've received 6 FOIA requests for correspondence and other documents that are likely in NLMs possession documenting the deletion of several early SARS-CoV-2 sequences from the SRA database. As you're probably aware, a preprint about these sequences was recently posted on biRxiv by Jesse Bloom at Fred Hutch (<https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1>). The slew of requests for NIH records related to this followed soon after. A copy of all of the requests are attached, as is a summary document of all 6, called "NLM SRA cases".

Almost all of the requesters are journalists and several have requested expedited processing. NIH FOIA is currently evaluating the expedited processing, but in the mean time I'm reaching out to your team to help figure out who the custodians of these files/correspondence might be so we can start collecting responsive documents. I should note that one of the requesters, a journalist from *Science*, mentioned Dr. Sherry, the Acting Director at NLM, in his request, though I am not sure if he is the most appropriate contact.

Please let me know if you have any questions or need any clarifications.

Thanks,
Nikki

Nikki Meadows [C], PhD

Policy Analyst

Freedom of Information and Privacy Act Branch/FOIA Service Center

National Heart, Lung and Blood Institute (NHLBI), NIH

Kelly Government Solutions

(b) (6)

Rockledge I, 4th Floor, MSC 7957

T: (b) (6)

From: Sherry, Steve (NIH/NLM/NCBI) [E]
Sent: Wed, 30 Jun 2021 07:46:49 -0400
To: Benson, Dennis (NIH/NLM/NCBI) [E]; Coleman, Janet (NIH/NLM/NCBI) [C]; Mizrachi, Ilene (NIH/NLM/NCBI) [E]; Pruitt, Kim (NIH/NLM/NCBI) [E]; Yaschenko, Eugene (NIH/NLM/NCBI) [E]
Subject: RE: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, and 56602

Hi Dennis, yes Larry Tabak said the same thing to Patti yesterday in the afternoon briefing. I need to confer with her this morning and verify she understands that the FOIA office will make the final decision.

From: Benson, Dennis (NIH/NLM/NCBI) [E] (b) (6)
Sent: Tuesday, June 29, 2021 12:49 PM
To: Coleman, Janet (NIH/NLM/NCBI) [C] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Mizrachi, Ilene (NIH/NLM/NCBI) [E] (b) (6); Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6); Yaschenko, Eugene (NIH/NLM/NCBI) [E] (b) (6)
Subject: Re: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, and 56602

Steve – Did you get guidance from the NIH FOIA Office on the types of deletions we can do. The exemption on privacy has a range of interpretation and there are factors that actually are considered to outweigh the standard redaction of even personal names, viz., if there is a public interest in doing so.

That said, an approach to take is for us to redact per your email, and let the NIH FOIA Office make the final decision.

Dennis

From: Janet Coleman (b) (6)
Date: Tuesday, June 29, 2021 at 12:33 PM
To: "Sherry, Steve (NIH/NLM/NCBI) [E]" (b) (6), "Mizrachi, Ilene (NIH/NLM/NCBI) [E]" (b) (6), "Pruitt, Kim (NIH/NLM/NCBI) [E]" (b) (6), "Yaschenko, Eugene (NIH/NLM/NCBI) [E]" (b) (6), Dennis Benson (b) (6)
Subject: Re: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, and 56602

Steve,

I'm not sure if legally we can omit all of the elements you suggested redacting (b) (5).

Dennis,
Can you please advise whether or not we can omit all of some of these items?

Thanks,
Janet

From: "Sherry, Steve (NIH/NLM/NCBI) [E]" (b) (6)
Date: Tuesday, June 29, 2021 at 9:13 AM
To: Janet Coleman (b) (6), Ilene Mizrachi (b) (6),
"Pruitt, Kim (NIH/NLM/NCBI) [E]" (b) (6), "Yaschenko, Eugene
(NIH/NLM/NCBI) [E]" (b) (6), Dennis Benson (b) (6)
Subject: FW: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, and 56602

We have received several FOIA requests yesterday for SRA. Three are expedited and we must reply in 24 hours. We have a week for the other three. (b) (5)

(b) (5) We can provide email correspondence after redaction of personal names, case & submission identifiers, and submitter department - We can leave institutional names, dates, and SRA/Project accession numbers. Communications should provide text of the exchange but with no details of the persons in communication to protect privacy. Here is an example of how I shared detail. We can use black boxes for redaction if that is more customary.

Janet, can you work with Ilene on assembling the response materials? I need to review it with Patti before we send anything back to OCPL.

Steve

(b) (5)

From: Nurik, Jody (NIH/NLM) [E] (b) (6)
Sent: Monday, June 28, 2021 4:48 PM
To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Cc: Mowery, Tara (NIH/NLM) [E] (b) (6); Tuncer, Diane (NIH/NLM) [E] (b) (6); Lemon, Alison (NIH/NLM) [E] (b) (6)
Subject: FW: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, and 56602

Hi Steve,

Please see attached and email below from Nikki Meadows. Tara reached out to Nikki for timeframes – will be back in touch once we learn more.

Thanks,

Jody

Jody Nurik
Communications Director, Office of Communications and Public Liaison
National Library of Medicine | National Institutes of Health
Office: (b) (6) 5



From: Mowery, Tara (NIH/NLM) [E] (b) (6)
Sent: Monday, June 28, 2021 1:57 PM
To: Nurik, Jody (NIH/NLM) [E] (b) (6); Tuncer, Diane (NIH/NLM) [E] (b) (6); Lemon, Alison (NIH/NLM) [E] (b) (6)
Subject: Fwd: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, and 56602

Just received. Keeping you in the loop.

Tara Mowery
Office of Communications and Public Liaison
National Library of Medicine | National Institutes of Health
8600 Rockville Pike, Lister Hill Building (#38A), Room 127
[Bethesda, MD 20894](#)

Office: (b) (6) Mobile: (b) (6)
(b) (6)

Begin forwarded message:

From: "Meadows, Nikki (NIH/NHLBI) [C]" (b) (6)
Date: June 28, 2021 at 1:55:21 PM EDT
To: "Mowery, Tara (NIH/NLM) [E]" (b) (6), "Nguyen, Pam (NIH/NLM) [E]" (b) (6)
Cc: "Danielson, Todd (NIH/NLM) [E]" (b) (6), "Manheim, Marianne (NIH/NHLBI) [E]" (b) (6), "Ma, Dongying (NIH/NHLBI) [C]" (b) (6)
Subject: NLM FOIA Requests- 56582, 56586, 56587, 56588, 56591, and 56602

Hi NLM team,

We've received 6 FOIA requests for correspondence and other documents that are likely in NLMs possession documenting the deletion of several early SARS-CoV-2 sequences from the SRA database. As you're probably aware, a preprint about these sequences was recently posted on biRxiv by Jesse Bloom at Fred Hutch (<https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1>). The slew of requests for NIH records related to this followed soon after. A copy of all of the requests are attached, as is a summary document of all 6, called "NLM SRA cases".

Almost all of the requesters are journalists and several have requested expedited processing. NIH FOIA is currently evaluating the expedited processing, but in the mean time I'm reaching out to your team to help figure out who the custodians of these files/correspondence might be so we can start collecting responsive documents. I should note that one of the requesters, a journalist from *Science*, mentioned Dr. Sherry, the Acting Director at NLM, in his request, though I am not sure if he is the most appropriate contact.

Please let me know if you have any questions or need any clarifications.

Thanks,
Nikki

Nikki Meadows [C], PhD

Policy Analyst

Freedom of Information and Privacy Act Branch/FOIA Service Center

National Heart, Lung and Blood Institute (NHLBI), NIH

Kelly Government Solutions

(b) (6)

Rockledge I, 4th Floor, MSC 7957

T: (b) (6)

From: Bloom PhD, Jesse D
Sent: Sun, 27 Jun 2021 09:09:53 -0400
To: Sherry, Steve (NIH/NLM/NCBI) [E]
Subject: Re: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Hi Steve,

I was writing to ask if the NCBI still plans to compile a detailed report of all the SRA deletions, and if so whether it will be shared? I have several meetings next week with congressional staffers who were interested in the deletions, and I'm sure they will be asking about this.

As mentioned before, I'd be happy to help analyze any SRA data for anything relevant to SARS-CoV-2. I'm also still really curious about the second Wuhan University BioProject mentioned in the e-mail you forwarded last Saturday, as I don't think I've been able to identify that one.

Thanks,
Jesse

--

Jesse Bloom
Associate Professor, Fred Hutchinson Cancer Research Center
Investigator, Howard Hughes Medical Institute

From: Sherry, Steve (NIH/NLM/NCBI) [E] [REDACTED] (b) (6)
Date: Saturday, June 19, 2021 at 7:34 AM
To: Collins, Francis (NIH/OD) [E] [REDACTED] (b) (6), Bloom PhD, Jesse D
<jbloom@fredhutch.org>, Fauci, Anthony (NIH/NIAID) [E] [REDACTED] (b) (6), Brennan, Patti (NIH/NLM) [E] [REDACTED] (b) (6)
Cc: Pruitt, Kim (NIH/NLM/NCBI) [E] [REDACTED] (b) (6)
Subject: RE: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Dear Francis and Jesse,

Below is the June 2020 exchange between Wuhan University and SRA submission staff. I have redacted names and the withdrawal request tracking ID for privacy. Please read from the bottom up.

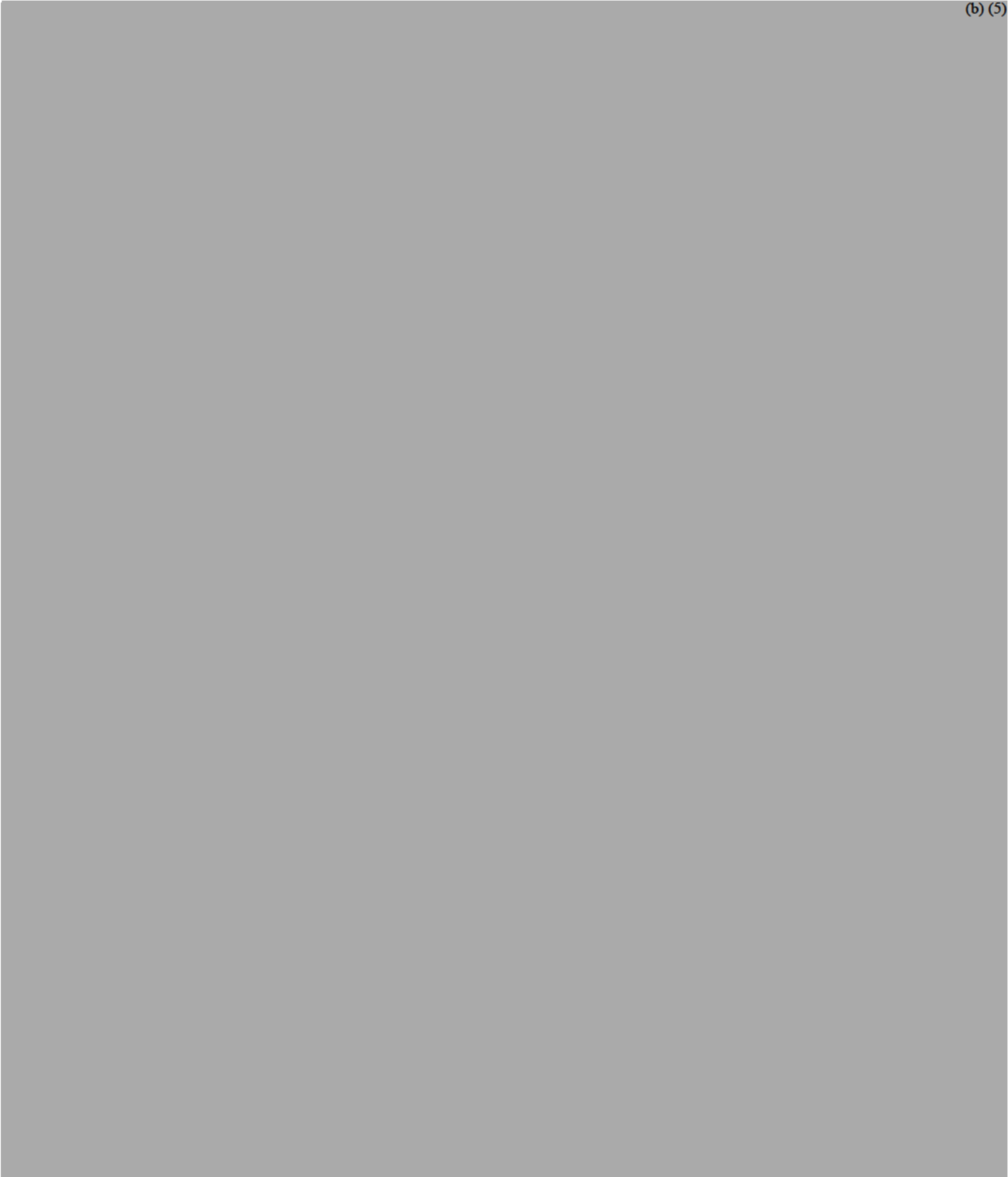
I would note that this request was received and processed according to SRA policy. As Jesse notes in his manuscript, submitters own their SRA records and can withdraw them upon request. SRA does not adjudicate the reason.

More generally, I have requested the SRA team to compile a report of all withdrawn SARS-COV2 data so there is transparency into the status of all SRA SARS-COV2 sequence submissions. I will share the report as soon as it is available.

Kind regards,

Steve

(data withdrawal correspondence) -----



(b) (5)

From: Collins, Francis (NIH/OD) [E] (b) (6)
Sent: Friday, June 18, 2021 10:01 PM
To: Bloom PhD, Jesse D <jbloom@fredhutch.org>; Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: RE: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Dear Jesse,

This is truly intriguing. I'll be interested in Steve's thoughts about the deleted SRA entries and whether there is any way to recover information about how that happened.

Francis

From: Bloom PhD, Jesse D <jbloom@fredhutch.org>
Sent: Friday, June 18, 2021 7:00 PM
To: Collins, Francis (NIH/OD) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Hi Francis, Stephen, and Toni,

I'm just writing to give you a heads up that I identified a data set of early Wuhan SARS-CoV-2 sequences that has been deleted from the NIH's Sequence Read Archive (SRA). I was able to recover the deleted files from the Google Cloud and analyze the sequences, and have attached a pre-print on the analysis that I just submitted for posting by *bioRxiv*.

Since SARS-CoV-2 origins and early spread has become a hot-button topic, I wanted to give you a heads up. I made sure to emphasize in the discussion that the SRA has many sequences and so isn't in a position to vet all deletions. Nonetheless, I think it would be highly worthwhile to do a comprehensive analysis of SRA (and other NIH) data that might be relevant to this topic that could have been deleted or otherwise overlooked. If I can be of any assistance, let me know.

I have been running a pipeline to identify additional deleted SRA data using various heuristics including those in described in the attached pre-print, but have not yet completed the analysis enough to know the extent that the data I have recovered is relevant to SARS-CoV-2's origins or early spread. But as I mention in the pre-print, there are two known SRR deletions that are worth looking at. I definitely think it would be good to perform a SRA side search as well, since that will obviously be easier and more efficient, and could identify deleted data not on the cloud.

Anyway, I hope overall this can be a good opportunity for the NIH to take the lead by using its remarkable data archives to make progress in resolving some of the important questions about the virus's origins.

Thanks,
Jesse

Jesse Bloom
Associate Professor, Fred Hutch Cancer Research Center
Affiliate Associate Professor, Genome Sciences & Microbiology, University of Washington
Investigator, Howard Hughes Medical Institute

From: Pruitt, Kim (NIH/NLM/NCBI) [E]
Sent: Wed, 23 Jun 2021 17:40:33 -0400
To: Coleman, Janet (NIH/NLM/NCBI) [C]; Mizrachi, Ilene (NIH/NLM/NCBI) [E]; Skripchenko, Yuriy (NIH/NLM/NCBI) [C]; Brister, James (NIH/NLM/NCBI) [E]
Cc: Hicks, Denise (NIH/NLM/NCBI) [C]; Fleischmann, Lydia (NIH/NLM/NCBI) [C]; Trawick, Bart (NIH/NLM/NCBI) [E]; Sherry, Steve (NIH/NLM/NCBI) [E]
Subject: RE: SRA was contacted by NY times reporter

A New York Times article is also out. I don't like its tone.

<https://www.nytimes.com/2021/06/23/science/coronavirus-sequences.html>

Kim D. Pruitt, Ph.D
Senior Scientist
Chief, Information Engineering Branch, NCBI/NLM/NIH

Telework hours: 8:30 – 5:00
Phone: (b) (6)

45 Center Drive
Building 45 Room 5AN44A
Bethesda, MD 20892-6511

From: Coleman, Janet (NIH/NLM/NCBI) [C] (b) (6)
Sent: Wednesday, June 23, 2021 5:36 PM
To: Mizrachi, Ilene (NIH/NLM/NCBI) [E] (b) (6); Skripchenko, Yuriy (NIH/NLM/NCBI) [C] (b) (6); Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6); Brister, James (NIH/NLM/NCBI) [E] (b) (6)
Cc: Hicks, Denise (NIH/NLM/NCBI) [C] (b) (6); Fleischmann, Lydia (NIH/NLM/NCBI) [C] (b) (6); Trawick, Bart (NIH/NLM/NCBI) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Subject: Re: SRA was contacted by NY times reporter

For anyone who didn't yet see it, The Bloom study is on the top section of the online Washington Post :
https://www.washingtonpost.com/health/coronavirus-origin-nih-gene-sequence-deletion/2021/06/23/186e87d0-d437-11eb-a53a-3b5450fdca7a_story.html

NIH doesn't come out badly, unless you read this paragraph as referring to NIH as well as, or instead of, the scientist who withdrew the data: "Bloom said in an email to The Washington Post that he was not accusing the NIH of wrongdoing. But Bloom's online paper suggests the deletion of data violates scientific norms and the code of trust essential to science"

Seattle scientist digs up deleted coronavirus genetic data, adding fuel to the covid origin debate

June 23, 2021 at 2:00 p.m. EDT

326

An American scientist has incited a new skirmish over the [origin of the coronavirus](#), reporting that he has retrieved potentially significant genetic data about SARS-CoV-2 that had been stored and later deleted from a digital archive at the National Institutes of Health.

Jesse Bloom, a computational biologist at the Fred Hutchinson Cancer Research Center in Seattle, [posted his findings](#) on the preprint server bioRxiv, where papers that have not yet been peer-reviewed or published in a journal have been landing by the thousands since the start of the pandemic.

The scientific significance of Bloom's research remained unclear Wednesday, but it stirred instant online reaction, favorable and unfavorable alike, among scientists who have been debating the flurry of theories about the initial [coronavirus](#) outbreak.

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Bloom, who retrieved the data through Google Cloud, does not claim that it advances one theory or another, but he contends it bolsters evidence that the virus was circulating in Wuhan, China, before a December outbreak of covid-19, the illness caused by the virus, that was linked to a market selling live animals.

What is not in dispute is that the data was deleted from a database at the NIH. The data was included in a preprint paper posted in March 2020 and [published](#) that June in the journal *Small*.

The NIH released a statement Wednesday saying that a researcher who originally published the genetic sequences asked for them to be removed from the NIH database so that they could be included in a different database. The NIH said it is standard practice to remove data if requested to do so. The NIH statement did not identify the scientist who requested that the material be excised from the agency's sequence read archive, known as the SRA.

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“These SARS-CoV-2 sequences were submitted for posting in SRA in March 2020 and subsequently requested to be withdrawn by the submitting investigator in June 2020. The requestor indicated the sequence information had been updated, was being submitted to another database, and wanted the data removed from SRA to avoid version control issues,” the NIH said.

The statement said the NIH “can’t speculate on motive beyond a submitter’s stated intentions.”

Bloom said in an email to The Washington Post that he was not accusing the NIH of wrongdoing. But Bloom’s online paper suggests the deletion of data violates scientific norms and the code of trust essential to science. On [Twitter](#), Bloom said the data was also taken down from a Chinese database.

“[T]he current study suggests that at least in one case, the trusting structures of science have been abused to obscure sequences relevant to the early spread of SARS-CoV-2 in Wuhan,” Bloom wrote.

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Efforts by The Post to reach the senior author of the sequencing [paper](#) have been unsuccessful.

Robert F. Garry, a Tulane University virologist who co-wrote an influential March 2020 paper saying SARS-CoV-2 was a natural virus and not engineered, took issue with the new Bloom paper.

“Jesse Bloom found exactly nothing new that is not already part of the scientific literature,” Garry wrote in an email. He called the Bloom paper “inflammatory.”

Bloom is no stranger to the debate over the virus’s origins. He was the lead author of a [letter](#) to the journal Science, signed by an additional 17 prominent scientists, that last month criticized a World Health Organization probe into the origins of the virus. The letter called for a deeper investigation of the “lab leak” hypothesis, which asserts that the coronavirus — accidentally or by design — potentially slipped out of [a laboratory in Wuhan](#).

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Stanford University microbiologist David H. Relman, another organizer of that letter, said of Bloom’s findings: “It shows how critical it is that early data be sought, preserved, and shared in trying to infer virus evolutionary paths and origins, since early data are always sparse

to begin with, and since analyses are therefore so sensitive to specific data that happen to be available.”

In his paper, Bloom does not claim that the data he retrieved advances the argument for a lab leak or a [natural zoonosis](#).

“This study provides no evidence either way,” Bloom said in an email. “But it does indicate that we probably have not exhausted all relevant data.”

He added, “I think as scientists we really need to focus on the following two questions: How can we get more data? How can we better analyze the data we have?”

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Bloom said the deleted sequences he recovered reinforce a notion supported by previous analyses, including a conclusion from the WHO-convened investigation into the virus’s origins conducted earlier this year: The virus probably infected people before the outbreak at the Huanan Seafood Market in December 2019. That spreading event, though large, was not necessarily the first instance of SARS-CoV-2 in humans.

W. Ian Lipkin, a Columbia University epidemiologist, said by email that Bloom’s paper offers “evidence of what many of us speculated — that the virus was circulating before the market outbreak. The retraction of sequence data is unprecedented and must be addressed.” University of California at San Diego evolutionary biologist Joel Wertheim, who has studied the emergence of the virus in Hubei province, said, “I actually don’t think this study adds much to the origins debate.”

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The sequences Bloom analyzed show greater similarities with coronavirus relatives in bats, when compared with the virus that infected many people at the seafood market. But researchers were already aware of two genetic lineages of the coronavirus that spread in Wuhan in January and February 2020, Wertheim said, and “these genome fragments further demonstrate this point.”

Speculation emerged on Twitter on Wednesday that Bloom’s findings could alter the timeline of the virus emergence, but Wertheim said that’s doubtful: “I’m not convinced that this paper makes a strong case for altering our molecular clock estimates, since similar — more complete — data were included in previous studies.”

President Biden has ordered the intelligence agencies to conduct a review of information that could shed light on the origins of the virus. In an interview with [Yahoo News](#) published Tuesday, Director of National Intelligence Avril Haines said the ultimate answer might never be found.

“We’re hoping to find a smoking gun,” Haines said, but “it’s challenging to do that.” She added: “It might happen, but it might not.”

Haines said that teams were seeking to collect new intelligence, in addition to taking a fresh look at information that was already gathered.

From: Ilene Mizrachi (b) (6)
Date: Wednesday, June 23, 2021 at 10:10 AM
To: "Skripchenko, Yuriy (NIH/NLM/NCBI) [C]" (b) (6), "Pruitt, Kim (NIH/NLM/NCBI) [E]" (b) (6), "Brister, James (NIH/NLM/NCBI) [E]" (b) (6), Janet Coleman (b) (6)
Cc: "Hicks, Denise (NIH/NLM/NCBI) [C]" (b) (6), "Fleischmann, Lydia (NIH/NLM/NCBI) [C]" (b) (6), "Trawick, Bart (NIH/NLM/NCBI) [E]" (b) (6)
Subject: RE: SRA was contacted by NY times reporter

I am adding Janet and Bart since I suspect that this will require a quick turnaround assuming Kim wants to comment.

Ilene

From: Skripchenko, Yuriy (NIH/NLM/NCBI) [C] (b) (6)
Sent: Wednesday, June 23, 2021 10:08 AM
To: Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6); Brister, James (NIH/NLM/NCBI) [E] (b) (6)
Cc: Mizrachi, Ilene (NIH/NLM/NCBI) [E] (b) (6); Hicks, Denise (NIH/NLM/NCBI) [C] (b) (6); Fleischmann, Lydia (NIH/NLM/NCBI) [C] (b) (6)
Subject: SRA was contacted by NY times reporter

Hello Kim, Rodney, and Ilene,

SRA was contacted by a NY Times columnist regarding the preprint by Jesse Bloom. I am passing on his initial email and contact information so we can reply to Carl Zimmer.

Best,
Yuriy

Details:

Greetings:

I am a columnist for the New York Times. I am writing about a preprint from Jesse Bloom, a virologist at the Fred Hutchinson Cancer Institute.

<https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1>

Dr. Bloom determined that SARS-CoV-2 sequences from early in the Covid-19 pandemic were deleted from SRA. He was then able to find copies of the sequences online and used them to create a revised phylogeny of the coronaviruses, offering important clues about the origin of the pandemic.

In his preprint, Dr. Bloom calls for the NIH to determine the reason that these significant sequences were deleted. I'd like to offer SRA an opportunity to provide a response for my article.

Thank you for your time.

Best wishes,

Carl Zimmer
Columnist



carl.zimmer@nytimes.com

Author website carlzimmer.com

From: Coleman, Janet (NIH/NLM/NCBI) [C]
Sent: Wed, 23 Jun 2021 12:35:48 -0400
To: Sherry, Steve (NIH/NLM/NCBI) [E]
Subject: Re: Question about removal of SARS-CoV-2 sequences from NCBI SRA

Will do.
Janet

From: "Sherry, Steve (NIH/NLM/NCBI) [E]" (b) (6)
Date: Wed, Jun 23, 2021, 12:34 PM
To: "Coleman, Janet (NIH/NLM/NCBI) [C]" (b) (6)
Subject: FW: Question about removal of SARS-CoV-2 sequences from NCBI SRA

Hi Janet, can you refer this inquiry to OCPL.

Thanks!
Steve

From: Ewen Callaway <e.callaway@nature.com>
Sent: Wednesday, June 23, 2021 11:45 AM
To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Subject: Question about removal of SARS-CoV-2 sequences from NCBI SRA

Dear Dr. Sherry,

I'm a journalist at Nature in the UK. I'm writing about a preprint that identifies a set of SARS-CoV-2 sequences that were removed from NCBI's SRA database, at the request of the depositing scientists: <https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1.full.pdf>.

The author of the preprint, Jesse Bloom, said that NCBI had shared the email requesting the removal with him. Jesse suggested I contact you to see if you could share the request, or details about it, with me.

All the best,
Ewen

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From: Coleman, Janet (NIH/NLM/NCBI) [C]
Sent: Wed, 23 Jun 2021 11:37:04 -0400
To: Sherry, Steve (NIH/NLM/NCBI) [E]
Subject: Re: Deletion of Wang et al. sequence data

Hi Steve,
Of course; I will send to OCPL.

From: "Sherry, Steve (NIH/NLM/NCBI) [E]" [REDACTED] (b) (6)
Date: Wednesday, June 23, 2021 at 11:36 AM
To: Janet Coleman [REDACTED] (b) (6)
Subject: Fwd: Deletion of Wang et al. sequence data

Hi Janet, can you please refer this science reporter to OCPL?

cheers,
Steve

From: Brennan, Patti (NIH/NLM) [E] [REDACTED] (b) (6)
Sent: Wednesday, June 23, 2021 10:33:30 AM
To: Sherry, Steve (NIH/NLM/NCBI) [E] [REDACTED] (b) (6); Pruitt, Kim (NIH/NLM/NCBI) [E]
[REDACTED] (b) (6)
Subject: Re: Deletion of Wang et al. sequence data

OCPL
Thanks
Patti

Patricia Flatley Brennan, RN, PhD
Director, National Library of Medicine
Investigator, National Institute of Nursing Research
National Institutes of Health
US Department of Health and Human Services

Telework: 830-5PM and by appointment



From: Steve Sherry [REDACTED] (b) (6)
Date: Wednesday, June 23, 2021 at 11:30 AM

To: "Pruitt, Kim (NIH/NLM/NCBI) [E]" (b) (6), Patti Brennan
(b) (6)

Subject: Fwd: Deletion of Wang et al. sequence data

Where should I refer these requests?

cheers,
Steve

From: Jon Cohen <jcohen@aaas.org>

Sent: Wednesday, June 23, 2021 8:50:18 AM

To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)

Subject: Deletion of Wang et al. sequence data

Dr. Sherry,

I'm a staff writer with Science.

Could you share with me the e-mail reason for deleting the sequence data Jesse Bloom refers to in his preprint?

I've filed a FOIA but that of course can take months or years.

Thanks,

Jon Cohen
Science
760-445-4674

From: Nurik, Jody (NIH/NLM) [E]
Sent: Wed, 23 Jun 2021 11:36:55 -0400
To: Sherry, Steve (NIH/NLM/NCBI) [E]; Brennan, Patti (NIH/NLM) [E]
Subject: FW: Deletion of Wang et al. sequence data

Thanks, Patti.

Steve, I spoke to Kim earlier asking that all media requests be sent to NLMCommunications@nlm.nih.gov.

Thanks,

Jody

Jody Nurik
Communications Director, Office of Communications and Public Liaison
National Library of Medicine | National Institutes of Health
Office: (b) (6)



From: Brennan, Patti (NIH/NLM) [E] (b) (6)
Sent: Wednesday, June 23, 2021 11:34 AM
To: Nurik, Jody (NIH/NLM) [E] (b) (6)
Subject: FW: Deletion of Wang et al. sequence data

Patricia Flatley Brennan, RN, PhD
Director, National Library of Medicine
Investigator, National Institute of Nursing Research
National Institutes of Health
US Department of Health and Human Services

Telework: 830-5PM and by appointment



From: Steve Sherry (b) (6)
Date: Wednesday, June 23, 2021 at 11:30 AM

To: "Pruitt, Kim (NIH/NLM/NCBI) [E]" (b) (6), Patti Brennan
(b) (6)

Subject: Fwd: Deletion of Wang et al. sequence data

Where should I refer these requests?

cheers,
Steve

From: Jon Cohen <jcohen@aaas.org>

Sent: Wednesday, June 23, 2021 8:50:18 AM

To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)

Subject: Deletion of Wang et al. sequence data

Dr. Sherry,

I'm a staff writer with Science.

Could you share with me the e-mail reason for deleting the sequence data Jesse Bloom refers to in his preprint?

I've filed a FOIA but that of course can take months or years.

Thanks,

Jon Cohen
Science
760-445-4674

From: Brennan, Patti (NIH/NLM) [E]
Sent: Tue, 22 Jun 2021 22:36:38 -0400
To: Sherry, Steve (NIH/NLM/NCBI) [E];Pruitt, Kim (NIH/NLM/NCBI) [E]
Subject: FW: WSJ Question about Bloom Paper

FYI

Patricia Flatley Brennan, RN, PhD
Director, National Library of Medicine
Investigator, National Institute of Nursing Research
National Institutes of Health
US Department of Health and Human Services

Telework: 830-5PM and by appointment



From: Patti Brennan (b) (6)
Date: Tuesday, June 22, 2021 at 10:34 PM
To: "Myles, Renate (NIH/OD) [E]" (b) (6), "Tabak, Lawrence (NIH/OD) [E]" (b) (6), "Collins, Francis (NIH/OD) [E]" (b) (6)
Cc: "Fine, Amanda (NIH/OD) [E]" (b) (6), "Wojtowicz, Emma (NIH/OD) [E]" (b) (6), "Pruitt, Kim (NIH/NLM/NCBI) [E]" (b) (6)
Subject: Re: WSJ Question about Bloom Paper

(b) (5)

Here are some considerations from the twitter sphere:

Bloom say: I discovered that even though the files were deleted from archive itself, they could be recovered from the Google Cloud at links like storage.googleapis.com/nih-sequence-r



(b) (5)

Bloom also says, (b) (5): Fortunately, Sequence Read Archive has rigorous data tracking enabling them to determine when data deleted & stated justification by authors. In fact,

[@NIHDirector](#)

[@NCBI](#)

have already determined this & generously shared info w me, but will let them share more widely. (21/n)

NIH Colleagues:



Please note that NLM/NCBI Policies and practices related to submission of sequence information can be found here: <https://www.ncbi.nlm.nih.gov/sra/docs/submit/>

Instructions related to with withdraw of data can be found here: <https://www.ncbi.nlm.nih.gov/sra/docs/submitquestions/#question3upd>

Please let me know how I can be of assistance

Patti

Patricia Flatley Brennan, RN, PhD
Director, National Library of Medicine
Investigator, National Institute of Nursing Research
National Institutes of Health
US Department of Health and Human Services

Telework: 830-5PM and by appointment



From: "Myles, Renate (NIH/OD) [E]" (b) (6)
Date: Tuesday, June 22, 2021 at 10:02 PM
To: Patti Brennan (b) (6), "Tabak, Lawrence (NIH/OD) [E]" (b) (6), "Collins, Francis (NIH/OD) [E]" (b) (6)
Cc: "Fine, Amanda (NIH/OD) [E]" (b) (6), "Wojtowicz, Emma (NIH/OD) [E]" (b) (6)
Subject: Re: WSJ Question about Bloom Paper

Thanks, Patty. Shall I wait or are you good with responding with the below?

From: Brennan, Patti (NIH/NLM) [E] (b) (6)
Sent: Tuesday, June 22, 2021 9:47:08 PM
To: Tabak, Lawrence (NIH/OD) [E] (b) (6); Myles, Renate (NIH/OD) [E] (b) (6); Collins, Francis (NIH/OD) [E] (b) (6)
Cc: Fine, Amanda (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6)
Subject: Re: WSJ Question about Bloom Paper

Will weigh in shortly

Renate's statement is acceptable

Patti

Patricia Flatley Brennan, RN, PhD
Director, National Library of Medicine
National Institutes of Health
US Department of Health and Human Services
Telework Hours 830-5 and by appt

From: Tabak, Lawrence (NIH/OD) [E] (b) (6)
Sent: Tuesday, June 22, 2021 9:38:03 PM
To: Myles, Renate (NIH/OD) [E] (b) (6); Collins, Francis (NIH/OD) [E] (b) (6); Brennan, Patti (NIH/NLM) [E] (b) (6)
Cc: Fine, Amanda (NIH/OD) [E] (b) (6); Wojtowicz, Emma (NIH/OD) [E] (b) (6)

(b) (6)

Subject: Re: WSJ Question about Bloom Paper

I had a conversation with Patti today – she needs to weigh in please.
Larry

From: "Myles, Renate (NIH/OD) [E]" (b) (6)

Date: Tuesday, June 22, 2021 at 9:27 PM

To: Francis Collins (b) (6), "Tabak, Lawrence (NIH/OD) [E]"

(b) (6), "Brennan, Patti (NIH/NLM) [E]" (b) (6)

Cc: "Fine, Amanda (NIH/OD) [E]" (b) (6), "Wojtowicz, Emma (NIH/OD) [E]"

(b) (6)

Subject: WSJ Question about Bloom Paper

Removing ASF and adding Patti

Bloom posted on twitter that there was some indication that NIH might be issuing a statement about new rules regarding submission of sequences to data bases. WSJ is asking: Are there any changes planned? Are any new policies being contemplated?

I believe the answer is (b) (5)

The NLM is (b) (5). The SRA is a database. (b) (5)

Thanks,
Renate

From: Myles, Renate (NIH/OD) [E]

Sent: Tuesday, June 22, 2021 6:31 PM

To: Collins, Francis (NIH/OD) [E] (b) (6); Tabak, Lawrence (NIH/OD) [E]

(b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6)

Subject: RE: pre-print posted

Hi all:

Some of the Twitter thread didn't paste, so I'm resending with the full thread. I'm also highlighting the information about the NIH SRA archive.

Thanks,
Renate

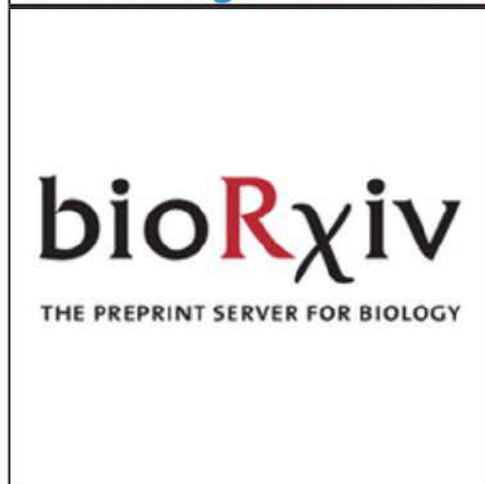


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@jbloom lab

In a new study, I identify and recover a deleted set of [#SARSCoV2](#) sequences that provide additional information about viruses from the early Wuhan outbreak:

[biorxiv.org/content/10.110 ...](https://doi.org/10.1101/2021.06.15.448111) (1/n)



[Recovery of deleted deep sequencing data sheds more light on the early Wuhan SARS-CoV-2 epidemic](#)

The origin and early spread of SARS-CoV-2 remains shrouded in mystery. Here I identify a data set containing SARS-CoV-2 sequences from early in the Wuhan epidemic that has been deleted from the NIH's...

[biorxiv.org](https://doi.org/10.1101/2021.06.15.448111)

5:09 PM · Jun 22, 2021 · Twitter Web App

31

Retweets

14

Quote Tweets

72

Likes



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22m

Replying to

@jbloom lab

Specifically, NIH maintains the Sequence Read Archive, where scientists around world deposit deep sequencing data for others to analyze. I noted peerj.com/articles/9255 lists all #SARSCoV2 data in archive as of March-31-2020. Most from a project by Wuhan University.

(2/n)

| | | | | | | | | | | |
|----|-------------|----------|------|----------|-------------|--------------|------------|----------|------------------|--------|
| 40 | SRR11313269 | AMPLICON | 998 | 103835 | PRJNA612766 | SAMN14381172 | Pathogen.c | 176103 | WUHAN UNIVERSITY | public |
| 41 | SRR11313270 | AMPLICON | 624 | 31239 | PRJNA612766 | SAMN14381111 | Pathogen.c | 109326 | WUHAN UNIVERSITY | public |
| 42 | SRR11313271 | AMPLICON | 698 | 53058 | PRJNA612766 | SAMN14381075 | Pathogen.c | 129329 | WUHAN UNIVERSITY | public |
| 43 | SRR11313272 | AMPLICON | 1058 | 22225 | PRJNA612766 | SAMN14381110 | Pathogen.c | 100844 | WUHAN UNIVERSITY | public |
| 44 | SRR11313273 | AMPLICON | 410 | 410 | PRJNA612766 | SAMN14381109 | Pathogen.c | 78348 | WUHAN UNIVERSITY | public |
| 45 | SRR11313274 | AMPLICON | 741 | 1466036 | PRJNA612766 | SAMN14381108 | Pathogen.c | 1423974 | WUHAN UNIVERSITY | public |
| 46 | SRR11313275 | AMPLICON | 697 | 139403 | PRJNA612766 | SAMN14381107 | Pathogen.c | 208445 | WUHAN UNIVERSITY | public |
| 47 | SRR11313276 | AMPLICON | 653 | 1790911 | PRJNA612766 | SAMN14381106 | Pathogen.c | 1722468 | WUHAN UNIVERSITY | public |
| 48 | SRR11313277 | AMPLICON | 624 | 152322 | PRJNA612766 | SAMN14381105 | Pathogen.c | 220445 | WUHAN UNIVERSITY | public |
| 49 | SRR11313278 | AMPLICON | 1386 | 48522 | PRJNA612766 | SAMN14381104 | Pathogen.c | 124781 | WUHAN UNIVERSITY | public |
| 50 | SRR11313279 | AMPLICON | 1258 | 1258 | PRJNA612766 | SAMN14381103 | Pathogen.c | 79449 | WUHAN UNIVERSITY | public |
| 51 | SRR11313280 | AMPLICON | 714 | 21328421 | PRJNA612766 | SAMN14381102 | Pathogen.c | 19626474 | WUHAN UNIVERSITY | public |
| 52 | SRR11313281 | AMPLICON | 695 | 1926994 | PRJNA612766 | SAMN14381101 | Pathogen.c | 1846539 | WUHAN UNIVERSITY | public |
| 53 | SRR11313282 | AMPLICON | 1151 | 94454 | PRJNA612766 | SAMN14381074 | Pathogen.c | 166664 | WUHAN UNIVERSITY | public |
| 54 | SRR11313283 | AMPLICON | 1497 | 28449 | PRJNA612766 | SAMN14381100 | Pathogen.c | 106563 | WUHAN UNIVERSITY | public |
| 55 | SRR11313284 | AMPLICON | 1458 | 1458 | PRJNA612766 | SAMN14381099 | Pathogen.c | 79719 | WUHAN UNIVERSITY | public |
| 56 | SRR11313285 | AMPLICON | 709 | 14759827 | PRJNA612766 | SAMN14381098 | Pathogen.c | 13606413 | WUHAN UNIVERSITY | public |
| 57 | SRR11313286 | AMPLICON | 690 | 1124662 | PRJNA612766 | SAMN14381097 | Pathogen.c | 1112254 | WUHAN UNIVERSITY | public |
| 58 | SRR11313287 | AMPLICON | 688 | 15397651 | PRJNA612766 | SAMN14381096 | Pathogen.c | 14198094 | WUHAN UNIVERSITY | public |
| 59 | SRR11313288 | AMPLICON | 527 | 2746094 | PRJNA612766 | SAMN14381311 | Pathogen.c | 2600463 | WUHAN UNIVERSITY | public |
| 60 | SRR11313289 | AMPLICON | 664 | 1210380 | PRJNA612766 | SAMN14381095 | Pathogen.c | 1191913 | WUHAN UNIVERSITY | public |
| 61 | SRR11313290 | AMPLICON | 530 | 109785 | PRJNA612766 | SAMN14381310 | Pathogen.c | 180549 | WUHAN UNIVERSITY | public |
| 62 | SRR11313291 | AMPLICON | 880 | 5446065 | PRJNA612766 | SAMN14381309 | Pathogen.c | 5059669 | WUHAN UNIVERSITY | public |
| 63 | SRR11313292 | AMPLICON | 865 | 2752369 | PRJNA612766 | SAMN14381308 | Pathogen.c | 2596911 | WUHAN UNIVERSITY | public |
| 64 | SRR11313293 | AMPLICON | 867 | 1394642 | PRJNA612766 | SAMN14381307 | Pathogen.c | 1355493 | WUHAN UNIVERSITY | public |
| 65 | SRR11313294 | AMPLICON | 883 | 706757 | PRJNA612766 | SAMN14381306 | Pathogen.c | 726413 | WUHAN UNIVERSITY | public |
| 66 | SRR11313295 | AMPLICON | 849 | 214139 | PRJNA612766 | SAMN14381305 | Pathogen.c | 276476 | WUHAN UNIVERSITY | public |

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22m

But when I went to Sequence Read Archive, I found entire project was gone! (Note that as detailed below, this does **not** imply malfeasance by NIH. Sequence Read Archive policy allows submitters to delete by e-mail request.) (3/n)

NCBI
Site map All databases Search

Sequence Read Archive

Main Browse Search Download Submit Software Trace Archive

Studies Samples Analyses **Run Browser** Run Selector Provisional SRA

! COVID-19 Information
[Public health information \(CDC\)](#) | [Research information \(NIH\)](#)
[SARS-CoV-2 data \(NCBI\)](#) | [Prevention and treatment information \(HHS\)](#) | [Español](#)

SRR11313485 is removed

Run Browser

Search and browse data for a single RUN

Accession: Search

[What can be entered in this field?](#)

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22m

I was able to determine deleted data corresponded to a study that partially sequenced "45 nasopharyngeal samples from [Wuhan] outpatients with suspected COVID-19 early in the epidemic" medrxiv.org/content/10.1101/2020.03.26.20078881v1 (4/n)

.

Nanopore target sequencing for accurate and comprehensive detection of SARS-CoV-2 and other...

The ongoing novel coronavirus pneumonia COVID-19 outbreak in Wuhan, China, has engendered numerous cases of infection and death. COVID-19 diagnosis relies upon nucleic acid detection; however,...

medrxiv.org

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I discovered that even though the files were deleted from archive itself, they could be recovered from the Google Cloud at links like storage.googleapis.com/nih-sequence-r... (5/n)

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Using this approach, I recovered files for the 34 early samples that were virus positive. I was able to use the data in the files to reconstruct partial viral sequences (from start of spike to end of ORF10) for 13 of these samples. (6/n)

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1h

Now I need to give background to explain a confusing scientific mystery about other early #SARSCoV2 sequences. Although events that led to emergence of #SARSCoV2 in Wuhan are unclear (zoonosis vs lab accident), everyone agrees deep ancestors are coronaviruses from bats. (7/n)

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1h

Therefore, we'd expect the first #SARSCoV2 sequences would be more similar to bat coronaviruses, and as #SARSCoV2 continued to evolve it would become more divergent from these ancestors. But that is *not* the case! (8/n)

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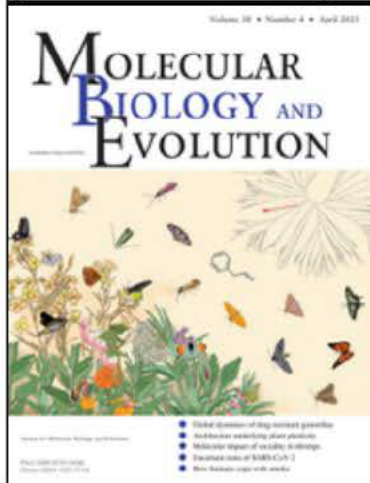
1h

Instead, early Huanan Seafood Market #SARSCoV2 viruses are more different from bat coronaviruses than #SARSCoV2 viruses collected later in China and even other countries.

@lpipes

@ras_nielsen

give nice technical analysis at academic.oup.com/mbe/article/38 (9/n)



Assessing Uncertainty in the Rooting of the SARS-CoV-2 Phylogeny

Abstract. The rooting of the SARS-CoV-2 phylogeny is important for understanding the origin and early spread of the virus. Previously published phylogenies have

academic.oup.com

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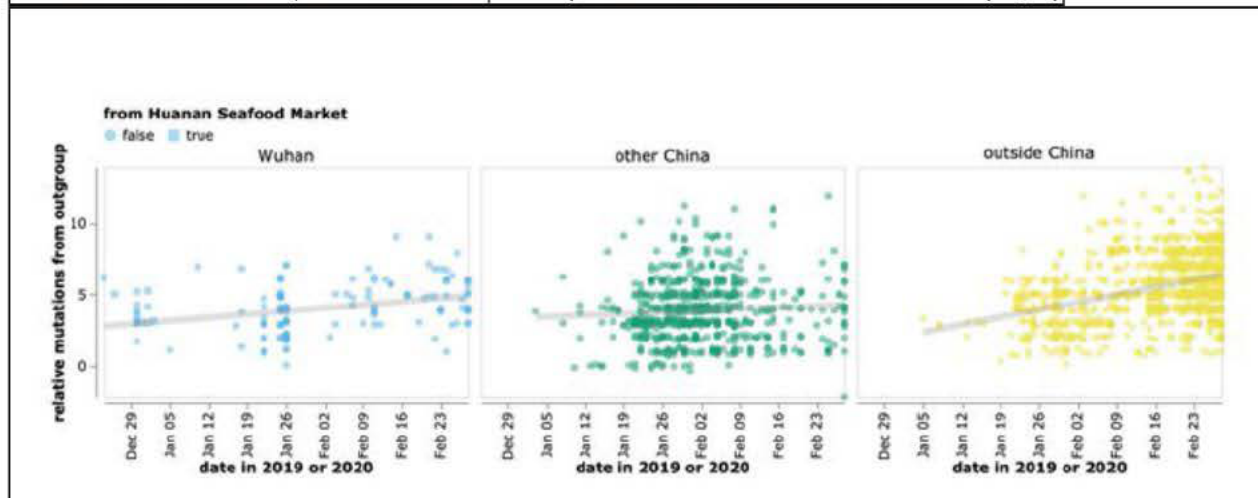
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1h

The conundrum is easily seen by plotting the relative differences from the bat coronavirus RaTG13 outgroup versus collection date for early #SARSCoV2. See how the first reported viruses from Wuhan (leftmost blue points) aren't the closest to RaTG13. (10/n)



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1h

Same result if we use other bat coronaviruses like RpYN06 or RmYN02. To see this, go to jbloom.github.io/SARS-CoV-2_PRJ for an interactive plot that allows you to select the bat coronavirus outgroup and mouse over points for strain details. (11/n)

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1h

How do deleted sequences I recovered relate to this conundrum? If we include those sequences, and note 4 sequences from Guangdong are from two groups of people infected in Wuhan in late Dec / early Jan, we get plausible scenarios that resolve above problems.

(12/n)

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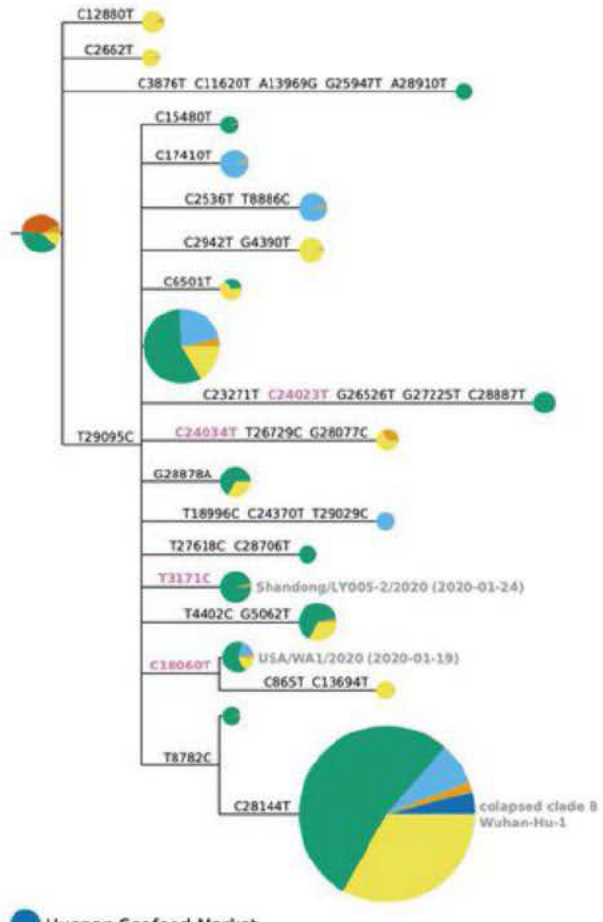
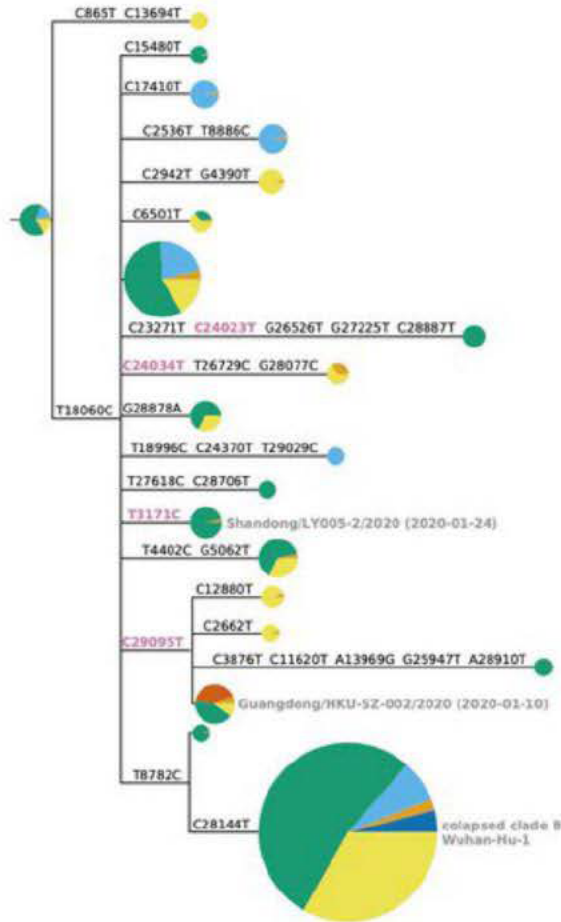
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These two scenarios are plotted below. Each has a different "progenitor", which is the sequence that gave rise to all *currently* known #SARSCoV2 sequences (still may not be virus that infected patient zero if other early sequences remain unknown). (13/n)

progenitor as USA/WA1/2020 (2020-01-19)
 mutations from proCoV2 (Kumar et al): none
 mutations from Wuhan-Hu-1: C8782T, C18060T, T28144C

progenitor as Guangdong/HKU-SZ-002/2020 (2020-01-10)
 mutations from proCoV2 (Kumar et al): T18060C, C29095T
 mutations from Wuhan-Hu-1: C8782T, T28144C, C29095T



- Huanan Seafood Market
- deleted early Wuhan
- Guangdong patient infected in Wuhan before Jan 5
- other Wuhan
- other China
- outside China

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1h

Both putative progenitors have 3 mutations relative to Seafood Market viruses that make them more similar to bat coronavirus. One is progenitor inferred by

[@kumar lab](#)

[@sergeilkp](#)

et al ([academic.oup.com/mbe/advance-ar.....](#)), other has C8782T, T28144C, and C29095T relative to Wuhan-Hu-1. (14/n)

Evolutionary Portrait of the Progenitor SARS-CoV-2 and Its Dominant Offshoots in COVID-19 Pandemic

Abstract. Global sequencing of genomes of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has continued to reveal new genetic variants that are the [academic.oup.com](#)

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1h

Both progenitors suggest [#SARSCoV2](#) was circulating in Wuhan before December outbreak at Huanan Seafood Market, which is corroborated by lots of other evidence, including news articles from China in early 2020 (see intro to my paper linked in first Tweet in this thread).

(15/n)

23m

There are also broader implications. First, fact this dataset was deleted should make us skeptical that all other relevant early Wuhan sequences have been shared. We already know many labs in China ordered to destroy early samples: [scmp.com/news/china/soc.....](#)

(16/n)

According to a provincial health commission notice issued in February, those handling virus samples were ordered not to provide them to any institutions or labs without approval. Unauthorised labs that obtained samples in the early stage of the outbreak had to destroy them or send them to a municipal centre for disease control and prevention for storage.

Chinese magazine *Caixin* reported in February that some hospitals had sent samples to private gene sequencing companies to identify the mystery virus early in the outbreak. Some of those results came back as early as December 27 and were identified as being from the same coronavirus family as Sars, the report said. One company had been told to destroy all virus samples, according to the report.

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23m

Sequence sharing could be further limited by fact that scientists in China are under an order from the State Council requiring central approval of all publications:

[apnews.com/article/united](https://apnews.com/article/united...) ... (17/n)

4. Strengthen coordination of the publication of scientific research information

During the epidemic prevention and control period, all localities and units must conscientiously implement the spirit of a series of important instructions on epidemic prevention and control by General Secretary Xi Jinping, further strengthen overall awareness and sense of responsibility, strengthen reviews and checks, and actively communicate and coordinate the publication of scientific research on COVID-19 in a pattern like "moves in a game of chess" across the country. Important and sensitive scientific research results must be repeatedly reviewed and checked, and if they are not certain, procedures should be followed to request instructions from the scientific research team and related departments in a timely manner.

5. Strengthen supervision and accountability.

Those who fail to apply for approval in accordance with the prescribed procedures and publish unconfirmed false information on scientific research, thereby causing serious adverse social impacts, shall be held accountable.

Contact: Zhao Qing, [REDACTED], [REDACTED]

Wu Yungao, [REDACTED], [REDACTED]

Fax: [REDACTED], Contact email: [REDACTED]

The State Council Novel Coronavirus Pneumonia
Epidemic Joint Prevention and Control Mechanism
Scientific Research Task Force
(Representative Stamp)

March 3, 2020

(This document is not public)

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23m

Second major implication is that it may be possible to obtain additional information about early spread of [#SARSCoV2](#) in Wuhan even if efforts for more on-the-ground investigations are stymied. (18/n)

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23m

Scientific communication and data sharing typically rely on trust. The NIH Sequence Read Archive has > 13,000,000 runs, so they have to trust authors when they request deletions as not feasible to validate reasons for all requests, some of which are legitimate. (19/n)

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23m

In case of data set I describe above, it seems possible that trust that the NIH Sequence Read Archive grants to scientific authors to delete data may have been used to obscure sequences informative for understanding early #SARSCoV2. (20/n)

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23m

Fortunately, Sequence Read Archive has rigorous data tracking enabling them to determine when data deleted & stated justification by authors. In fact,

@NIHDirector

@NCBI

have already determined this & generously shared info w me, but will let them share more widely. (21/n)

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23m

It is important to examine if other trust-based systems in science conceivably may have also been used to hide data relevant to origins / early spread of [#SARSCoV2](#). This includes not only looking more at sequence databases, but also paper reviews, grant reporting, etc.

(22/n)

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23m

Third major implication is that scientists need to stay focused on data-driven study of [#SARSCoV2](#) origins / early spread. After spending the last 4 months studying this closely, I am cautiously optimistic that additional relevant data are still likely to come to light. (23/n)

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23m

We should therefore avoid dogmatic arguments about [#SARSCoV2](#) origins / early spread, and instead focus on following two questions: (1) How can we get more data? (2) How can we better analyze the data we have? (24/n)

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23m

Finally, my analysis is on GitHub at github.com/jbloom/SARS-CoV-2_PRJNA612766 where you can access all code, data, & paper drafts. All updates are via time-stamped commits. This ensures transparency/reproducibility of this study are not in doubt, regardless of your views on interpretation. (25/n)

The screenshot shows the GitHub repository page for 'jbloom/SARS-CoV-2_PRJNA612766'. The repository title is 'jbloom/SARS-CoV-2_PRJNA612766'. The description is 'Analysis of early Wuhan SARS-CoV-2 sequences from deleted SRA BioProject PRJNA612766'. The repository has 1 contributor, 0 issues, 0 stars, and 0 forks. A profile picture of the user 'jbloom' is visible on the right side of the repository header.

[jbloom/SARS-CoV-2 PRJNA612766](https://github.com/jbloom/SARS-CoV-2_PRJNA612766)

[Analysis of early Wuhan SARS-CoV-2 sequences from deleted SRA BioProject PRJNA612766](https://github.com/jbloom/SARS-CoV-2_PRJNA612766)

[- jbloom/SARS-CoV-2 PRJNA612766](https://github.com/jbloom/SARS-CoV-2_PRJNA612766)

github.com

From: Collins, Francis (NIH/OD) [E] (b) (6)

Sent: Tuesday, June 22, 2021 5:29 PM

To: Myles, Renate (NIH/OD) [E] (b) (6); Tabak, Lawrence (NIH/OD) [E]

(b) (6); Fauci, Anthony (NIH/NIAID) [E]

(b) (6)

Subject: FW: pre-print posted

FYI

From: Bloom PhD, Jesse D <jbloom@fredhutch.org>

Sent: Tuesday, June 22, 2021 5:15 PM

To: Collins, Francis (NIH/OD) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E]

(b) (6); Embry, Alan (NIH/NIAID) [E]

(b) (6)

Subject: pre-print posted

Hi Francis, Steve, and Alan,

Just wanted to let you know that the pre-print recently posted on *bioRxiv* at:

<https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1>

I also posted a Twitter thread that goes through and summarizes it:

https://twitter.com/jbloom_lab/status/1407445604029009923

Thanks again for handling and looking into this all so responsively even over last weekend, and let me know if I can be of any help in continued efforts to better understand the early spread of the virus.

Thanks,

Jesse

Jesse Bloom

Associate Professor, Fred Hutch Cancer Research Center

Affiliate Associate Professor, Genome Sciences & Microbiology, University of Washington

Investigator, Howard Hughes Medical Institute

From: Trevor Bedford
Sent: Mon, 21 Jun 2021 13:19:56 -0400
To: Collins, Francis (NIH/OD) [E]
Cc: Tabak, Lawrence (NIH/OD) [E];Fauci, Anthony (NIH/NIAID) [E];Embry, Alan (NIH/NIAID) [E];Sherry, Steve (NIH/NLM/NCBI) [E];Kristian G. Andersen;Bloom PhD, Jesse D;Garry, Robert F;rasmus_nielsen@berkeley.edu;spnd
Subject: Re: URGENT: Seeking your expert advice

Hi all,

My apologies for missing the meeting yesterday. I don't generally check my @fredhutch.org email address on weekends and I missed this entirely.

I'm not sure what the consensus was on the call, but my general take is as follows:

Although there were clearly confirmed cases that were non-market associated in early December, the large market outbreak had remained a major datapoint for me in a zoonotic scenario, as emergence outside the market would require a very early transmission chain make it to the market and be amplified (not impossible, but less parsimonious).

However, these new sequences add to phylogenetic evidence that the root of the SARS-CoV-2 phylogeny may well lie in lineage A rather than lineage B and support a root that's the outside the market.

Rasmus, Sergei and Jesse have all worked on this rooting issue. If we could have confidence that the root of the phylogeny does not match with market-associated genomes this would be strong evidence for me that the market is a secondary foci and not the site of emergence. I view this rooting issue as highly important to analyze properly and to determine uncertainty between different root locations.

Best,

- Trevor

On Jun 20, 2021, at 11:33 AM, Collins, Francis (NIH/OD) [E] (b) (6) wrote:

Allow me to suggest this agenda:

1. Introductions
2. Retrieval of SARS-CoV-2 reads deleted from SRA by submitter – Jesse Bloom
3. NCBI SOPs for handling submitter requests to delete reads in SRA – Steve Sherry
4. Likelihood of other sequence deletions from SRA? – Steve Sherry
5. Significance of this new sequence information for origin of SARS-CoV-2 – Jesse, Kristian, Trevor, Bob, Rasmus, Sergei
6. Discussion and next steps – All

Looking forward to the discussion.

Francis

From: Tabak, Lawrence (NIH/OD) [E] (b) (6)
Sent: Sunday, June 20, 2021 2:07 PM
To: Collins, Francis (NIH/OD) [E] (b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6); Embry, Alan (NIH/NIAID) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Cc: Kristian G. Andersen (b) (6); Bedford, Trevor <tbedford@fredhutch.org>; Bloom PhD, Jesse D <jbloom@fredhutch.org>; Garry, Robert F <rfgarry@TULANE.EDU>; rasmus_nielsen@berkeley.edu; spond@temple.edu
Subject: Re: URGENT: Seeking your expert advice

A zoom call will be held instead of the phone call:

Join ZoomGov Meeting

<https://nih.zoomgov.com/join/1234567890?pwd=TmVPTUdMdHZVVS9EbXFpMncrNOlLdz09>

Meeting ID: (b) (6)

Passcode: (b) (6)

One tap mobile

+16692545252, (b) (6) US (San Jose)

+16468287666, (b) (6) US (New York)

Dial by your location

+1 669 254 5252 US (San Jose)

+1 646 828 7666 US (New York)

+1 551 285 1373 US

+1 669 216 1590 US (San Jose)

Meeting ID: (b) (6)

Passcode: (b) (6)

Find your local number: <https://nih.zoomgov.com/u/aebeXjaOqb>

Join by SIP

[sip:\(b\) \(6\)@sip.zoomgov.com](mailto:(b) (6)@sip.zoomgov.com)

Join by H.323

161.199.138.10 (US West)

161.199.136.10 (US East)

Meeting ID: (b) (6)

Passcode (b) (6)

From: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Date: Sunday, June 20, 2021 at 1:58 PM
To: Anthony Fauci (b) (6), "Kristian G. Andersen" (b) (6), "Bloom PhD, Jesse D" <jbloom@fredhutch.org>
Cc: Francis Collins (b) (6), "Garry, Robert F" <rfgarry@TULANE.EDU>, "spond@temple.edu" <spond@temple.edu>, "rasmus_nielsen@berkeley.edu" <rasmus_nielsen@berkeley.edu>, "Bedford, Trevor" <tbedford@fredhutch.org>, "Embry, Alan

(NIH/NIAID) [E]" [REDACTED] (b) (6), "Sherry, Steve (NIH/NLM/NCBI) [E]"
[REDACTED] (b) (6)

Subject: Re: URGENT: Seeking your expert advice

Setting it up now.

From: Anthony Fauci [REDACTED] (b) (6)

Date: Sunday, June 20, 2021 at 1:53 PM

To: "Tabak, Lawrence (NIH/OD) [E]" [REDACTED] (b) (6), "Kristian G. Andersen"
[REDACTED] (b) (6), "Bloom PhD, Jesse D" <jbloom@fredhutch.org>

Cc: Francis Collins [REDACTED] (b) (6), "Garry, Robert F" <rfgarry@TULANE.EDU>, "spond@temple.edu" <spond@temple.edu>, "rasmus_nielsen@berkeley.edu" <rasmus_nielsen@berkeley.edu>, "Bedford, Trevor" <tbedford@fredhutch.org>, "Embry, Alan (NIH/NIAID) [E]" [REDACTED] (b) (6)

Subject: RE: URGENT: Seeking your expert advice

I am fine with Zoom if you so decide. Just let me know and send a link. I believe that Francis may still be able to join the link by phone. Thanks.

From: Tabak, Lawrence (NIH/OD) [E] [REDACTED] (b) (6)

Sent: Sunday, June 20, 2021 12:37 PM

To: Kristian G. Andersen [REDACTED] (b) (6); Bloom PhD, Jesse D <jbloom@fredhutch.org>

Cc: Collins, Francis (NIH/OD) [E] [REDACTED] (b) (6); Garry, Robert F <rfgarry@TULANE.EDU>; spond@temple.edu; rasmus_nielsen@berkeley.edu; Bedford, Trevor <tbedford@fredhutch.org>; Fauci, Anthony (NIH/NIAID) [E] [REDACTED] (b) (6); Embry, Alan (NIH/NIAID) [E] [REDACTED] (b) (6)

Subject: Re: URGENT: Seeking your expert advice

Francis will be in transit; I can set this up if it is preference.

Best wishes,

Larry

From: "Kristian G. Andersen" [REDACTED] (b) (6)

Date: Sunday, June 20, 2021 at 12:35 PM

To: "Bloom PhD, Jesse D" <jbloom@fredhutch.org>

Cc: Francis Collins [REDACTED] (b) (6), "Garry, Robert F" <rfgarry@TULANE.EDU>, "spond@temple.edu" <spond@temple.edu>, "rasmus_nielsen@berkeley.edu" <rasmus_nielsen@berkeley.edu>, "Bedford, Trevor" <tbedford@fredhutch.org>, Anthony Fauci [REDACTED] (b) (6), "Embry, Alan (NIH/NIAID) [E]" [REDACTED] (b) (6), "Tabak, Lawrence (NIH/OD) [E]" [REDACTED] (b) (6)

Subject: Re: URGENT: Seeking your expert advice

Hi everybody,

Looking forward to the discussion in a few hours. Would it be possible to set this up as a Zoom call instead of a teleconference? A few visuals might be useful.

Best,
Kristian

On Sat, Jun 19, 2021 at 2:48 PM Bloom PhD, Jesse D <jbloom@fredhutch.org> wrote:
By the way, I just wanted to add one last piece of information prior to the meeting that might be relevant.

Because the e-mail Steve Sherry found from Wuhan University about the request to delete PRJNA612766 mentioned deleting two projects, I pointed my pipeline that is currently scanning for SRA deletions to that range of SRRs. It appears that the other largest chunk of contiguous deleted accessions of SARS-CoV-2 sequencing is from SRR11313377 to SRR11313509, which comes immediately after the PRJNA612766 accessions. I suspect that this might be the other sequencing project that Wuhan University requested to delete in their e-mail to the SRA? It might be informative if NCBI is able to confirm that just so we know that we have the both project deletions covered before meeting tomorrow.

I'm not going to have time to properly analyze the runs from SRR11313377 to SRR11313509 before tomorrow, but on an extremely cursory glance nothing looks that striking from those runs. Some of them contain the mutation A15090T which is not a mutation that I've come across before in early-ish isolates, but there isn't obvious significance of that mutation as the identity is A in most of the closely related bat coronaviruses (other than PrC31).

--

Jesse Bloom
Associate Professor, Fred Hutchinson Cancer Research Center
Investigator, Howard Hughes Medical Institute

From: Collins, Francis (NIH/OD) [E] [REDACTED] (b) (6)
Date: Saturday, June 19, 2021 at 8:08 AM
To: [REDACTED] (b) (6), Garry, Robert F <rfgarry@TULANE.EDU>, spond@temple.edu<spond@temple.edu>, rasmus.nielsen@berkeley.edu<rasmus.nielsen@berkeley.edu>, Bedford, Trevor <tbedford@fredhutch.org>
Cc: Fauci, Anthony (NIH/NIAID) [E] [REDACTED] (b) (6), Bloom PhD, Jesse D <jbloom@fredhutch.org>, Embry, Alan (NIH/NIAID) [E] [REDACTED] (b) (6), Tabak, Lawrence (NIH/OD) [E] [REDACTED] (b) (6)
Subject: URGENT: Seeking your expert advice

Hi Kristian, Bob, Sergei, Rasmus, and Trevor,

Tony Fauci and I would like to get your advice on the interpretation and significance of a preprint that Jesse Bloom has just submitted to BioRxiv (attached). As you will see, through some clever sleuthing, Jesse has been able to discover 13 sequences of SARS-CoV-2 spike protein that were deposited (and then deleted) from the SRA by a Chinese investigator at Wuhan University. The sequences are

incomplete but interesting, in that they appear to represent a slightly closer relationship to RaTG13 than the prior root of the phylogenetic tree.

Would you be willing to have a close read of the paper and then join a conference call with Jesse, Tony, and me tomorrow (Sunday 6/20) at 3 PM EDT? Steve Sherry of NCBI will also join – he has been digging out information about how these reads were removed from SRA by a request from the submitter, and assessing whether there might have been any other similar requests in early 2020.

Let me know if you can be available.

Thanks, Francis

From: Benson, Dennis (NIH/NLM/NCBI) [E]
Sent: Mon, 21 Jun 2021 08:40:03 -0400
To: Sherry, Steve (NIH/NLM/NCBI) [E]
Subject: Re: Bloom preprint call debrief

Hi Steve. Thanks for sending; let me read through the materials. It looks like [REDACTED] (b) (5)
[REDACTED] And I don't see [REDACTED] (b) (5)

So, don't want to hold up your trip preparations; I hope you have a restful and relaxing break. Don't hesitate to phone or txt if there's anything I can do to help.

Thanks,

Dennis

From: "Sherry, Steve (NIH/NLM/NCBI) [E]" [REDACTED] (b) (6)
Date: Monday, June 21, 2021 at 8:23 AM
To: Dennis Benson [REDACTED] (b) (6)
Subject: FW: Bloom preprint call debrief

Hi Dennis,

I am forwarding you a few threads of activity around the SRA SARS2 data. We need to prepare talking points for bldg1 about the data removal – [REDACTED] (b) (5)
[REDACTED]
[REDACTED]

There is some confusion [REDACTED] (b) (5)
[REDACTED] If we decide [REDACTED] (b) (5)
[REDACTED]
[REDACTED] We will need to ensure [REDACTED] (b) (5)
[REDACTED]

The other burning issue is that [REDACTED] (b) (5)
[REDACTED]
[REDACTED] It will be
meaningless [REDACTED] (b) (5)
[REDACTED]

Happy to chat on the phone if you like. [REDACTED] (b) (6)
[REDACTED]

Cheers
Steve

From: Brennan, Patti (NIH/NLM) [E] (b) (6)
Sent: Sunday, June 20, 2021 5:17 PM
To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6)
Subject: Re: Bloom preprint call debrief

Thanks Very helpful - I have heard from NLM OCPL - recommend that Kim and I speak to them tomorrow per Kim's availability

From my perspective I recommend (b) (5)

Thanks again

Patti

Patricia Flatley Brennan, RN, PhD
Director, National Library of Medicine
National Institutes of Health
US Department of Health and Human Services
Telework Hours 830-5 and by appt

From: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Sent: Sunday, June 20, 2021 4:42:05 PM
To: Brennan, Patti (NIH/NLM) [E] (b) (6)
Subject: Bloom preprint call debrief

Patti, here is my email to Kim and the SRA team for your awareness.

(b) (5)
We will need to
tabulate (b) (5)

(b) (5) please work with (b) (5)
We will need to point out all relevant points:
(b) (5)

[REDACTED] (b) (5)
[REDACTED]
[REDACTED] so we do not have much time [REDACTED] (b) (5)
[REDACTED]

[REDACTED] (b) (5)
[REDACTED]
[REDACTED] If
we could point [REDACTED] (b) (5)
[REDACTED]
[REDACTED]
[REDACTED]

From: Sherry, Steve (NIH/NLM/NCBI) [E]
Sent: Sun, 20 Jun 2021 10:10:29 -0400
To: Tabak, Lawrence (NIH/OD) [E]
Subject: RE: URGENT: Seeking your expert advice

Perfect. I just replied a few minutes ago with updates on the 2 additional runs from Texas and Utah. Here is that additional background.

Good morning, Jesse. We did some more digging on status of the runs you mentioned. A full report of all withdrawn samples will come later this week when staff are back in the office.

Kind regards,
Steve

SRR11607649 (Utah) was not deleted. It is still public at <https://www.ncbi.nlm.nih.gov/sra/?term=SRR11607649+>

SRR13075049 (Texas) was withdrawn from SRA on Nov 20, 2020. Here is the email request from Texas Dept of State Health Services.

From: NLM Support <nlm-support@nlm.nih.gov>
Sent: Friday, November 20, 2020 11:19 AM
To: XXXX (DSHS) [REDACTED] (b) (6)
Subject: case #zzzzz: RE: Biosample/SRA retraction

WARNING: This email is from outside the HHS system. Do not click on links or attachments unless you expect them from the sender and know the content is safe.

Hello [SRA Submitter],
All requested objects have been withdrawn.
Feel free to contact us with any questions or concerns.
Thanks,
[SRA curator]

==
[SRA submissions staff]
NCBI/NLM/NIH

----- Original Message -----

From: [SRA submitter] (DSHS);
Received: Thu Nov 19 2020 12:49:15 GMT-0500 (Eastern Standard Time)
To: Biosample Support;
Cc: [REDACTED] (b) (6);
Subject: Biosample/SRA retraction

Hello,

We submitted a biosample and SRA for this sample below by mistake. Can you please retract or delete this sample from NCBI?

| Sample | SAMN | SRR | Comments |
|----------------------|--------------|-------------|----------------|
| TX- DSHS- 1014 | SAMN16818263 | SRR13075049 | Not SARS-CoV-2 |

Thank you very much for your help!
[SRA Submitter]

From: Tabak, Lawrence (NIH/OD) [E] (b) (6)
Sent: Sunday, June 20, 2021 10:08 AM
To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Subject: Re: URGENT: Seeking your expert advice

FC sent to me. Thanks

Sent from my iPhone

On Jun 20, 2021, at 10:05 AM, Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6) wrote:

Thanks Larry. I will join at 3 pm. Shall I forward you the email exchange with Jesse and FC with the data withdrawal requests for background?

Cheers
Steve

From: Tabak, Lawrence (NIH/OD) [E] (b) (6)
Sent: Sunday, June 20, 2021 6:51 AM
To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Subject: FW: URGENT: Seeking your expert advice

Steve,
Sorry to have omitted you.
Larry

From: Tabak, Lawrence (NIH/OD) [E] (b) (6)
Sent: Saturday, June 19, 2021 12:31 PM

To: Collins, Francis (NIH/OD) [E] (b) (6); (b) (6); Garry, Robert F <rfgarry@TULANE.EDU>; spond@temple.edu; rasmus_nielsen@berkeley.edu; tbedford@fredhutch.org
Cc: Fauci, Anthony (NIH/NIAID) [E] (b) (6); Bloom PhD, Jesse D <jbloom@fredhutch.org>; Embry, Alan (NIH/NIAID) [E] (b) (6)
Subject: Re: URGENT: Seeking your expert advice

Colleagues,

When: tomorrow (Sunday 6/20) at 3 PM EDT

Please call: (b) (6)

Passcode: (b) (6)

Many thanks,
Larry

From: Francis Collins (b) (6)
Date: Saturday, June 19, 2021 at 11:07 AM
To: (b) (6), "Garry, Robert F" <rfgarry@TULANE.EDU>, "spond@temple.edu" <spond@temple.edu>, "rasmus_nielsen@berkeley.edu" <rasmus_nielsen@berkeley.edu>, "tbedford@fredhutch.org" <tbedford@fredhutch.org>
Cc: Anthony Fauci (b) (6), "Bloom PhD, Jesse D" <jbloom@fredhutch.org>, "Embry, Alan (NIH/NIAID) [E]" (b) (6), "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Subject: URGENT: Seeking your expert advice

Hi Kristian, Bob, Sergei, Rasmus, and Trevor,

Tony Fauci and I would like to get your advice on the interpretation and significance of a preprint that Jesse Bloom has just submitted to BioRxiv (attached). As you will see, through some clever sleuthing, Jesse has been able to discover 13 sequences of SARS-CoV-2 spike protein that were deposited (and then deleted) from the SRA by a Chinese investigator at Wuhan University. The sequences are incomplete but interesting, in that they appear to represent a slightly closer relationship to RaTG13 than the prior root of the phylogenetic tree.

Would you be willing to have a close read of the paper and then join a conference call with Jesse, Tony, and me tomorrow (Sunday 6/20) at 3 PM EDT? Steve Sherry of NCBI will also join – he has been digging out information about how these reads were removed from SRA by a request from the submitter, and assessing whether there might have been any other similar requests in early 2020.

Let me know if you can be available.

Thanks, Francis

From: Brennan, Patti (NIH/NLM) [E]
Sent: Sat, 19 Jun 2021 09:34:52 -0400
To: Pruitt, Kim (NIH/NLM/NCBI) [E]; Sherry, Steve (NIH/NLM/NCBI) [E]
Subject: Re: URGENT: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Thanks that is a helpful update- [REDACTED] (b) (5)

Patti

Patricia Flatley Brennan, RN, PhD
Director, National Library of Medicine
National Institutes of Health
US Department of Health and Human Services
Telework Hours 830-5 and by appt

From: Pruitt, Kim (NIH/NLM/NCBI) [E] [REDACTED] (b) (6)

Sent: Saturday, June 19, 2021 9:13:21 AM

To: Brennan, Patti (NIH/NLM) [E] [REDACTED] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E]

[REDACTED] (b) (6)

Subject: RE: URGENT: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Patti,

We are trying to find a way to contact people who work on SRA and trying to search Dynamics for prior communications. We don't have home phone numbers, trying to contact others who might possibly have that info.

The only way data is removed from SRA (per SOP) is if a submitter notifies us that the submission was in error. We would not delete data ourselves. Only submitters have that authority over their data.

Kim

Kim D. Pruitt, Ph.D
Senior Scientist
Chief, Information Engineering Branch, NCBI/NLM/NIH

Telework hours: 8:30 – 5:00

Phone: [REDACTED] (b) (6)

45 Center Drive
Building 45 Room 5AN44A
Bethesda, MD 20892-6511

From: Brennan, Patti (NIH/NLM) [E] [REDACTED] (b) (6)

Sent: Saturday, June 19, 2021 8:16 AM

To: Pruitt, Kim (NIH/NLM/NCBI) [E] [REDACTED] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E]

(b) (6)

Subject: Re: URGENT: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Please note the mailing list to the previous message and do not reply all!

Patti

Patricia Flatley Brennan, RN, PhD
Director, National Library of Medicine
National Institutes of Health
US Department of Health and Human Services
Telework Hours 830-5 and by appt

From: Brennan, Patti (NIH/NLM) [E] (b) (6)

Sent: Saturday, June 19, 2021 8:05:11 AM

To: Collins, Francis (NIH/OD) [E] (b) (6); Pruitt, Kim (NIH/NLM/NCBI) [E]
(b) (6)

Cc: Fauci, Anthony (NIH/NIAID) [E] (b) (6); Bloom PhD, Jesse D
(b) (6)

Subject: Re: URGENT: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Good morning colleagues

I just spoke to Francis and Steve Sherry. Steve is investigating the situation and will brief Francis later this morning

Patti

Patricia Flatley Brennan, RN, PhD
Director, National Library of Medicine
National Institutes of Health
US Department of Health and Human Services
Telework Hours 830-5 and by appt

From: Collins, Francis (NIH/OD) [E] (b) (6)

Sent: Saturday, June 19, 2021 7:37:59 AM

To: Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6)

Cc: Brennan, Patti (NIH/NLM) [E] (b) (6); Fauci, Anthony (NIH/NIAID) [E]
(b) (6); Bloom PhD, Jesse D <jbloom@fredhutch.org>

Subject: URGENT: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Hi Kim,

See note below and the attached rather stunning preprint. (b) (5)

(b) (5) I got an "out of office" from Steve saying he was gone until June 28. (b) (5)

(b) (5)

Please let me know right away what can be learned about this.

Francis

From: Collins, Francis (NIH/OD) [E]
Sent: Friday, June 18, 2021 10:01 PM
To: Bloom PhD, Jesse D <jbloom@fredhutch.org>; Sherry, Steve (NIH/NLM/NCBI) [E]
(b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: RE: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Dear Jesse,

This is truly intriguing. I'll be interested in Steve's thoughts about the deleted SRA entries and whether there is any way to recover information about how that happened.

Francis

From: Bloom PhD, Jesse D <jbloom@fredhutch.org>
Sent: Friday, June 18, 2021 7:00 PM
To: Collins, Francis (NIH/OD) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E]
(b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Hi Francis, Stephen, and Toni,

I'm just writing to give you a heads up that I identified a data set of early Wuhan SARS-CoV-2 sequences that has been deleted from the NIH's Sequence Read Archive (SRA). I was able to recover the deleted files from the Google Cloud and analyze the sequences, and have attached a pre-print on the analysis that I just submitted for posting by *bioRxiv*.

Since SARS-CoV-2 origins and early spread has become a hot-button topic, I wanted to give you a heads up. I made sure to emphasize in the discussion that the SRA has many sequences and so isn't in a position to vet all deletions. Nonetheless, I think it would be highly worthwhile to do a comprehensive analysis of SRA (and other NIH) data that might be relevant to this topic that could have been deleted or otherwise overlooked. If I can be of any assistance, let me know.

I have been running a pipeline to identify additional deleted SRA data using various heuristics including those in described in the attached pre-print, but have not yet completed the analysis enough to know the extent that the data I have recovered is relevant to SARS-CoV-2's origins or early spread. But as I mention in the pre-print, there are two known SRR deletions that are worth looking at. I definitely think it would be good to perform a SRA side search as well, since that will obviously be easier and more efficient, and could identify deleted data not on the cloud.

Anyway, I hope overall this can be a good opportunity for the NIH to take the lead by using its remarkable data archives to make progress in resolving some of the important questions about the virus's origins.

Thanks,
Jesse

Jesse Bloom
Associate Professor, Fred Hutch Cancer Research Center
Affiliate Associate Professor, Genome Sciences & Microbiology, University of Washington
Investigator, Howard Hughes Medical Institute

From: [Bloom PhD, Jesse D](#)
To: [Sherry, Steve \(NIH/NLM/NCBI\) \[E\]](#)
Subject: Question regarding two deleted and then restored deep sequencing runs
Date: Tuesday, October 12, 2021 1:20:00 AM

Hi Steve,

I'm writing to inquire about some more deleted deep sequencing runs from China on the SRA.

As you may know, two runs related to pangolin coronavirus sequences from China, SRR11119760 and SRR11119761 were deleted from the SRA on March-16-2020 by curator (b) (6) at the request of the submitter (b) (6) of South China Agricultural University under the stated rationale that they were accidental uploads unrelated to the project.

But a puzzling thing about these accessions is that they then re-appeared on the SRA over a year later, on or about June-16-2021.

To understand why they reappeared over a year after being deleted, an investigative entity sent a request to the NLM / NIH for all correspondence related to these accessions in the period spanning March of 2020 through June of 2021.

The documents that were provided in response to this request did not indicate any further correspondence between the submitters in China and the SRA after March of 2020 regarding these two samples.

We are therefore trying to understand the process and rationale by which the two deleted sequencing runs were again made available on the SRA. My understanding from your previous explanations is that once datasets are removed at a submitter's request, they are only restored if the submitter requests that. Yet the documents provided by NLM / NIH do not indicate that South China Agricultural University made any request to restore these accessions.

I am therefore wondering, which of the following is the case:

1. Was there in fact a request from South China Agricultural University to restore these sequences that was omitted from the documents provided by NLM / NIH?
2. Did the NCBI restore these sequences to public access without a request from South China Agricultural University? If so, what was the rationale and process for this restoration?

Thanks for your help in looking into this.

--Jesse

--

Jesse Bloom
Professor, Fred Hutchinson Cancer Research Center
Investigator, Howard Hughes Medical Institute

From: [Bloom PhD, Jesse D](#)
To: [Sherry, Steve \(NIH/NLM/NCBI\) \[E\]](#)
Subject: Re: Proposal for searching all deleted/suppressed SRA datasets
Date: Tuesday, October 5, 2021 4:36:28 PM

OK, thanks for at least considering and getting back in touch about the idea.

Thanks,
Jesse

Jesse Bloom
Professor, Fred Hutch Cancer Research Center
Affiliate Professor, Genome Sciences & Microbiology, University of Washington
Investigator, Howard Hughes Medical Institute

From: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Date: Tuesday, October 5, 2021 at 10:05 AM
To: Bloom PhD, Jesse D <jbloom@fredhutch.org>
Subject: RE: Proposal for searching all deleted/suppressed SRA datasets

Hi Jesse,

I appreciate you reaching out. As you know, when data are withdrawn from the database, that status does not permit use for further analyses. Withdrawn data are kept purely for preservation purposes; therefore, we are unable to collaborate with you to perform the analyses you have suggested.

Steve

From: Bloom PhD, Jesse D <jbloom@fredhutch.org>
Sent: Monday, September 27, 2021 12:25 AM
To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Subject: Proposal for searching all deleted/suppressed SRA datasets

Hi Steve,

Hope all is well.

I wanted to reach out to you with a proposal to search all deleted deep sequencing datasets on the SRA for sequences that might be relevant to SARS-CoV-2. Apologies if you also hear about this idea from others as I have been running it by various others for feedback too, but I figured maybe I should directly get in touch with you as well.

As you probably know, the question is whether any datasets might have been deleted or suppressed

that contained sequences relevant to SARS-CoV-2. These could either be viral sequences or sequences with just contamination from viral reads.

I have been able to build a list of 122,904 accessions (SRR, ERR, and DRR) that became “suppressed” (which includes both suppressed and killed in the terminology of the INSDC status document) between 2018-12-02 and 2021-08-10. For most of them, I’ve also been able assemble relevant metadata such as dates of status changes, number of reads, md5 checksums, and in some cases other information. From this information, I’ve been able to partially prioritize them. I downloaded and analyzed as many as are still available through the SRA or Google / Amazon cloud, which is unfortunately only 1829 of the 122,904. Of the remaining, based on the metadata I rank 565 as being of the highest priority, 2822 of medium priority, 29160 of moderate priority, and 88528 of lower priority. I am trying to obtain more of these datasets from other sources (there are a few organizations that download and store large amounts of SRA data), but I’m sure I will not be able to get many of them.

I read in the [Wall Street Journal article a few weeks ago](#) how the SRA keeps copies of all accessions even if they have been removed from public access. So my proposal is that we come up with some strategy to analyze all of these deleted accessions. I have scalable Snakemake pipelines that can process this number of sequences, first to identify those with SARS-CoV-2 reads, and then place those reads in a phylogenetic context to identify any more “ancestral” looking sequences. Here on the Hutch cluster I could process ~100,000 accessions in somewhere between 2-6 weeks depending on how much time is needed to transfer the files, and the pipelines should be relatively portable to run on another cluster if that is preferable.

I think that doing this type of analysis could be consistent with INSDC policy. For instance, the [main INSDC policy page](#) actually says that data submitted to the INSD will always remain permanently accessible. Although [the INSDC status page](#) conflictingly says in rare cases data can be killed, it still says there is no prior restraint on its use. Furthermore, the analysis would naturally discard all non-coronavirus reads, which would be the entirety of most datasets.

This approach could also help resolve some of the confusion about sequence deletions. I am now getting inquiries from congressional staff who are asking if the deletion of PRJNA612766 by Wuhan University was “proper” or should be investigated more. I explain that this question sort of misses the point: under INSDC status document policy, it is allowed for submitters to remove data. The correct question is not if the SRA was wrong to remove that project, but rather we are now doing everything we can to see if there is anything else of relevance now that we know these deletions can occur. I think this is especially important given the [recent revelations about the DARPA DEFUSE proposal](#) that highlight the possibility that there could be information relevant to SARS-CoV-2 that has been overlooked in the public discussion.

Finally, this could all be set up in a totally transparent way. For instance, the pipelines could be made available ahead of time along with the lists of accessions, and summary statistics could be output publicly. Therefore, in contrast to the brewing battles and investigations related to COVID-19 origins, for this part everything could be done totally transparently in a scientific framework that isn’t susceptible to speculation and doubt.

Anyway, let me know if you have any interest in chatting more about the possibility of some approach along these lines.

Also, I just wanted to mention that it turns out that I think there was an error in the statement the [NIH gave to the *Washington Post*](#) about the original Wuhan University deletions, where they said there were just 8 deletions and the rest were from submitters “predominantly in the US.” There were *at least* two other full-BioProject deletions that involves SARS-CoV-2-related reads: PRJNA637497 and PRJNA640246.

Thanks for considering all of this, and just let me know if there might be a chance to chat more.

--Jesse

--

Jesse Bloom
Professor, Fred Hutchinson Cancer Research Center
Investigator, Howard Hughes Medical Institute

From: [Bloom PhD, Jesse D](#)
To: [Sherry, Steve \(NIH/NLM/NCBI\) \[E\]](#)
Subject: Re: SARS-CoV-2 data deleted from the NIH/NCBI SRA
Date: Sunday, June 27, 2021 9:10:09 AM

Hi Steve,

I was writing to ask if the NCBI sill plans to compile a detailed report of all the SRA deletions, and if so whether it will be shared? I have several meetings next week with congressional staffers who were interested in the deletions, and I'm sure they will be asking about this.

As mentioned before, I'd be happy to help analyze any SRA data for anything relevant to SARS-CoV-2. I'm also still really curious about the second Wuhan University BioProject mentioned in the e-mail you forwarded last Saturday, as I don't think I've been able to identify that one.

Thanks,
Jesse

--

Jesse Bloom
Associate Professor, Fred Hutchinson Cancer Research Center
Investigator, Howard Hughes Medical Institute

From: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Date: Saturday, June 19, 2021 at 7:34 AM
To: Collins, Francis (NIH/OD) [E] (b) (6), Bloom PhD, Jesse D <jbloom@fredhutch.org>, Fauci, Anthony (NIH/NIAID) [E] (b) (6), Brennan, Patti (NIH/NLM) [E] (b) (6)
Cc: Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6)
Subject: RE: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Dear Francis and Jesse,

Below is the June 2020 exchange between Wuhan University and SRA submission staff. I have redacted names and the withdrawal request tracking ID for privacy. Please read from the bottom up.

I would note that this request was received and processed according to SRA policy. As Jesse notes in his manuscript, submitters own their SRA records and can withdraw them upon request. SRA does not adjudicate the reason.

More generally, I have requested the SRA team to compile a report of all withdrawn SARS-COV2 data so there is transparency into the status of all SRA SARS-COV2 sequence submissions. I will share the report as soon as it is available.

Kind regards,
Steve

(data withdrawal correspondence) -----

Dear [SRA],

Thanks for your replay. Yes, I want to withdraw both 2 submissions XXXXX and YYYYY. The Bioprojects, Biosamples and all SRA objects should be withdrawn as well.

Best regards,

[Submitter]

Wuhan University

From: [NLM Support](#)
Date: 2020-06-16 21:00
To: [\[submitter\]](#)
Subject: Re: SUBXXXXX/subs/sra/SUBXXXXX/overview
Dear [Submitter],

Do you want to withdraw all SRA objects created in your account?
here are 2 submissions XXXX and YYYYY.
Also, bioprojects and biosamples whould be withdrawn as well, right?

Best regards,

[SRA curator]

If you have any questions or concerns regarding your **SRA** submission please don't hesitate to contact sra@ncbi.nlm.nih.gov (applies to new questions).

We normally respond within 2 business days.

[SRA curator]
The NCBI SRA database submission staff

Summary: Re: SUBXXXXX/subs/sra/SUBXXXXX/overview

Details:
Dear Mr/Ms,

Recently, I found that it's hard to visit my submitted SRA data, and it would also be very difficult for me to update the data. I have submitted an updated version of this SRA data to another website, so I want to withdraw the old one at NCBI in order to avoid the data version issue. The Submission ID is XXXX. I would appreciate your help.

Best regard,

—
[Submitter]

Wuhan University

From: Collins, Francis (NIH/OD) [E] (b) (6)
Sent: Friday, June 18, 2021 10:01 PM
To: Bloom PhD, Jesse D <jbloom@fredhutch.org>; Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: RE: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Dear Jesse,

This is truly intriguing. I'll be interested in Steve's thoughts about the deleted SRA entries and whether there is any way to recover information about how that happened.

Francis

From: Bloom PhD, Jesse D <jbloom@fredhutch.org>
Sent: Friday, June 18, 2021 7:00 PM
To: Collins, Francis (NIH/OD) [E] (b) (6); Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Hi Francis, Stephen, and Toni,

I'm just writing to give you a heads up that I identified a data set of early Wuhan SARS-CoV-2 sequences that has been deleted from the NIH's Sequence Read Archive (SRA). I was able to recover the deleted files from the Google Cloud and analyze the sequences, and have attached a pre-print on the analysis that I just submitted for posting by *bioRxiv*.

Since SARS-CoV-2 origins and early spread has become a hot-button topic, I wanted to give you a heads up. I made sure to emphasize in the discussion that the SRA has many sequences and so isn't in a position to vet all deletions. Nonetheless, I think it would be highly worthwhile to do a comprehensive analysis of SRA (and other NIH) data that might be relevant to this topic that could have been deleted or otherwise overlooked. If I can be of any assistance, let me know.

I have been running a pipeline to identify additional deleted SRA data using various heuristics including those in described in the attached pre-print, but have not yet completed the analysis enough to know the extent that the data I have recovered is relevant to SARS-CoV-2's origins or early spread. But as I mention in the pre-print, there are two known SRR deletions that are worth looking at. I definitely think it would be good to perform a SRA side search as well, since that will obviously

be easier and more efficient, and could identify deleted data not on the cloud.

Anyway, I hope overall this can be a good opportunity for the NIH to take the lead by using its remarkable data archives to make progress in resolving some of the important questions about the virus's origins.

Thanks,
Jesse

Jesse Bloom
Associate Professor, Fred Hutch Cancer Research Center
Affiliate Associate Professor, Genome Sciences & Microbiology, University of Washington
Investigator, Howard Hughes Medical Institute

(b) (6)

From: Sherry, Steve (NIH/NLM/NCBI) [E]
Sent: Wednesday, June 23, 2021 8:38 AM
To: Bloom PhD, Jesse D
Subject: Re: NCBI deletion explanation e-mail

Hi Jesse, please refer them to NIH or NLM. NIH should communicate about submission activities.

cheers,
Steve

From: Bloom PhD, Jesse D <jbloom@fredhutch.org>
Sent: Tuesday, June 22, 2021 9:28:08 PM
To: Sherry, Steve (NIH/NLM/NCBI) [E] (b) (6)
Subject: NCBI deletion explanation e-mail

Hi Steve,

A number of people have started asking me what is the reason that was given for the e-mail request to delete the project. At this point I have just said that you shared that e-mail request with me (redacted), but that they should go to you (or NIH) to ask for it.

Should I continue to do that, or should I just directly share the redacted e-mail request you set me?

Thanks,
Jesse

--
Jesse Bloom
Associate Professor, Fred Hutchinson Cancer Research Center
Investigator, Howard Hughes Medical Institute

From: [Bloom PhD, Jesse D](#)
To: [Collins, Francis \(NIH/OD\) \[E\]](#); [Sherry, Steve \(NIH/NLM/NCBI\) \[E\]](#); [Embry, Alan \(NIH/NIAID\) \[E\]](#)
Subject: pre-print posted
Date: Tuesday, June 22, 2021 5:16:45 PM

Hi Francis, Steve, and Alan,

Just wanted to let you know that the pre-print recently posted on *bioRxiv* at:

<https://www.biorxiv.org/content/10.1101/2021.06.18.449051v1>

I also posted a Twitter thread that goes through and summarizes it:

https://twitter.com/jbloom_lab/status/1407445604029009923

Thanks again for handling and looking into this all so responsively even over last weekend, and let me know if I can be of any help in continued efforts to better understand the early spread of the virus.

Thanks,
Jesse

Jesse Bloom

Associate Professor, Fred Hutch Cancer Research Center

Affiliate Associate Professor, Genome Sciences & Microbiology, University of Washington

Investigator, Howard Hughes Medical Institute

From: [Brennan, Patti \(NIH/NLM\) \[E\]](#)
To: [Bloom PhD, Jesse D](#); [Collins, Francis \(NIH/OD\) \[E\]](#); [Pruitt, Kim \(NIH/NLM/NCBI\) \[E\]](#); [Sherry, Steve \(NIH/NLM/NCBI\) \[E\]](#)
Cc: [Fauci, Anthony \(NIH/NIAID\) \[E\]](#)
Subject: Re: URGENT: SARS-CoV-2 data deleted from the NIH/NCBI SRA
Date: Saturday, June 19, 2021 9:08:25 AM

Thanks Jesse

Copying Steve for coordination

Patti

Patricia Flatley Brennan, RN, PhD
Director, National Library of Medicine
National Institutes of Health
US Department of Health and Human Services
Telework Hours 830-5 and by appt

From: Bloom PhD, Jesse D <jbloom@fredhutch.org>
Sent: Saturday, June 19, 2021 8:49:10 AM
To: Brennan, Patti (NIH/NLM) [E] (b) (6); Collins, Francis (NIH/OD) [E] (b) (6); Pruitt, Kim (NIH/NLM/NCBI) [E] (b) (6)
Cc: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: Re: URGENT: SARS-CoV-2 data deleted from the NIH/NCBI SRA

By the way, one important point that could be helpful for generally explaining SRA deletions so people don't become *overly* conspiratorial: it is possible to identify what appear to be non-suspicious SRA deletions as well. It might be worth seeing if NCBI can validate information on these non-suspicious deletions to make clear that there is such a thing as a legitimate deletion.

I wholeheartedly agree with Francis's suggestion that it's crucial to identify any other deletions that could shed light on the origins or early spread of the virus. But I would also hate for anyone to misconstrue that a SRA curator has done anything personally wrong by removing an accession, given that these curators are responsible for handling >13-million accessions. For this reason, it would also be helpful to be able to point to the existence of legitimate deletions as well as highly suspicious ones. Below are two examples of what I *think* are probably legitimate deletions based just on looking at SRR numbers. If NCBI can validate that fact, we can be sure to mention these examples as well if there are questions about how deletions work.

Specifically, SRR13075049 is another SARS-CoV-2 related sequencing run that is also deleted (<https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR13075049>). But at least based on the nearby SRR numbers, this appears to be a run from a sequencing project by the Texas State Department of Public Health (<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA639066>), and so probably they deleted it after making some mistake in the upload or sample labeling. Similarly with SRR11607649 and a Utah public health lab.

--

Jesse Bloom
Associate Professor, Fred Hutchinson Cancer Research Center
Investigator, Howard Hughes Medical Institute

From: Brennan, Patti (NIH/NLM) [E] [REDACTED] (b) (6)
Date: Saturday, June 19, 2021 at 5:05 AM
To: Collins, Francis (NIH/OD) [E] [REDACTED] (b) (6), Pruitt, Kim (NIH/NLM/NCBI) [E]
[REDACTED] (b) (6)
Cc: Fauci, Anthony (NIH/NIAID) [E] [REDACTED] (b) (6), Bloom PhD, Jesse D
<jbloom@fredhutch.org>
Subject: Re: URGENT: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Good morning colleagues

I just spoke to Francis and Steve Sherry. Steve is investigating the situation and will brief Francis later this morning

Patti

Patricia Flatley Brennan, RN, PhD
Director, National Library of Medicine
National Institutes of Health
US Department of Health and Human Services
Telework Hours 830-5 and by appt

From: Collins, Francis (NIH/OD) [E] [REDACTED] (b) (6)
Sent: Saturday, June 19, 2021 7:37:59 AM
To: Pruitt, Kim (NIH/NLM/NCBI) [E] [REDACTED] (b) (6)
Cc: Brennan, Patti (NIH/NLM) [E] [REDACTED] (b) (6); Fauci, Anthony (NIH/NIAID) [E]
[REDACTED] (b) (6); Bloom PhD, Jesse D <jbloom@fredhutch.org>
Subject: URGENT: SARS-CoV-2 data deleted from the NIH/NCBI SRA

Hi Kim,

See note below and the attached rather stunning preprint. [REDACTED] (b) (5)
[REDACTED]. I got an "out of office" from Steve saying he was gone until June
28. [REDACTED] (b) (5)

[REDACTED]
[REDACTED]

Please let me know right away what can be learned about this.

Francis

From: Collins, Francis (NIH/OD) [E]
Sent: Friday, June 18, 2021 10:01 PM
To: Bloom PhD, Jesse D <jbloom@fredhutch.org>; Sherry, Steve (NIH/NLM/NCBI) [E]
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