From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Fri, 28 Feb 2020 00:47:19 +0000
To: Mark Zuckerberg
Subject: RE:

Mark:

Thanks for the note. If we start in April (~6-7 weeks from now) with a phase 1 trial of 45 subjects, it will take another 3-4 months to determine safety and some immunogenicity. The next step is phase 2 for efficacy. We may need help with resources for the phase 2 trial if we do not get our requested budget supplement. I believe that we will be OK. If this goes off track, I will contact you. Many thanks for the offer. Much appreciated.

Best regards,

Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: (b) (6)
FAX: (301) 496-4409
E-mail: (b) (6)
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From: Mark Zuckerberg (b) (6)
Sent: Thursday, February 27, 2020 7:16 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)>
Subject:

Tony:

I was glad to hear your statement that the covid-19 vaccine will be ready for human trials in six weeks. Are there any resources our foundation can help provide to potentially accelerate this or at least make sure it stays on track?

Mark

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Tue, 3 Mar 2020 03:26:29 +0000
To: Collins, Francis (NIH/OD) [E];Giroir, Brett (HHS/OASH)
Cc: Steele, Danielle (HHS/IOS);Tabak, Lawrence (NIH/OD) [E]
Subject: RE: SARS CoV-2 in humanized mice

Ditto.

From: Collins, Francis (NIH/OD) [E] (b) (6)
Sent: Monday, March 2, 2020 9:32 PM
To: Giroir, Brett (HHS/OASH) (b) (6)>
Cc: Fauci, Anthony (NIH/NIAID) [E] < (b) (6)>; Steele, Danielle (HHS/IOS) (b) (6); Tabak, Lawrence (NIH/OD) [E] < (b) (6)
Subject: RE: SARS CoV-2 in humanized mice

Larry has it right. Tony may want to add.

Francis

From: Tabak, Lawrence (NIH/OD) [E] (b) (6)
Sent: Monday, March 2, 2020 8:14 PM
To: Giroir, Brett (HHS/OASH) (b) (6)>
Cc: Collins, Francis (NIH/OD) [E] (b) (6)>; Fauci, Anthony (NIH/NIAID) [E] (b) (6)>; Steele, Danielle (HHS/IOS) (b) (6)
Subject: Re: SARS CoV-2 in humanized mice

Brett,

Tony or Francis may offer additional insight, but the (b) (5)
.

I hope this helps.
Larry

From: "Giroir, Brett (HHS/OASH)" < (b) (6)>
Date: Monday, March 2, 2020 at 7:25 PM
To: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)>
Cc: Francis Collins (b) (6)>, Anthony Fauci (b) (6)>, "Steele, Danielle (HHS/IOS)" (b) (6)>, "Giroir, Brett (HHS/OASH)" (b) (6)
Subject: RE: SARS CoV-2 in humanized mice

Dear Larry,

Thank you for your patience. The question has been raised, [redacted] (b) (5)

I appreciate your willingness to continue to work on this and respond to the questions that I am receiving.

V/r
Brett

Brett P. Giroir, MD
ADM, US Public Health Service
Assistant Secretary for Health (ASH)
200 Independence Avenue, SW
Washington, DC 20201
Office Phone: [redacted] (b) (6)

From: Tabak, Lawrence (NIH/OD) [E] [redacted] (b) (6)
Sent: Thursday, February 20, 2020 5:29 PM
To: Giroir, Brett (HHS/OASH) [redacted] (b) (6)>
Cc: Collins, Francis (NIH/OD) [E] [redacted] (b) (6)>; Fauci, Anthony (NIH/NIAID) [E] [redacted] (b) (6); Steele, Danielle (HHS/IOS) [redacted] (b) (6)>
Subject: Re: SARS CoV-2 in humanized mice

Brett,
I have discussed with both Francis and Tony [redacted] (b) (5)

With regard to your questions:

[redacted] (b) (5)

(b) (5)



Hope this is helpful. Please let me know if you require additional information.
Best wishes,
Larry

From: "Giroir, Brett (HHS/OASH)" (b) (6)>
Date: Thursday, February 20, 2020 at 12:32 PM
To: "Tabak, Lawrence (NIH/OD) [E]" < (b) (6)
Cc: "Steele, Danielle (HHS/IOS)" (b) (6)
Subject: RE: SARS CoV-2 in humanized mice

Can you give me a quick call?

(b) (5)

Brett P. Giroir, MD
ADM, US Public Health Service
Assistant Secretary for Health (ASH)
200 Independence Avenue, SW
Washington, DC 20201
Office Phone: (b) (6)

From: Tabak, Lawrence (NIH/OD) [E] (b) (6)
Sent: Thursday, February 20, 2020 12:19 PM
To: Giroir, Brett (HHS/OASH) (b) (6)>
Cc: Steele, Danielle (HHS/IOS) (b) (6)>
Subject: Re: SARS CoV-2 in humanized mice

(b) (5)

Thanks
Larry

From: "Giroir, Brett (HHS/OASH)" (b) (6)>
Date: Thursday, February 20, 2020 at 12:17 PM
To: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Cc: "Steele, Danielle (HHS/IOS)" (b) (6)
Subject: RE: SARS CoV-2 in humanized mice

Larry

(b) (5)

Brett P. Giroir, MD
ADM, US Public Health Service
Assistant Secretary for Health (ASH)
200 Independence Avenue, SW
Washington, DC 20201
Office Phone: (b) (6)

From: Tabak, Lawrence (NIH/OD) [E] (b) (6)
Sent: Wednesday, February 19, 2020 11:04 PM
To: Giroir, Brett (HHS/OASH) (b) (6)
Cc: Steele, Danielle (HHS/IOS) (b) (6)
Subject: FW: SARS CoV-2 in humanized mice

Brett,

(b) (5)

Thanks for your consideration,
Larry

From: "Hasenkrug, Kim (NIH/NIAID) [E]" (b) (6)
Date: Wednesday, February 19, 2020 at 5:50 PM

To: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Subject: SARS CoV-2 in humanized mice

Hi Dr. Tabak, (b) (5)

(b) (5)

Best regards,

Kim

Kim J Hasenkrug, Ph.D.
Senior Investigator
Chief, Retroviral Immunology Section
Laboratory of Persistent Viral Diseases
Rocky Mountain Laboratories
National Institute of Allergy and Infectious Diseases
National Institutes of Health
903 S. 4th Street
Hamilton, MT 59840
(b) (6)

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From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Mon, 2 Mar 2020 00:48:25 +0000
To: Cassetti, Cristina (NIH/NIAID) [E];Giroir, Brett (HHS/OASH)
Cc: Conrad, Patricia (NIH/NIAID) [E]
Subject: RE: COVID and Chloroquine

Thanks, Cristina

From: Cassetti, Cristina (NIH/NIAID) [E] (b) (6)>
Sent: Sunday, March 1, 2020 7:06 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6) Giroir, Brett (HHS/OASH)
(b) (6)
Cc: Conrad, Patricia (NIH/NIAID) [E] (b) (6)>
Subject: RE: COVID and Chloroquine

Hi,

Sorry for the late response, I just flew back from (b) (6).

NIAD doesn't have ongoing trials with chloroquine and I heard that such trials are being conducted in China.

We are planning to evaluate chloroquine in animal models ASAP. If any therapeutic with a good clinical safety profile (like chloroquine) appears to be effective in vivo against COVID-19, we are planning to quickly add to them to the Remdesivir therapeutic trial as another arm.

Let me know if you have other questions.

Kind regards,

Cristina

Cristina Cassetti, Ph.D.
Deputy Director
Division of Microbiology and Infectious Diseases
National Institute of Allergy and Infectious Diseases, NIH
5601 Fishers Lane, Room 7G51
Rockville, MD 20852
Tel: (b) (6)
(b) (6)

From: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Sent: Saturday, February 29, 2020 8:20 PM

To: Giroir, Brett (HHS/OASH) (b) (6)>
Cc: Cassetti, Cristina (NIH/NIAID) [E] (b) (6)>; Conrad, Patricia (NIH/NIAID) [E] (b) (6)>
Subject: RE: COVID and Chloroquine
Importance: High

Brett:
Thanks for the note. I will run this by the people in our Program and get back to you.
Best,
Tony

Cristina:
Are we or anyone else doing anything with clinical trials and chloroquine for COVID-19? Please respond directly to ADM Giroir.
Thanks,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
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From: Giroir, Brett (HHS/OASH) (b) (6)>
Sent: Saturday, February 29, 2020 9:31 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: COVID and Chloroquine

You know the old data and the new data. New in vitro look promising.
Do you have good visibility on the trials being conducted? Or is NIH running any of these?

Your time is precious, so 10 word response sufficient.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 22 Feb 2020 12:06:10 +0000
To: Cassetti, Cristina (NIH/NIAID) [E]
Subject: FW: DEAR TONY: CORONAVIRUS

Please handle.

From: Dr. Michael Jacobs (b) (6) >
Sent: Friday, February 21, 2020 6:14 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6) >
Cc: Alexander Tarakhovsky (b) (6); Lockshin, Michael MD (b) (6); Dr. Michael Jacobs (b) (6) >
Subject: DEAR TONY: CORONAVIRUS

dear tony:

i am a cornell medical school cumc (b) (6) graduate. i am associate professor of dermatology at weill-cornell in private practice. (b) (6) alexander tarakhovsky is (b) (6) and a professor at rockefeller university. he is a virologist.

we have been following the corona virus pandemic closely, and a few days ago became alarmed at the news that the chinese government is sterilizing their paper money from hubei province.

we think that there is a possibility that the virus was released from a lab in wuhan, the biotech area of china. we also think that the virus might be complexed with another organism, such as a yeast or fungus, to make it more sticky.

we would like to discuss this with you further. we feel that immediate action must be taken by united states scientists to try to neutralize this threat.

please contact alexander and me at your earliest convenience at above emails or my mobile (b) (6) or office (b) (6) michael lockshin gave me your email.

with kind regards

michael jacobs

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Tue, 5 May 2020 13:00:29 +0000
To: Lipkin, Ian W.
Subject: RE: SARS-CoV-2

Thanks, Ian. I hope that you are well.
Best,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: (b) (6)
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From: Lipkin, Ian W. (b) (6)
Sent: Tuesday, May 5, 2020 8:39 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: Fwd: SARS-CoV-2

Tony,
(b) (4) This prompted the letter I sent to him last evening to which he responded this morning. I dont expect a response but wanted to keep you updated. We deeply appreciate your efforts in steering and messaging.

All my best,
Ian

Ps. Skoll just invested $5M in piloting the GIDEoN international capacity building and surveillance network that includes Cliff and others in your intramural team.

Begin forwarded message:

From: ZhuChen (b) (6)>
Subject: Re:SARS-CoV-2
Date: May 5, 2020 at 8:16:23 AM EDT
To: Lipkin, Ian W. (b) (6)>

Dear Ian,
Thank you for your email detailing the (b) (4)
(b) (4)
(b) (4). I shall keep you informed of any progress in the coming weeks.
Best,
Zhu

---------- Original ----------
From: "Lipkin, Ian W. (b) (6);
Date: Tue, May 5, 2020 06:06 AM
To: "ZhuChen' (b) (6)>;
Subject: SARS-CoV-2

Dear Zhu,
The COVID-19 pandemic poses an unprecedented threat not only to global public health but also to economic and political stability. Uncertainty about the origin of COVID-19 pandemic is causing friction worldwide, particularly between China and the United States. There is agreement that the causative agent, SARS-CoV-2 originated in a bat. There is also a high level of confidence that the virus was not deliberately modified in any laboratory. What we do not know is the answers to two questions: (1) whether a precursor virus circulated in the human population before it evolved to become a pandemic virus and (2) whether a precursor virus adapted to humans by first passing through another animal. (b) (4)



With great affection,
Ian
W. Ian Lipkin, MD
John Snow Professor of Epidemiology and Director
Center for Infection and Immunity
Mailman School of Public Health

Professor of Pathology and Neurology
College of Physicians & Surgeons
Columbia University
722 West 168th Street, 17th Floor
New York, NY 10032
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Email: (b) (6)

Administrative Coordinator
(b) (6)

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From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Mon, 20 Apr 2020 01:25:42 +0000
To: bgertz@washingtontimes.com
Cc: Miller, Katie R. EOP/OVP;Short, Marc T. EOP/OVP
Subject: Scientific paper on origin of coronavirus

Bill:

Here are the links to the scientific papers and a commentary about the scientific basis of the origins of SARS-Cov-2.

The proximal origin of SARS-CoV-2. Andersen KG, Rambaut A, Lipkin WI, **Holmes** EC, Garry RF. Nat Med. 2020 Apr;26(4):450-452. doi: 10.1038/s41591-020-0820-9. No abstract available.
A Genomic Perspective on the Origin and Emergence of SARS-CoV-2.Zhang YZ, **Holmes** EC. Cell. 2020 Apr 16;181(2):223-227. doi: 10.1016/j.cell.2020.03.035. Epub 2020 Mar 26.
Also this statement from Eddie Holmes
https://bit.ly/2ym1UGe

Best regards,
Tony

Anthony S. Fauci, MD
Director
National Institute of Allergy and Infectious Diseases
Building 31, Room 7A-03
31 Center Drive, MSC 2520
National Institutes of Health
Bethesda, MD 20892-2520
Phone: (b) (6)
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> On Apr 19, 2020, at 2:21 PM, Bill Gertz <bgertz@washingtontimes.com> wrote:
>
> Katie,
>
> Dr. Fauci on Friday said he would share a scientific paper with the press on the origin of the coronavirus. Can you please help me get a copy of that paper? Thanks in advance.
>
> Bill Gertz
>
> ---

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 19 Apr 2020 03:29:42 +0000
To: Peter Daszak
Subject: RE: Thank you for your public comments re COVID-19's origins

Peter:
Many thanks for your kind note.
Best regards,
Tony

From: Peter Daszak (b) (6)
Sent: Saturday, April 18, 2020 9:43 PM
To: Morens, David (NIH/NIAID) [E] (b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6)>
Cc: Stemmy, Erik (NIH/NIAID) [E] (b) (6)>; Erbelding, Emily (NIH/NIAID) [E] (b) (6)>; Aleksei Chmura (b) (6)
Subject: Thank you for your public comments re COVID-19's origins
Importance: High

Tony (cc'ing David so that you might pass this on to Tony once he has a spare second)

As the PI of the R01 grant publicly targeted by Fox News reporters at the Presidential press briefing last night, I just wanted to say a personal thankyou on behalf of our staff and collaborators, for publicly standing up and stating that the scientific evidence supports a natural origin for COVID-19 from a bat-to-human spillover, not a lab release from the Wuhan Institute of Virology.

(b) (7)(A)

From my perspective, your comments are brave, and coming from your trusted voice, will help dispel the myths being spun around the virus' origins.

Once this pandemic's over I look forward thanking you in person and let you know how important your comments are to us all.

Cheers,

Peter

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Thu, 19 Mar 2020 01:59:12 +0000
To: Lerner, Andrea (NIH/NIAID) [E]
Subject: FW: Coronavirus

Please respond to this person.

-----Original Message-----
From: Beth Abramson (b) (6)>
Sent: Wednesday, March 18, 2020 9:58 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)>
Subject: Coronavirus

Wondering whether it has been considered that only the vulnerable population (those over 60 and/or those with underlying health conditions)be isolated ? I am a (b) (6)psychiatrist and after contemplating this option was wondering if this could still reduce the risk to healthcare Systems with less disruption to our society. I await your response and appreciate all you are doing. Beth Abramson MD (b) (6)

Sent from my iPhone

From: (b) (6)
Sent: Sun, 8 Mar 2020 09:23:28 -0400
To: Kristian G. Andersen
Cc: Jeremy Farrar;Collins, Francis (NIH/OD) [E];Robert Garry;Edward Holmes;Andrew Rambaut;Ian Lipkin;Chris Emery
Subject: Re: SARS-CoV-2 article to be published in Nature Medicine

Kristian:
Thanks for your note. Nice job on the paper.
Tony

On Mar 6, 2020, at 4:23 PM, Kristian G. Andersen (b) (6) wrote:

Dear Jeremy, Tony, and Francis,

Thank you again for your advice and leadership as we have been working through the SARS-CoV-2 'origins' paper. We're happy to say that the paper was just accepted by Nature Medicine and should be published shortly (not quite sure when).

To keep you in the loop, I just wanted to share the accepted version with you, as well as a draft press release. We're still waiting for proofs, so please let me know if you have any comments, suggestions, or questions about the paper or the press release.

Tony, thank you for your straight talk on CNN last night - it's being noticed.

Best,
Kristian

Kristian G. Andersen, PhD
Associate Professor, Scripps Research
Director of Infectious Disease Genomics, Scripps Research Translational Institute
Director, Center for Viral Systems Biology

The Scripps Research Institute
10550 North Torrey Pines Road, SGM-300A
Department of Immunology and Microbial Science
La Jolla, CA 92037

(b) (6)

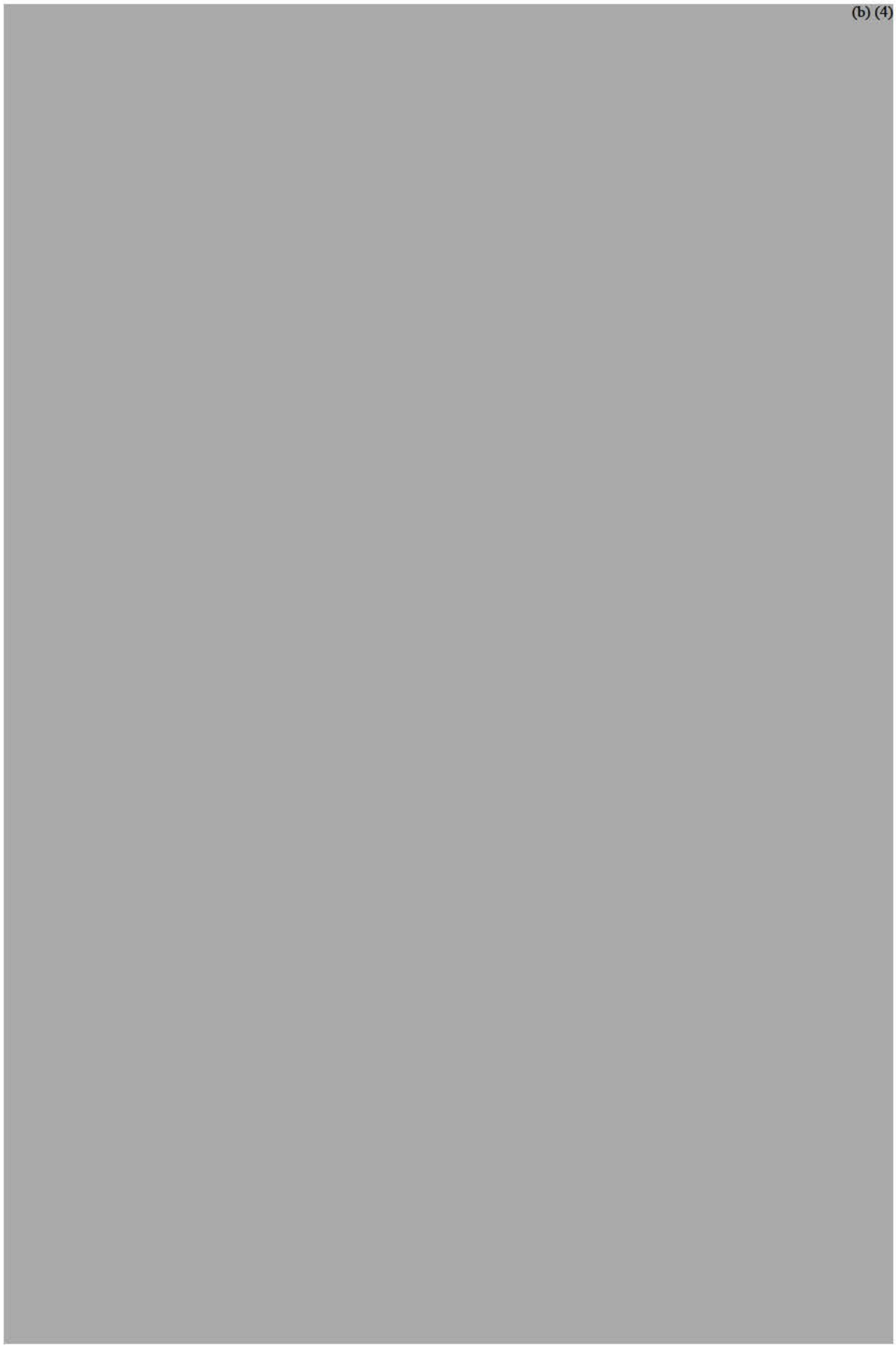
From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 7 Mar 2020 13:23:54 +0000
To: (b) (6)
Subject: FW: (b) (4)

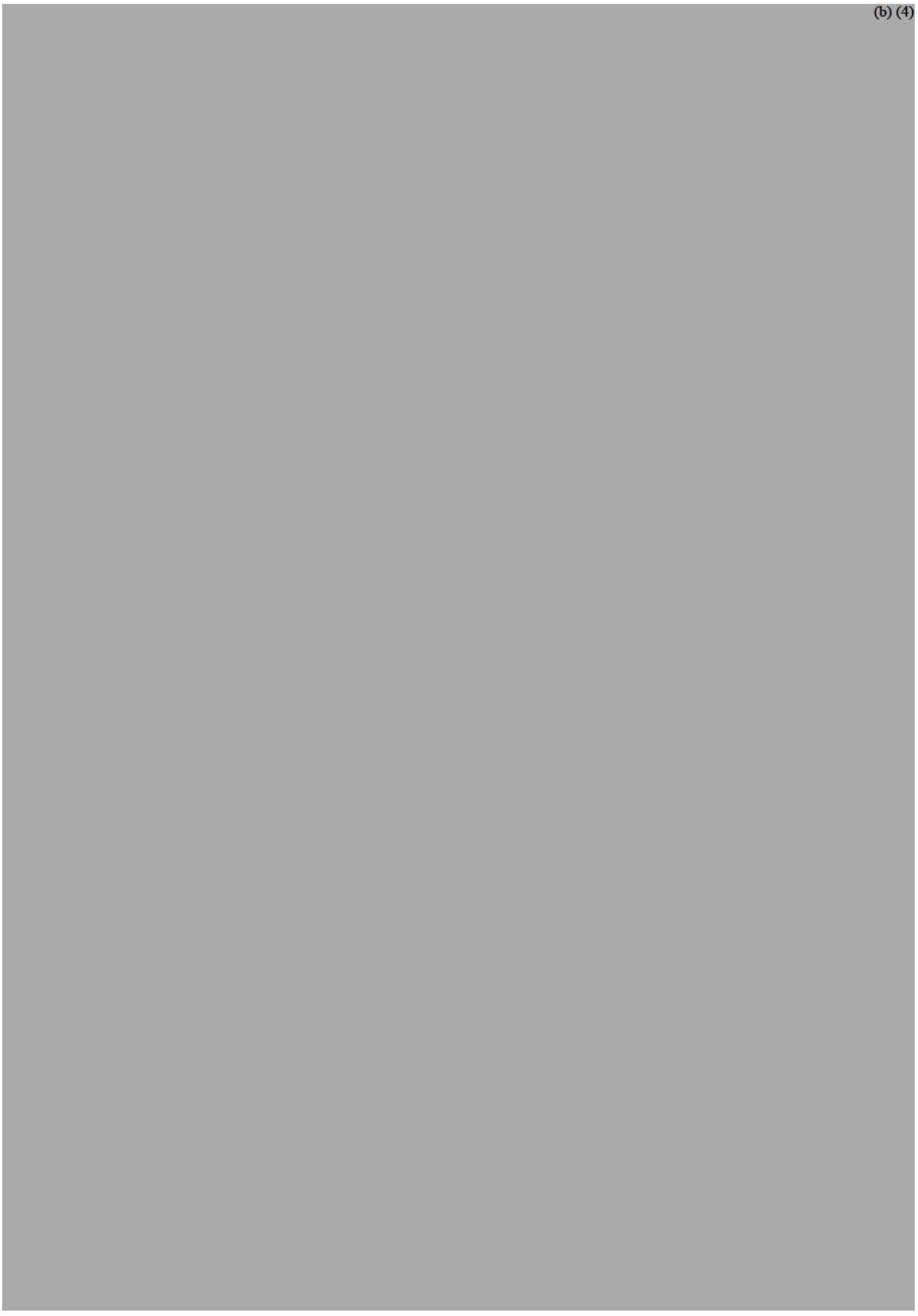
fyi

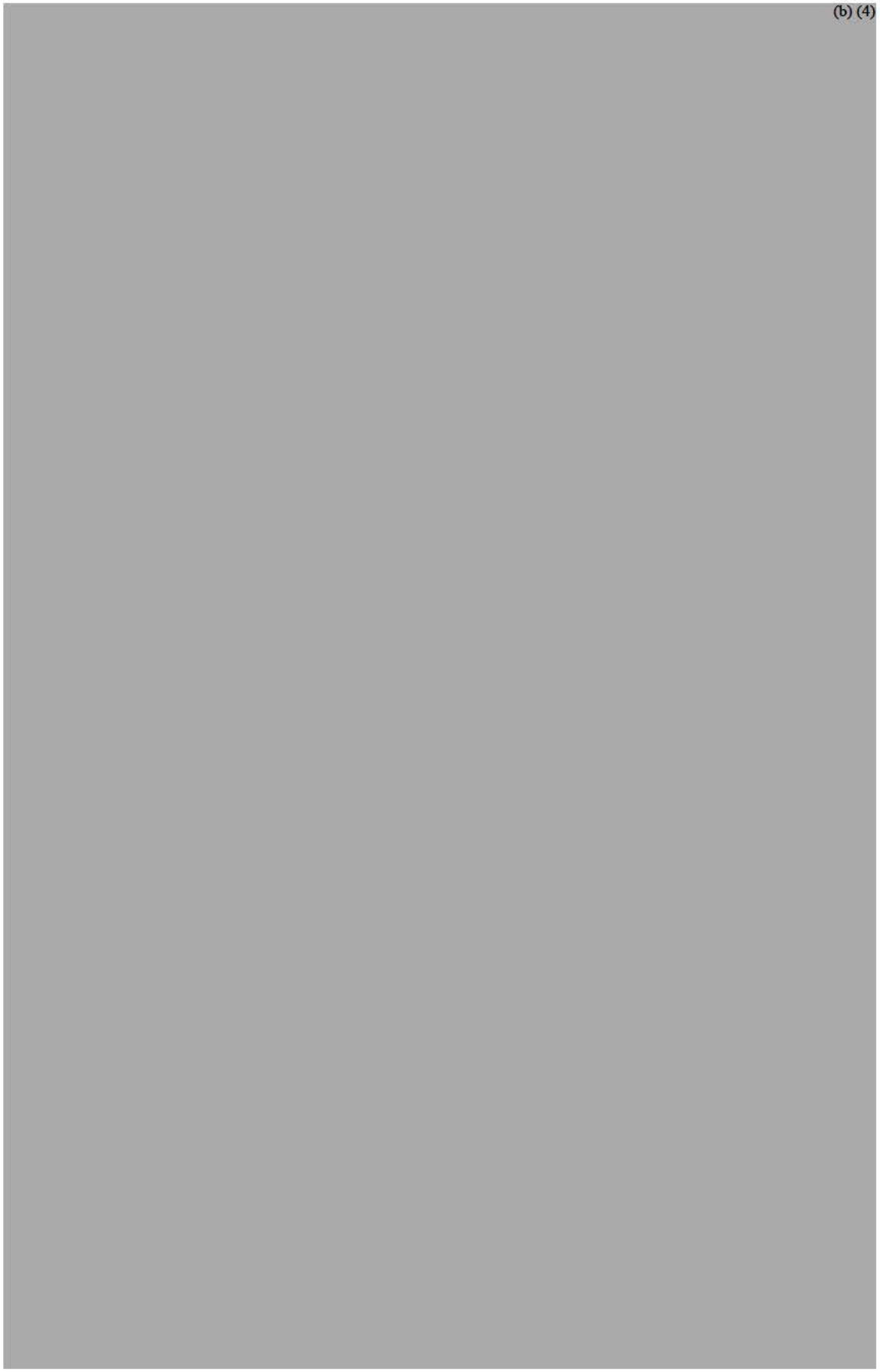
From: Lipkin, Ian W. (b) (6) >
Sent: Saturday, March 7, 2020 8:20 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: (b) (4)

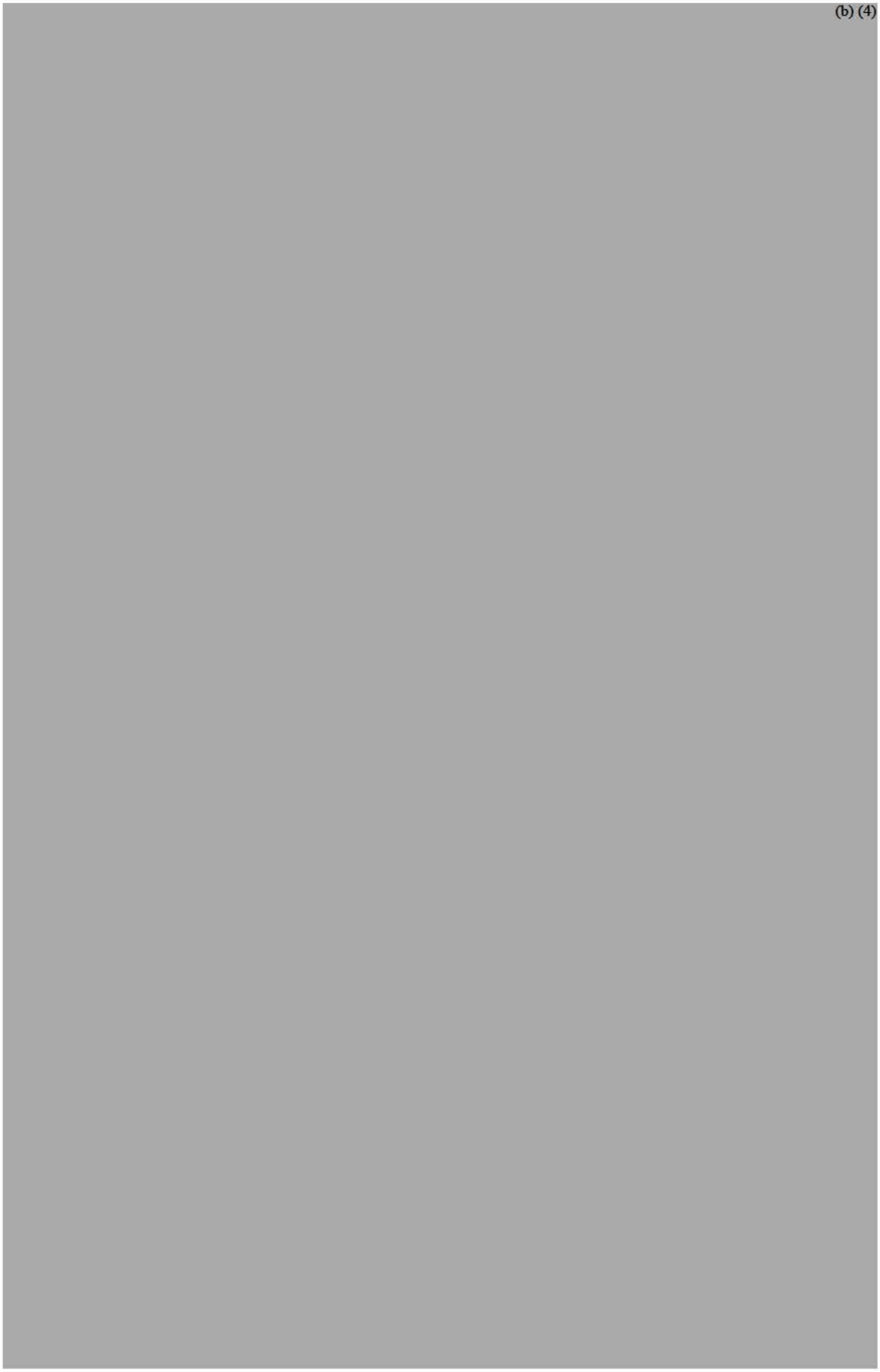
Tony,
Happy to connect you with Zhu. (b) (4)

(b) (4)


(b) (4)


(b) (4)


(b) (4)


(b) (4)

(b) (4)

>>>> With best regards,
>>>>
>>>> Zhu
>>>>
>>>>
>>>> 发件人: Lipkin, Ian W. (b) (6)
>>>> 发送时间: 2020年2月9日 23:01
>>>> 收件人: Zhu Chen
>>>> 抄送: George Gao; zhangzongwei
>>>> 主题: Re: important info
>>>>
>>>> Zhu,
>>>> Please call me on (b) (6)
>>>>
>>>> Ian
>>>>
>>>>
>>>>
>>>> W. Ian Lipkin, MD
>>>> John Snow Professor of Epidemiology and Director
>>>> Center for Infection and Immunity
>>>> Mailman School of Public Health
>>>>
>>>> Professor of Pathology and Neurology
>>>> College of Physicians & Surgeons
>>>> Columbia University
>>>> 722 West 168th Street, 17th Floor
>>>> New York, NY 10032
>>>> Voice: (b) (6)
>>>> Fax: (212) 342-9044
>>>> Email: (b) (6)

>>>>
>>>> Administrative Coordinator
>>>> (b) (6)
>>>> Voice: (b) (6)
>>>> Email: (b) (6)
>>>>
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>>>>
>>>>
>>>>
>>>>
>>>>
>>>>
>>>> On Feb 9, 2020, at 9:43 AM, ZhuChen (b) (6) > wrote:
>>>>
>>>> Dear Ian,
>>>> I have an important info to be shared with you. According to the latest report from the National Health Commission, the number of confirmed cases of NCP (2019-nCoV pneumonia) in other Provinces than Hubei (Wuhan is the capital city) was decreased from 890/day on Feb 3rd to 509/day on Feb 8th. So it is still possible for this outbreak to be basically contained in China.
>>>> Therefore, my suggestion is that we support the current public health policies and strategy to concentrate quality medical human resources and other resources to save more life of severe patients, even though the cost is high, very high. And then, we shall continuously analyze the situation for possible adjustment of policies and measures.
>>>> Best,
>>>> Zhu
>>>>
>>

possible. We (NIAID/ USG) do not expect to be the only source, but will likely be one of the main sources for this research resource based on experience with Zika.

5. If someone wishes to travel to China to work on the live virus, are there any travel restrictions other than the self isolation/quarantine already in place (and of course subject to change over time)?

For that, contacting CDC directly would make sense. If you would like us to inquire, we can. For high consequence viruses, use of proper PPE has been a mitigating factor in quarantine consideration.

Please feel free to contact me if you have additional questions.

Thanks,
Alan

Alan Embry, Ph.D.
Chief, Respiratory Diseases Branch
Division of Microbiology and Infectious Diseases, NIAID, NIH
5601 Fishers Lane, Room 8E31
Rockville, MD 20892
(b) (6)
(b) (6)

From: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Sent: Thursday, February 13, 2020 6:35 PM
To: Fried, Linda P. (b) (6)>; Redfield, Robert R. (CDC/OD) (b) (6)>
Cc: Conrad, Patricia (NIH/NIAID) [E] < (b) (6); Goldman, Lee (b) (6)>; Booth, Jane < (b) (6)>; Katznelson, Ira I. (b) (6)>; Marston, Hilary (NIH/NIAID) [E] (b) (6)>; Embry, Alan (NIH/NIAID) [E] (b) (6); Eisinger, Robert (NIH/NIAID) [E] (b) (6)>
Subject: RE: Institutional request for information

Linda:

There is a "sample sharing" working group involving NIH and CDC. I have copied both Hilary Marston and Alan Embry from NIAID who are involved in this group and will ask them by this e-mail to respond to items #1 through 4. Regarding returning travelers from China (item #5) if in Wuhan (Hubei province) within previous 14 days, they submit to institutional quarantine; if in non-Hubei province part of China, then they face self-isolation.

Hope that this is helpful.

Best regards,
Tony

Anthony S. Fauci, MD
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From: Fried, Linda P. (b) (6)
Sent: Thursday, February 13, 2020 12:45 PM
To: Redfield, Robert R. (CDC/OD) (b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Cc: Conrad, Patricia (NIH/NIAID) [E] (b) (6); Goldman, Lee (b) (6)>; Booth, Jane (b) (6)>; Katznelson, Ira I. (b) (6)
Subject: Institutional request for information

Dear Drs. Redfield and Fauci,

I am writing on behalf of Columbia University, which has received a request from Dr. Ian Lipkin to transfer live novel coronavirus from Hong Kong to his BSL3 facility at the University. As we evaluate his request, we note that he has approval from a CDC official to import the virus (see attached). However, as we consider the risks and benefits of Dr. Lipkin's proposal, we ask the two of you:

1. Is the CDC or NIH overseeing the distribution of the live virus in the U.S.?
2. Will you be the sole source of distribution in the U.S., or will institutions be permitted to obtain it directly from other sources?
3. If it can be obtained from other sources, what sources will be permitted? For example, the China or Hong Kong CDC or University of Hong Kong?
4. If you are to be the sole source, when would you expect to have a process for considering requests?
5. If someone wishes to travel to China to work on the live virus, are there any travel restrictions other than the self isolation/quarantine already in place (and of course subject to change over time)?

Thank you very much for your help with these important questions as we all try to do our best to contribute solutions to this health crisis.

With best regards,
Linda

From: (b) (6)
Sent: Thu, 6 Feb 2020 15:09:43 -0500
To: Folkers, Greg (NIH/NIAID) [E]
Cc: Conrad, Patricia (NIH/NIAID) [E];Eisinger, Robert (NIH/NIAID) [E];Lerner, Andrea (NIH/NIAID) [E];Marston, Hilary (NIH/NIAID) [E]
Subject: Re: ASF --- Morens + Daszak +Taubeneberger paper

I agree. I will not be a co-author

On Feb 6, 2020, at 1:59 PM, Folkers, Greg (NIH/NIAID) [E] (b) (6) >wrote:

(b) (4)



So the question to you – do you want to be part of this? ie be a coauthor

I would vote no – it wud look weird to add you as a coauthor now. Plus, plate too full……

Disclaimer: Any third-party material in this email has been shared for internal use under fair use provisions of U.S. copyright law, without further verification of its accuracy/veracity. It does not necessarily represent my views nor those of NIAID, NIH, HHS, or the U.S. government.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Thu, 6 Feb 2020 00:00:36 +0000
To: Jeremy Farrar;Collins, Francis (NIH/OD) [E]
Cc: Josie Golding;Tabak, Lawrence (NIH/OD) [E]
Subject: RE: Prevalence of infection and stage of the epidemic in Wuhan

Jeremy:
I left out an important name for the coronavirus evolution working group. Please include her: Pardis Sabeti at the Broad Institute of MIT and Harvard
Thanks,
Tony

Anthony S. Fauci, MD
Director
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From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Wednesday, February 5, 2020 5:25 PM
To: Jeremy Farrar < (b) (6) >; Collins, Francis (NIH/OD) [E] (b) (6)
Cc: Josie Golding < (b) (6) >; Tabak, Lawrence (NIH/OD) [E]
(b) (6)
Subject: RE: Prevalence of infection and stage of the epidemic in Wuhan

Jeremy:
Thanks for the note. Looks like things are moving along with WHO. I will list below a number of names for potential members of the working group to examine the evolutionary origin of the 2019-nCoV in addition to the individuals who were on the call with us last Saturday:

Harold Varmus – Weill Cornell Medical Center – New York City
Feng Zhang – MIT (CRISPR expert)
Joseph DeRisi - Chan Zuckerberg (CZ) BioHub (he's paying close attention to the Wuhan strain vs other bat viruses and the SARS virus)

Don Ganem - University of California at San Francisco (UCSF) and the CZ BioHub (knows more about hepadnaviruses but an outstanding clinical and basic virologist)
John Coffin - Tufts and National Cancer Institute, NIH (worked out the confusion over the alleged Chronic Fatigue Syndrome retrovirus that proved to be a xenotropic MLV)
Eugene Koonin - NCBI/National Libreary of Medicine, NIH; https://www.ncbi.nlm.nih.gov/research/groups/koonin/)
Wayne Hendrickson – Columbia University and the New York Structural Biology Center
Gary Nabel – Sanofi (Boston)

Best regards,
Tony

Anthony S. Fauci, MD
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From: Jeremy Farrar (b) (6)
Sent: Wednesday, February 5, 2020 6:21 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6); Collins, Francis (NIH/OD) [E] (b) (6)>
Cc: Josie Golding (b) (6)
Subject: Re: Prevalence of infection and stage of the epidemic in Wuhan

Francis and Tony

Couple of things:

- I spoke again with WHO this morning. I believe they have listened and acted. Let me know if you agree
    - At the WHO meeting next week they will set up the Group who will "look at the origins and evolution of 2019n-CoV"
    - They have asked for names to sit on that Group – please do send any names

- We can have a call this week with a core group of that to frame the work of the Group including – if you could join?
- I think this puts it under the umbrella of WHO, with action this week and into next
- With names to be put forward into the Group from us and pressure on this group from your and our teams next week.

- The team will update the draft today and I will forward immediately – they will add further comments on the glycans

Does that sound reasonable to you?

Jeremy

From: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6)
Date: Tuesday, 4 February 2020 at 13:18
To: Francis Collins <(b) (6)>, Jeremy Farrar (b) (6)
Subject: RE: Prevalence of infection and stage of the epidemic in Wuhan

?? (b) (4)

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From: Collins, Francis (NIH/OD) [E] (b) (6)
Sent: Tuesday, February 4, 2020 6:12 AM
To: Jeremy Farrar (b) (6)
Cc: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: RE: Prevalence of infection and stage of the epidemic in Wuhan

Yes, (b) (4)

Francis

From: Jeremy Farrar (b) (6)
Sent: Tuesday, February 4, 2020 6:08 AM
To: Collins, Francis (NIH/OD) [E] (b) (6)>
Cc: Fauci, Anthony (NIH/NIAID) [E] (b) (6)>
Subject: Re: Prevalence of infection and stage of the epidemic in Wuhan

(b) (4)

On 4 Feb 2020, at 10:58, Collins, Francis (NIH/OD) [E] (b) (6)> wrote:

Very thoughtful analysis. (b) (4)
(b) (4)

Francis

From: Jeremy Farrar (b) (6)
Sent: Tuesday, February 4, 2020 2:01 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)>; Collins, Francis (NIH/OD) [E] <(b) (6)
Subject: FW: Prevalence of infection and stage of the epidemic in Wuhan

Please treat in confidence – a very rough first draft from Eddie and team – they will send on the edited, cleaner version later.

Pushing WHO again today

From: Edward Holmes (b) (6)>
Date: Tuesday, 4 February 2020 at 06:33
To: Jeremy Farrar (b) (6)>
Subject: Re: Prevalence of infection and stage of the epidemic in Wuhan

Here's our summary so far. Will be edited further.

It's fundamental science and completely neutral as written. Did not mention other anomalies as this will make us look like loons. As it stands it is excellent basic science I think, which is a service in itself.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Thu, 13 Feb 2020 22:36:17 +0000
To: Messonnier, Nancy (CDC/DDID/NCIRD/OD)
Subject: RE: NAS

Nancy:

The official USG group will be convened by NAS. Bob Kadlec is the person with direct knowledge of that. In addition, there is an ad hoc group informally led by Jeremy Farrar of Wellcome Trust. This group has about 15 people, all of whom are highly respected scientists, mostly evolutionary biologists who are convening by e-mail and conference calls (I have been on 2 of these calls since Jeremy invited me) to look at all of the bat, pangolin and human coronavirus sequences to try and determine the evolutionary origin. This is not my area of expertise and so I have backed off and am leaving it all to Jeremy.

Best,

Tony

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From: Messonnier, Nancy (CDC/DDID/NCIRD/OD) (b) (6)>
Sent: Thursday, February 13, 2020 5:28 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)>
Subject: RE: NAS

Thanks. Is someone convening them?

From: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Sent: Thursday, February 13, 2020 5:07 PM

To: Messonnier, Nancy (CDC/DDID/NCIRD/OD) (b) (6)
Subject: RE: NAS

Nancy:

It is not a report. It is a letter from NAS to OSTP saying that it is important to bring together a group of experts to study the evolutionary origin the COVID19. I am attaching it here. I have no idea if it has been widely distributed and so please keep it internal.

Best,

Tony

Anthony S. Fauci, MD
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From: Messonnier, Nancy (CDC/DDID/NCIRD/OD) (b) (6)
Sent: Thursday, February 13, 2020 1:31 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Subject: NAS

Either you or Bob Kadlec made reference to a NAS report on the origins of SARS – COV2. (b) (5)

Thanks.

Nancy

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 9 Feb 2020 23:54:27 +0000
To: (b) (6)
Subject: FW: WHO advance team on coronavirus on way to China - Tedros tweet

Anthony S. Fauci, MD
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From: Grigsby, Garrett (HHS/OS/OGA) <(b) (6)>
Sent: Sunday, February 9, 2020 6:35 PM
To: Fauci, Anthony (NIH/NIAID) [E] <(b) (6); Harrison, Brian (HHS/IOS) (b) (6)
Cc: Kerr, Lawrence (HHS/OS/OGA) <(b) (6); Elvander, Erika (OS/OGA) (b) (6)>; Zebley, Kyle (HHS/OS/OGA) (b) (6) Redfield, Robert R. (CDC/OD) (b) (6); Kadlec, Robert (OS/ASPR/IO) <(b) (6); Abram, Anna (FDA/OC) <(b) (6)>; Bright, Rick (OS/ASPR/BARDA) (b) (6)>
Subject: RE: WHO advance team on coronavirus on way to China - Tedros tweet

Dr F,

(b) (5)

From: Fauci, Anthony (NIH/NIAID) [E] (b) (6)>
Sent: Sunday, February 9, 2020 6:24 PM
To: Grigsby, Garrett (HHS/OS/OGA) (b) (6)>; Harrison, Brian (HHS/IOS) (b) (6)>

Cc: Kerr, Lawrence (HHS/OS/OGA) <(b) (6)>; Elvander, Erika (OS/OGA) (b) (6); Zebley, Kyle (HHS/OS/OGA) <(b) (6)>; Redfield, Robert R. (CDC/OD) (b) (6)>; Kadlec, Robert (OS/ASPR/IO) (b) (6)>; Abram, Anna (FDA/OC) (b) (6)>; Bright, Rick (OS/ASPR/BARDA) (b) (6)
Subject: RE: WHO advance team on coronavirus on way to China - Tedros tweet

(b) (5)

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From: Grigsby, Garrett (HHS/OS/OGA) <(b) (6)
Sent: Sunday, February 9, 2020 6:03 PM
To: Harrison, Brian (HHS/IOS) (b) (6)
Cc: Kerr, Lawrence (HHS/OS/OGA) (b) (6); Elvander, Erika (OS/OGA) <(b) (6); Zebley, Kyle (HHS/OS/OGA) (b) (6)>; Redfield, Robert R. (CDC/OD) (b) (6); Fauci, Anthony (NIH/NIAID) [E] <(b) (6)>; Kadlec, Robert (OS/ASPR/IO) (b) (6)>; Abram, Anna (FDA/OC) (b) (6)>; Bright, Rick (OS/ASPR/BARDA) <(b) (6)
Subject: FW: WHO advance team on coronavirus on way to China - Tedros tweet

Brian – more clarity from "the horse's mouth" on this advance trip…see below.

From: Grigsby, Garrett (HHS/OS/OGA)
Sent: Sunday, February 9, 2020 6:01 PM
To: SCHWARTLANDER, Bernhard F. (b) (6)
Cc: SIMONSON, Stewart (b) (6)>
Subject: RE: WHO advance team on coronavirus on way to China - Tedros tweet

Many thanks, Bernard! I know I'll be asked, so I will pass your email up the chain…

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 2 Feb 2020 18:02:22 +0000
To: Billet, Courtney (NIH/NIAID) [E]
Subject: RE: Seeking comment on Indian paper about new Coronavirus

Geeeez

From: Billet, Courtney (NIH/NIAID) [E] (b) (6)
Sent: Sunday, February 2, 2020 12:53 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Cc: Marston, Hilary (NIH/NIAID) [E] (b) (6); Folkers, Greg (NIH/NIAID) [E] (b) (6)>; Conrad, Patricia (NIH/NIAID) [E] (b) (6)>; Stover, Kathy (NIH/NIAID) [E] (b) (6)>; Routh, Jennifer (NIH/NIAID) [E] (b) (6)>
Subject: Fwd: Seeking comment on Indian paper about new Coronavirus

FYI re the paper from the Indian researchers.
Talk about trying to put the genie back in the bottle! Yeesh.

From: "Mascola, John (NIH/VRC) [E]" <(b) (6)
Date: Sunday, February 2, 2020 at 10:39:42 AM
To: "Routh, Jennifer (NIH/NIAID) [E]" (b) (6)>, "Graham, Barney (NIH/VRC) [E]" (b) (6) "Hiatt, Nissa (NIH/VRC) [C]" (b) (6)>
Cc: "Marston, Hilary (NIH/NIAID) [E]" <(b) (6)>, "Billet, Courtney (NIH/NIAID) [E]" (b) (6)>, "Stover, Kathy (NIH/NIAID) [E]" (b) (6)>
Subject: RE: Seeking comment on Indian paper about new Coronavirus

Also note the following from the author on the BioRxiv comment section:

Prashant Pradhan • 8 hours ago

This is a preliminary study. Considering the grave situation, it was shared in BioRxiv as soon as possible to have creative discussion on the fast evolution of SARS-like corona viruses. It was not our intention to feed into the conspiracy theories and no such claims are made here. While we appreciate the criticisms and comments provided by scientific colleagues at BioRxiv forum and elsewhere, the story has been differently interpreted and shared by social media and news platforms. We have positively received all criticisms and comments. To avoid further misinterpretation and confusions world-over, we have decided to withdraw the current version of the preprint and will get back with a revised version after reanalysis, addressing the comments and concerns. Thank you to all who contributed in this open-review process.
: Authors of the Manuscript

From: Routh, Jennifer (NIH/NIAID) [E] (b) (6)
Sent: Sunday, February 2, 2020 10:35 AM
To: Graham, Barney (NIH/VRC) [E] (b) (6); Hiatt, Nissa (NIH/VRC) [C] (b) (6)
Cc: Marston, Hilary (NIH/NIAID) [E] (b) (6); Mascola, John (NIH/VRC) [E] (b) (6)>; Billet, Courtney (NIH/NIAID) [E] (b) (6)>; Stover, Kathy (NIH/NIAID) [E] < (b) (6)
Subject: RE: Seeking comment on Indian paper about new Coronavirus

Hi Barney –

We consulted with HHS and ASF. OCGR is going to send a note to the reporter to decline, noting that the paper is not peer-reviewed. Please let us know if you receive similar requests.

Thanks,
Jen

Jennifer Routh [E]
News and Science Writing Branch
Office of Communications and Government Relations
National Institute of Allergy and Infectious Diseases (NIAID)
NIH/HHS
31 Center Drive Room 7A17C
Bethesda, MD 20892
Direct: (b) (6)
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From: Graham, Barney (NIH/VRC) [E] (b) (6)
Sent: Saturday, February 1, 2020 2:11 PM
To: Hiatt, Nissa (NIH/VRC) [C] (b) (6)>; Routh, Jennifer (NIH/NIAID) [E] (b) (6)>
Cc: Marston, Hilary (NIH/NIAID) [E] (b) (6)>; Mascola, John (NIH/VRC) [E] (b) (6)
Subject: FW: Seeking comment on Indian paper about new Coronavirus

Hi Nissa and Jen,

This is one we don't want to answer without high-level input, but wanted you to know about the rising controversy.

BG

From: Issam AHMED <Issam.AHMED@afp.com>
Sent: Friday, January 31, 2020 5:27 PM
To: Graham, Barney (NIH/VRC) [E] (b) (6)
Subject: Seeking comment on Indian paper about new Coronavirus

Dear Dr Graham,

I'm a science journalist with news agency Agence France-Presse writing with a request -- apologies for reaching out on a Friday evening! I was told by a contact you may be willing to give an opinion on this paper that has just gone live https://www.biorxiv.org/content/10.1101/2020.01.30.927871v1.full.pdf it suggests the new Coronavirus has four inserts similar to HIV-1 and this is not a coincidence.

Thanks you very much, if you are able.

Issam Ahmed

Issam AHMED
Health, Science and Environment Correspondent
1500 K St. NW - 20005 Washington
Tel: (202) 414-0521



June 24, 2020
Virus death toll nears half a million as cases surge in US, Latin America

Join us on:



afp.com

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 2 Feb 2020 16:49:35 +0000
To: Collins, Francis (NIH/OD) [E]
Cc: Tabak, Lawrence (NIH/OD) [E]
Subject: FW: Teleconference

Francis:
Do you have a minute for a quick call?
Tony

From: Jeremy Farrar (b) (6)
Sent: Sunday, February 2, 2020 11:28 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6); Collins, Francis (NIH/OD) [E] (b) (6)
Cc: Tabak, Lawrence (NIH/OD) [E] (b) (6)>
Subject: Re: Teleconference

Tedros and Bernhard have apparently gone into conclave....they need to decide today in my view. If they do prevaricate, I would appreciate a call with you later tonight or tomorrow to think how we might take forward.

Meanwhile....

https://www.zerohedge.com/geopolitical/coronavirus-contains-hiv-insertions-stoking-fears-over-artificially-created-bioweapon

---

From: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6)>
Date: Sunday, 2 February 2020 at 15:30
To: Jeremy Farrar (b) (6)>, Francis Collins (b) (6)>
Cc: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Subject: RE: Teleconference

Jeremy:
Sorry that I took so long to weigh in on your e-mails with Francis and me. I was on conference calls. (b) (5)
(b) (5)
Best regards,
Tony

From: Jeremy Farrar (b) (6)>
Sent: Sunday, February 2, 2020 7:13 AM

To: Collins, Francis (NIH/OD) [E] (b) (6)>
Cc: Fauci, Anthony (NIH/NIAID) [E] (b) (6)>; Tabak, Lawrence (NIH/OD) [E]
< (b) (6)
Subject: Re: Teleconference

....Really appreciate us thinking through the options... (b) (5)

From: Francis Collins < (b) (6)>
Date: Sunday, 2 February 2020 at 12:03
To: Jeremy Farrar < (b) (6)>
Cc: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6), "Tabak, Lawrence (NIH/OD) [E]"
(b) (6)
Subject: RE: Teleconference

Hi Jeremy,

Thanks for forwarding these additional reflections from Mike and Bob. (b) (5)
(b) (5)

Francis

From: Jeremy Farrar (b) (6)
Sent: Sunday, February 2, 2020 6:53 AM
To: Collins, Francis (NIH/OD) [E] (b) (6)
Cc: Fauci, Anthony (NIH/NIAID) [E] (b) (6)>; Tabak, Lawrence (NIH/OD) [E]
(b) (6)
Subject: Re: Teleconference

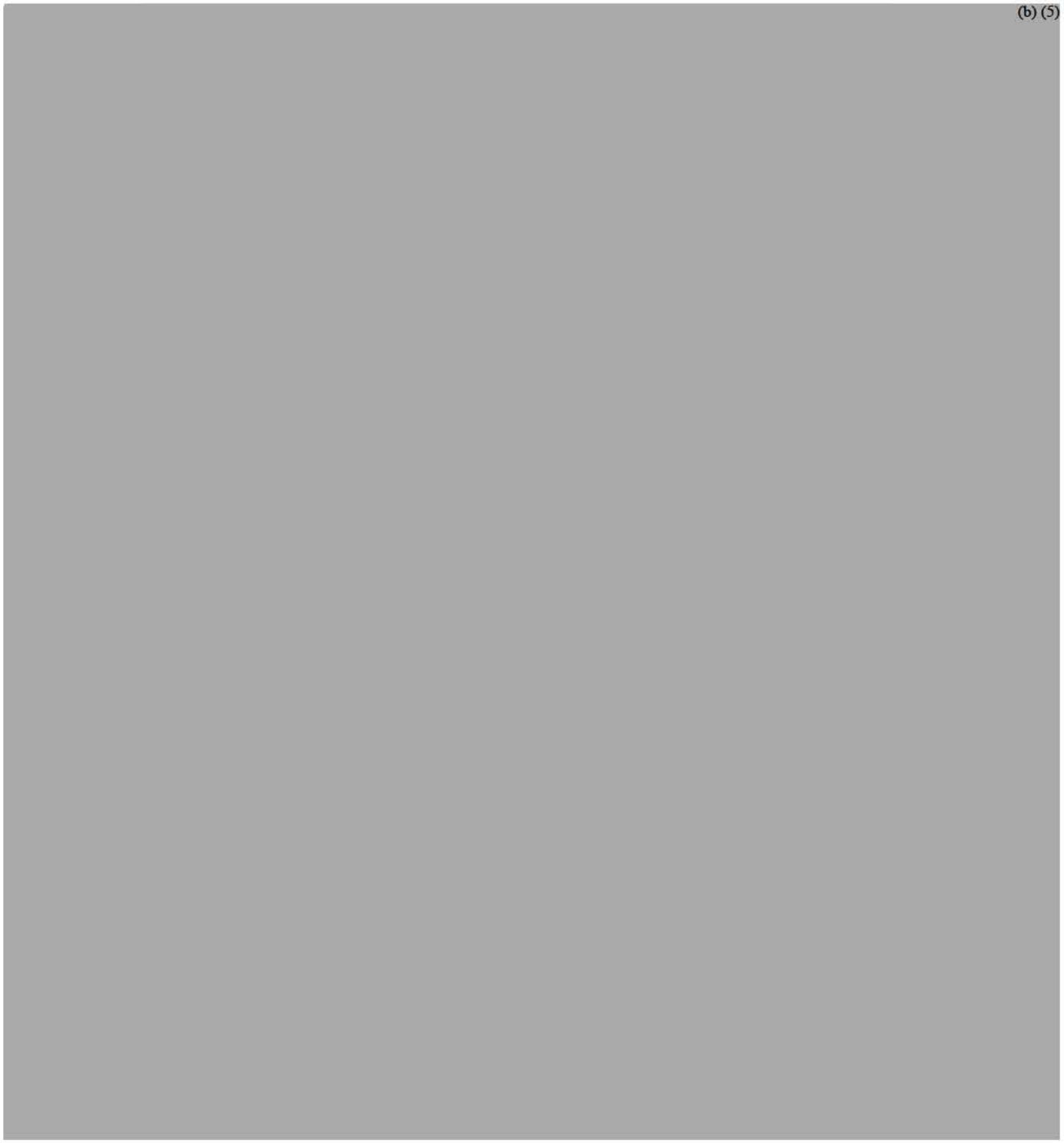
Thank you

See thoughts overnight from others.

(b) (5)

Jeremy

(b) (5)



From: Francis Collins (b) (6)>
Date: Sunday, 2 February 2020 at 10:27
To: Jeremy Farrar (b) (6)
Cc: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6), "Tabak, Lawrence (NIH/OD) [E]" (b) (6)
Subject: RE: Teleconference

Jeremy,

(b) (5)

I'm available any time today except 3:15 – 5:45 pm EST (on a plane) for a call to Tedros. Let me know if I can help get through his thicket of protectors.

Francis

From: Jeremy Farrar (b) (6)
Sent: Sunday, February 2, 2020 4:48 AM
To: Andrew Rambaut < (b) (6)>
Cc: R.A.M. Fouchier (b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6) Patrick Vallance (b) (6); Drosten, Christian (b) (6)>; M.P.G. Koopmans (b) (6); Eddie Holmes (b) (6); Kristian G. Andersen (b) (6); Paul Schreier (b) (6); Ferguson, Mike (b) (6); Collins, Francis (NIH/OD) [E] (b) (6)>; Tabak, Lawrence (NIH/OD) [E] (b) (6)>; Josie Golding (b) (6)
Subject: Re: Teleconference

This is a very complex issue.

I will:

(b) (5)

(b) (5)

I suggest we don't get into a further scientific discussion here, but wait for that group to be established.

Jeremy

From: ' (b) (6)
Date: Sunday, 2 February 2020 at 09:38
To: Jeremy Farrar < (b) (6) >
Cc: (b) (6) >, "Fauci, Anthony (NIH/NIAID) [E]" (b) (6), Patrick Vallance (b) (6) >, "Drosten, Christian" (b) (6), Marion Koopmans < (b) (6), Edward Holmes (b) (6) (b) (6), "Kristian G. Andersen" (b) (6), Paul Schreier (b) (6) Michael FMedSci (b) (6) >, Francis Collins (b) (6) (b) (6) Josie Golding (b) (6)
Subject: Re: Teleconference

Dear Jeremey, Ron and all,

Thanks for inviting me on the call yesterday. (b) (5)

(b) (5)

(b) (5)

Best,
Andrew

On 2 Feb 2020, at 08:40, Jeremy Farrar (b) (6)> wrote:

Thanks Ron

(b) (5)

Thoughts on that very welcome.

On 2 Feb 2020, at 08:30, R.A.M. Fouchier (b) (6)> wrote:

Dear Jeremy and others,

This was a very useful teleconference. (b) (5)

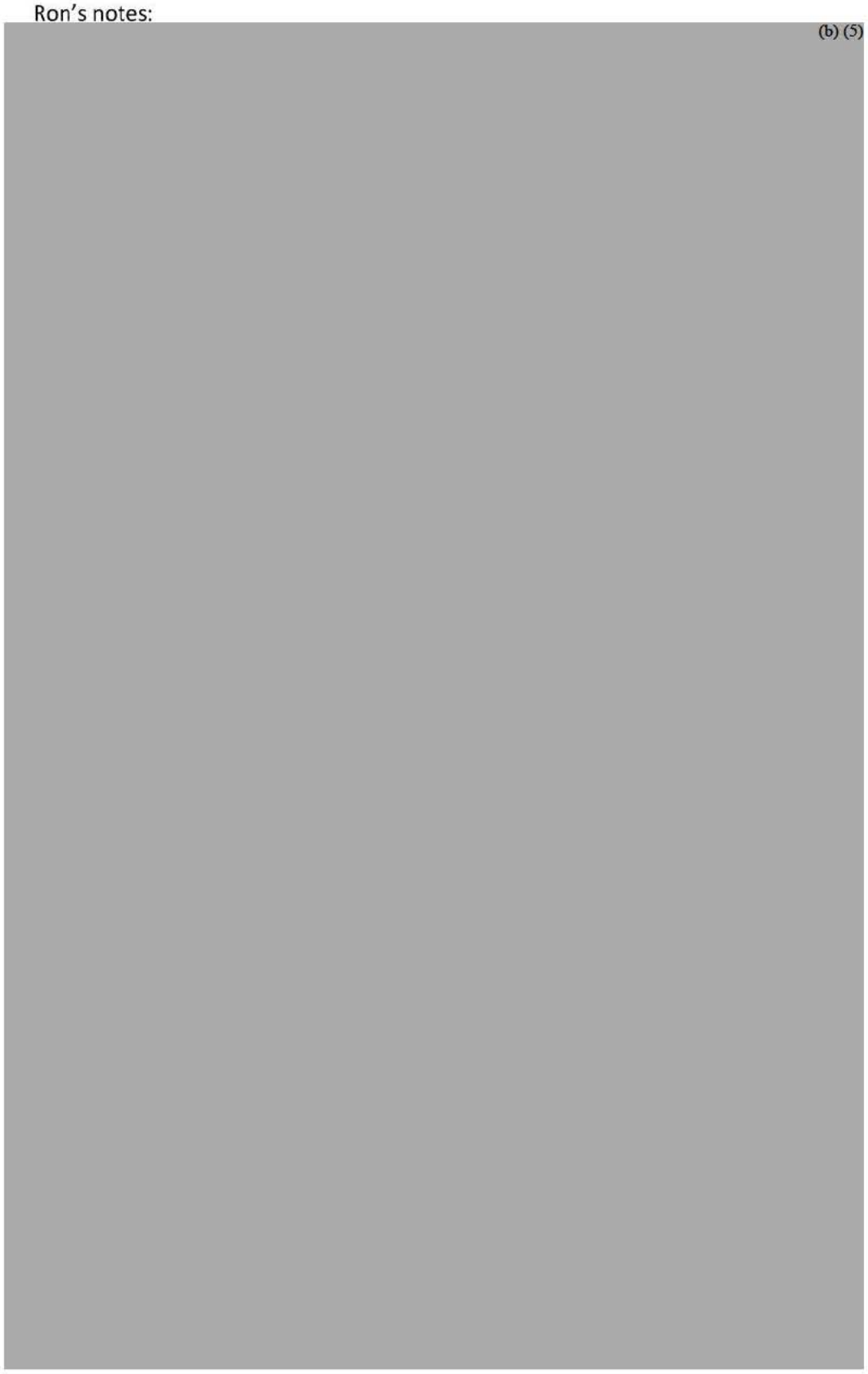
(b) (5)

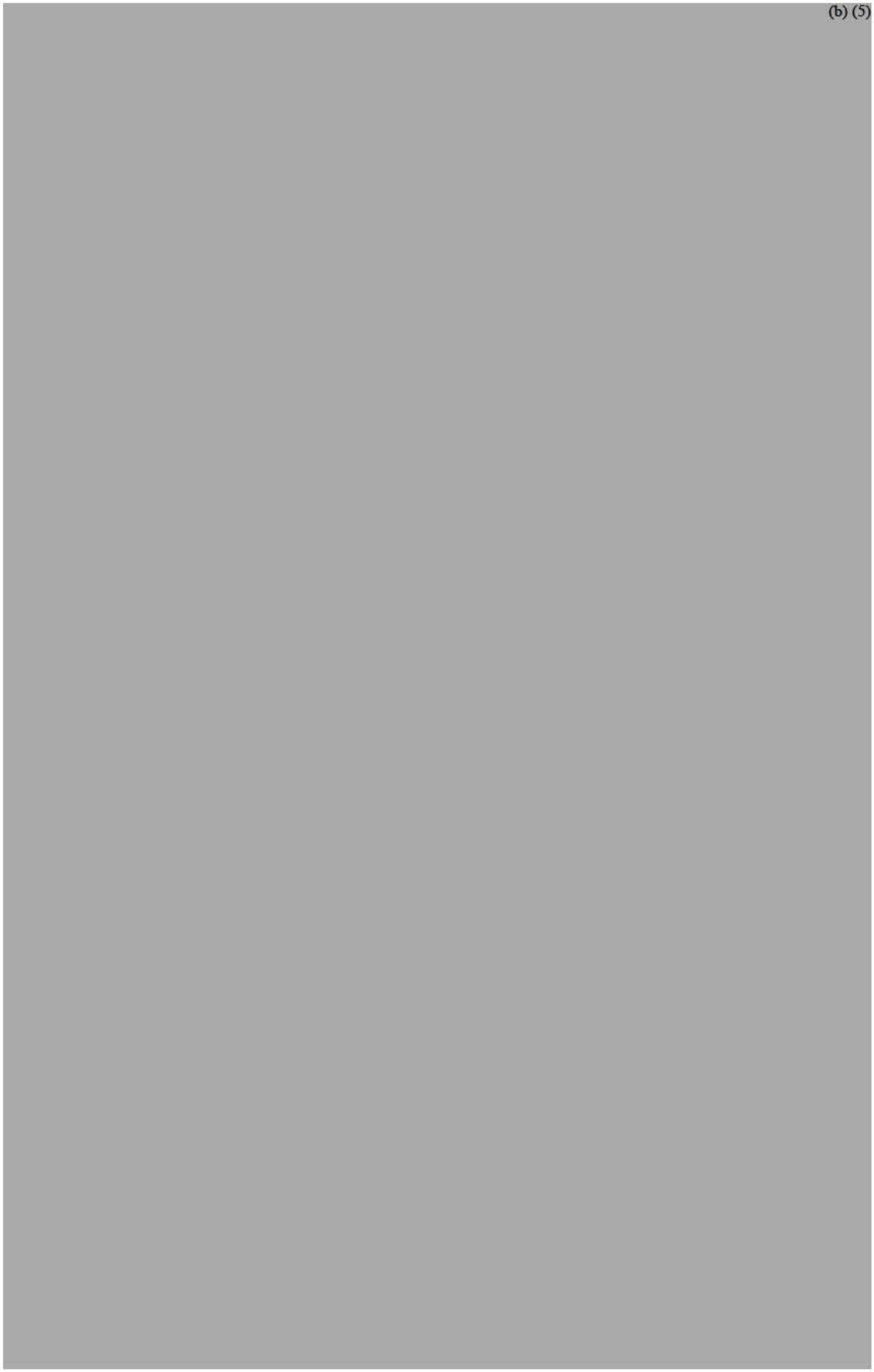
Thanks for organizing this on such short notice,
Kind regards

Ron

Ron's notes:

(b) (5)




(b) (5)

(b) (5)

Van: Jeremy Farrar (b) (6)
Datum: zaterdag 1 februari 2020 om 21:59
Aan: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6)>, Patrick Vallance (b) (6)
CC: Christian Drosten (b) (6) "M. Koopmans" (b) (6), "R.A.M. Fouchier" (b) (6), Edward Holmes (b) (6) (b) (6), Andrew Rambaut (b) (6) "Kristian G. Andersen" (b) (6), Paul Schreier (b) (6) (b) (6), "Ferguson, Mike" (b) (6) Francis Collins (b) (6), ' (b) (6)>, Josie Golding (b) (6)
Onderwerp: Re: Teleconference

Thank you to everyone for joining.

There is clearly much to understand understand in this. This call was very helpful to hear some of our current understanding and the many gaps in our knowledge. (b) (5)

(b) (5)

(b) (5)

I hope that is a reasonable approach, please send any thoughts or suggestions.

Once again, thank you for making time over a weekend and for such an informed discussion on a complex issue.

Thank you and best wishes Jeremy

From: Jeremy Farrar (b) (6)
Date: Saturday, 1 February 2020 at 15:34
To: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6)>, Patrick Vallance <(b) (6)
Cc: "Drosten, Christian" (b) (6)>, Marion Koopmans (b) (6)
"(b) (6) Edward Holmes (b) (6)
(b) (6)
(b) (6) "Kristian G. Andersen"
(b) (6), Paul Schreier (b) (6)
(b) (6)>, Michael FMedSci
(b) (6)
Subject: Teleconference

1st February (2nd Feb for Eddie)
Information and discussion is shared in total confidence and not to be shared until agreement on next steps.

Dial in details attached.
Please mute phones.
I will be on email throughout – email Paul or I Paul if any problems
If you cannot make it, I will phone you afterwards to update.

One Hour

6am Sydney
8pm CET
7pm GMT
2pm EST
11am PST
(Hope I have the times right!)

Thank you for the series of calls and for agreeing to join this call.

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Marion Koopmans
Stefan Pohlmann
Andrew Rambaut
Paul Schreier
Patrick Vallance

Andrew Rambaut
Institute for Evolutionary Biology
Ashworth Laboratories, University of Edinburgh, Edinburgh, EH9 3FL, UK

contact – (b) (6) | http://tree.bio.ed.ac.uk | tel (b) (6)

The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sun, 2 Feb 2020 11:26:13 +0000
To: Collins, Francis (NIH/OD) [E];Tabak, Lawrence (NIH/OD) [E];Wolinetz, Carrie (NIH/OD) [E]
Subject: RE: More on evolution of coronavirus

The Indian paper is really outlandish. Agree about Jon Cohen's nice summary.

From: Collins, Francis (NIH/OD) [E] (b) (6)
Sent: Sunday, February 2, 2020 5:58 AM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6); Tabak, Lawrence (NIH/OD) [E] (b) (6)>; Wolinetz, Carrie (NIH/OD) [E] (b) (6)>
Subject: More on evolution of coronavirus

In case you haven't seen, attached is the Indian paper claiming HIV sequences have been inserted into 2019-nCoV, which has been roundly debunked.

I found Jon Cohen's piece in Science to be a pretty useful summary:

https://www.sciencemag.org/news/2020/01/mining-coronavirus-genomes-clues-outbreak-s-origins

FC

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 22:06:26 +0000
To: Jeremy Farrar;Collins, Francis (NIH/OD) [E]
Subject: RE: Teleconference

Thanks, Jeremy. We really appreciate what you are doing here. Pleasure to work with you.
Best,
Tony

From: Jeremy Farrar [redacted]>
Sent: Saturday, February 1, 2020 4:00 PM
To: Collins, Francis (NIH/OD) [E] <[redacted]>
Cc: Fauci, Anthony (NIH/NIAID) [E] [redacted]
Subject: Re: Teleconference

We are altogether as you know! Conversations with you and Tony, and Patrick and others – always great working with you both

---

From: Francis Collins [redacted]>
Date: Saturday, 1 February 2020 at 20:50
To: Jeremy Farrar [redacted]
Cc: "Fauci, Anthony (NIH/NIAID) [E]" [redacted]
Subject: Re: Teleconference

Hi Jeremy,
I can make myself available at any time 24/7 for the call with Tedros. Just let me know.
Thanks for your leadership on this critical and sensitive issue.
Francis

Sent from my iPhone

> On Feb 1, 2020, at 3:07 PM, Jeremy Farrar [redacted]> wrote:
>
> I have rejoined so a line is open if any help to rejoin.
>
> ---
>
> **From:** Jeremy Farrar [redacted]>
> **Date:** Saturday, 1 February 2020 at 19:56
> **To:** "Fauci, Anthony (NIH/NIAID) [E]" [redacted], Francis Collins [redacted]>, Michael FMedSci [redacted], Patrick Vallance [redacted]
> **Subject:** Re: Teleconference

Can I suggest we shut down the call and then redial in?

Just for 5-10mins?

From: Marion Koopmans (b) (6)
Date: Saturday, 1 February 2020 at 19:43
To: Jeremy Farrar (b) (6)>
Cc: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6)>, Patrick Vallance (b) (6) "Drosten, Christian" (b) (6) (b) (6)>, Edward Holmes (b) (6), (b) (6) (b) (6)>, "Kristian G. Andersen" (b) (6), Paul Schreier (b) (6) < (b) (6) Michael FMedSci (b) (6) Francis Collins (b) (6)>
Subject: Re: Teleconference

(b) (5)

On 1 Feb 2020, at 19:12, Jeremy Farrar (b) (6)> wrote:

Kristen and Eddie have shared this and will talk through it on the call. Thank you.

Hope it will help frame the discussions.

From: Jeremy Farrar (b) (6)>
Date: Saturday, 1 February 2020 at 15:34

1st February (2nd Feb for Eddie)
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Stefan Pohlmann
Andrew Rambaut

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 20:03:12 +0000
To: Jeremy Farrar
Subject: RE: Teleconference

Yes

From: Jeremy Farrar (b) (6)
Sent: Saturday, February 1, 2020 2:56 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6); Collins, Francis (NIH/OD) [E] (b) (6); Ferguson, Mike (b) (6); Patrick Vallance (b) (6)
Subject: Re: Teleconference

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Cc: "Fauci, Anthony (NIH/NIAID) [E]" (b) (6), Patrick Vallance (b) (6), "Drosten, Christian" (b) (6), (b) (6) Edward Holmes (b) (6), (b) (6) "Kristian G. Andersen" (b) (6), Paul Schreier (b) (6) Michael FMedSci (b) (6), Francis Collins (b) (6)
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(b) (5)

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>
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Hope it will help frame the discussions.

From: Jeremy Farrar [redacted] (b) (6)>
Date: Saturday, 1 February 2020 at 15:34

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Marion Koopmans
Stefan Pohlmann
Andrew Rambaut
Paul Schreier
Patrick Vallance

<Coronavirus sequence comparison[1].pdf>

(b) (6), "NIAID NEWS (NIH/NIAID)" <NIAIDNEWS@niaid.nih.gov>
Subject: FW: coronavirus speaking opportunity

Obviously given the current environment (not to mention some of the names involved in the event), I want to make sure I'm in lockstep with you all from square one. How would you like me to proceed with the request below? The event is open to the public / press.

From: Chertow, Daniel (NIH/CC/CCMD) [E] (b) (6)>
Sent: Thursday, January 30, 2020 6:16 PM
To: Cohen, Justin (NIH/CC/OD) [E] (b) (6)>; Freimuth, Molly (NIH/CC/OC) [E] (b) (6)>
Cc: Suffredini, Anthony (NIH/CC/CCMD) [E] (b) (6)>; Masur, Henry (NIH/CC/CCMD) [E] (b) (6)
Subject: FW: Hudson Institute speaking request

Dear Justin,

I am checking back in with you regarding the below invitation to speak.

I would like to participate in this if possible.

Please confirm that you have received my email.

Thank you.

Sincerely,

Dan

From: "Asha M. George" <asha.george@biodefensecommission.org>
Date: Thursday, January 30, 2020 at 6:09 PM
To: "Chertow, Daniel (NIH/CC/CCMD) [E]" (b) (6)>
Subject: Re: Hudson Institute speaking request

Dear Dan,
Sorry, we have changed something slightly. Instead of taking questions directly from the audience, we will obtain questions from the audience via email while the first part of the event occurs, curate them, and then have them available for Senator Lieberman to ask them of the speakers.
Asha

Asha M. George, DrPH
Executive Director

BIPARTISAN COMMISSION ON BIODEFENSE

202.974.2416

biodefensecommission.org

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From: Asha M. George <asha.george@biodefensecommission.org>
Sent: Thursday, January 30, 2020 6:02 PM
To: Chertow, Daniel (NIH/CC/CCMD) [E] (b) (6)
Subject: Re: Hudson Institute speaking request

Dear Dan,
Here are some more specifics regarding the event we will holding at Hudson Institute on novel coronavirus. The meeting will be on February 10th, from 2:00 - 3:30 pm in the Stern Conference Center at Hudson Institute, which is located at 1201 Pennsylvania Avenue, NW, 4th floor, Washington, DC 20004.

We also have the executive conference room reserved from 1:30 pm on. Please plan to arrive around then, so that you can talk with Senator Lieberman and the other speakers before the event starts at 2:00 pm. Just ask the receptionist to direct you where to go.

Here are the speakers:

- Former Senator Joe Lieberman, co-chair, Bipartisan Commission on Biodefense
- Dr. Julie Gerberding, Executive Vice President & Chief Patient Officer, Strategic Communications, Global Public Policy and Population Health, Merck; former Director, Centers for Disease Control and Prevention
- Dr. Billy Karesh, ex officio, Bipartisan Commission on Biodefense; Executive VP, EcoHealth Alliance
- The Honorable Tim Morrison, Senior Fellow, Hudson Institute; former Deputy Assistant to President Trump for National Security; former Special Assistant to the President and Senior Director for Weapons of Mass Destruction and Biodefense
- Mr. Eric Brown, Senior Fellow, Hudson Institute

- Dr. Daniel S. Chertow (CAPT - US Public Health Service), Head, Emerging Pathogens Section, Critical Care Medicine Department, Clinical Center & Laboratory of Immunoregulation, National Institute of Allergy and Infectious Diseases, National Institutes of Health *(invited)*

The setting will be relatively informal. Scooter Libby will first introduce Senator Lieberman. Then Senator Lieberman will make a short opening statement, and look to Billy to set the stage and talk about the zoonotic nature of the disease, associated disease management considerations, etc., in about 5 minutes. The Senator will then ask each of the other speakers to say a few words from their perspectives. After that, Senator Lieberman will ask some questions of the group, allowing you all to answer and converse. All of this should take about 45 minutes. Then we will allow the audience to ask questions.

We are planning for Senator Lieberman to moderate the discussion and take questions from the audience, but if for some reason he cannot do so, then Billy Karesh will.

I hope you will be able to make it, Dan. Let me know if you have any questions (and if you will be able to make it, of course) and I look forward to seeing you on February 10th.

Asha

Asha M. George, DrPH
Executive Director

BIPARTISAN COMMISSION ON BIODEFENSE

202.974.2416

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From: Chertow, Daniel (NIH/CC/CCMD) [E] (b) (6)>
Sent: Tuesday, January 28, 2020 7:18 PM
To: Asha M. George <asha.george@biodefensecommission.org>
Subject: Re: Hudson Institute speaking request

Dear Asha,

Given that this is a public/press event, I will require additional clearance from my organization in order to participate.

I will reach out to them now and get back to you.

Thank you.

Dan

From: "Asha M. George" <asha.george@biodefensecommission.org>
Date: Tuesday, January 28, 2020 at 7:15 PM
To: "Chertow, Daniel (NIH/CC/CCMD) [E]" (b) (6)>
Subject: Re: Hudson Institute speaking request

Dear Dan,
Thank you! The meeting will be held on February 10th. We are still trying to nail down a time with Senator Lieberman and Governor Ridge, so I will get back to you about that as soon as possible, hopefully tomorrow.

The meeting will be open to the public and to the press, but Hudson Institute is a think tank, so it's never a negative or rowdy crowd.

Asha

Asha M. George, DrPH
Executive Director

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Beyond the blueprint

From: Chertow, Daniel (NIH/CC/CCMD) [E] (b) (6)
Sent: Tuesday, January 28, 2020 5:53 PM
To: Asha M. George <asha.george@biodefensecommission.org>
Subject: Re: Hudson Institute speaking request

Dear Asha,

I am available Feb 10th or 13th and would be happy to present to the group.

Please clarify who will be in attendance and if the event is open or closed to press/public as this would require additional clearance on my end.

Thank you.

Sincerely,

Dan

Daniel S. Chertow, MD, MPH, FCCM, FIDSA
CAPT, United States Public Health Service
Head, Emerging Pathogens Section
Critical Care Medicine Department, NIH Clinical Center &
Laboratory of Immunoregulation, NIAID

From: "Asha M. George" <asha.george@biodefensecommission.org>
Date: Monday, January 27, 2020 at 6:09 PM

To: "Chertow, Daniel (NIH/CC/CCMD) [E]" <(b) (6)
Subject: Hudson Institute speaking request

Dear Dr. Chertow,
I am the Executive Director of the Bipartisan Commission on Biodefense, co-chaired by former Senator Joe Lieberman and Governor Tom Ridge. Our fiscal sponsor is Hudson Institute, one of the think tanks here in DC. Hudson Institute's chair of the board of trustees (Sarah May Stern) has asked Hudson Institute to run a 90 minute meeting on the novel coronavirus situation. Hudson has asked us to help them pull a brief meeting together in short order.

Considering your experience on the ground dealing with other outbreaks, Hudson Institute invites you to speak at this event. In addition to one of Hudson Institute's China experts, we are also seeing whether Senator Lieberman and Governor Ridge are available to speak.

Here are the dates they are a looking at: February 6, February 10, and February 13. Could you let me know if you are available and if so, when on those dates?

Thank you for your consideration, Dan. I look forward to hearing from you soon.

Asha

Asha M. George, DrPH
Executive Director

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202.974.2416

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BIPARTISAN COMMISSION ON BIODEFENSE
Beyond the blueprint

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 18:43:31 +0000
To: Kristian G. Andersen
Subject: RE: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Thanks, Kristian. Talk soon on the call.

From: Kristian G. Andersen (b) (6)>
Sent: Friday, January 31, 2020 10:32 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)
Cc: Jeremy Farrar (b) (6)>
Subject: Re: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Hi Tony,

Thanks for sharing. Yes, I saw this earlier today and both Eddie and myself are actually quoted in it. It's a great article, but the problem is that our phylogenetic analyses aren't able to answer whether the sequences are unusual at individual residues, except if they are completely off. On a phylogenetic tree the virus looks totally normal and the close clustering with bats suggest that bats serve as the reservoir. The unusual features of the virus make up a really small part of the genome (<0.1%) so one has to look really closely at all the sequences to see that some of the features (potentially) look engineered.

We have a good team lined up to look very critically at this, so we should know much more at the end of the weekend. I should mention that after discussions earlier today, Eddie, Bob, Mike, and myself all find the genome inconsistent with expectations from evolutionary theory. But we have to look at this much more closely and there are still further analyses to be done, so those opinions could still change.

Best,
Kristian

On Fri, Jan 31, 2020 at 18:47 Fauci, Anthony (NIH/NIAID) [E] (b) (6)> wrote:

> Jeremy/Kristian:
> This just came out today. You may have seen it. If not, it is of interest to the current discussion.
> Best,
> Tony
>
> ---
>
> **From:** Folkers, Greg (NIH/NIAID) [E] (b) (6)
> **Sent:** Friday, January 31, 2020 8:43 PM
> **Subject:** Science: Mining coronavirus genomes for clues to the outbreak's origins



As part of a long-running effort to see what viruses bats harbor, researchers in China collect one from a cave in Guandong.
EcoHealth Alliance

Mining coronavirus genomes for clues to the outbreak's origins

By Jon CohenJan. 31, 2020 , 6:20 PM

attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct ...

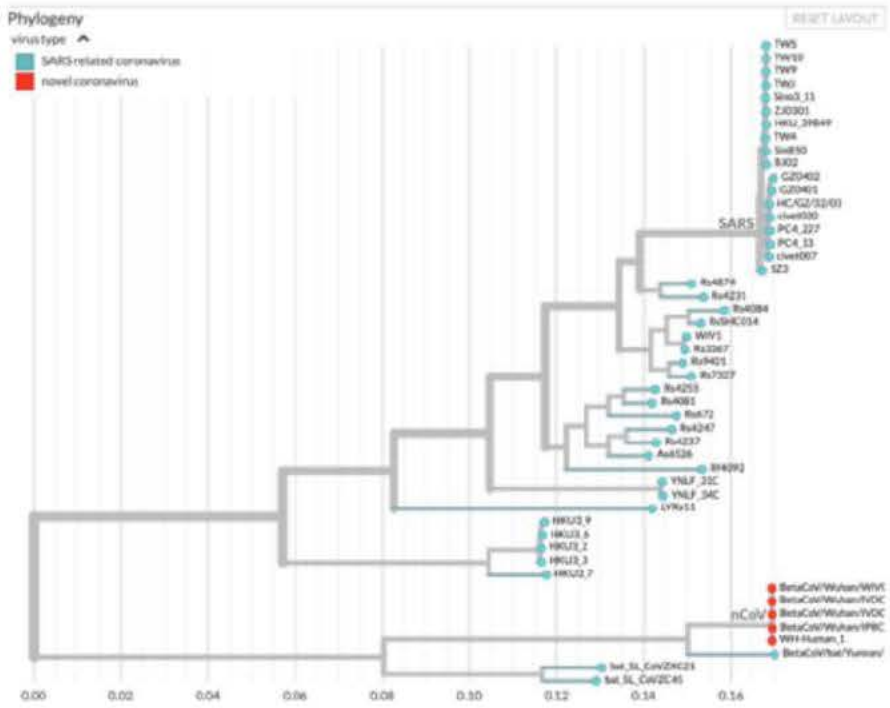
That string of apparent gibberish is anything but: It's a snippet of a DNA sequence from the viral pathogen, dubbed 2019 novel coronavirus (2019-nCoV), that is overwhelming China and frightening the entire world. Scientists are publicly sharing an ever-growing number of full sequences of the virus from patients—53 at last count in the Global Initiative on Sharing All Influenza Data database. These viral genomes are being intensely studied to try to understand the origin of 2019-nCoV and how it fits on the family tree of related viruses found in bats and other species. They have also given glimpses into what this newly discovered virus physically looks like, how it's changing, and how it might be stopped.

"One of the biggest takeaway messages [from the viral sequences] is that there was a single introduction into humans and then human-to-human spread," says Trevor Bedford, a bioinformatics specialist at the University of Washington, Seattle. The role of Huanan Seafood Wholesale Market in Wuhan, China, in spreading 2019-nCoV remains murky, though such sequencing, combined with sampling the market's environment for the presence of the virus, is clarifying that it indeed had an important early role in amplifying the outbreak. The viral sequences, most researchers say, also knock down the idea the pathogen came from a virology institute in Wuhan.

In all, 2019-nCoV has nearly 29,000 nucleotides bases that hold the genetic instruction book to produce the virus. Although it's one of the many viruses whose genes are in the form of RNA, scientists convert the viral genome into DNA, with bases known in shorthand as A, T, C, and G, to make it easier to study. Many analyses of 2019-nCoV's sequences have already appeared on virological.org, nextstrain.org, preprint servers like bioRxiv, and even in peer-reviewed journals. The sharing of the sequences by Chinese researchers allowed public health labs around the world to develop their own diagnostics for the virus, which now has been found in 18 other countries. (*Science*'s news stories on the outbreak can be found here.)

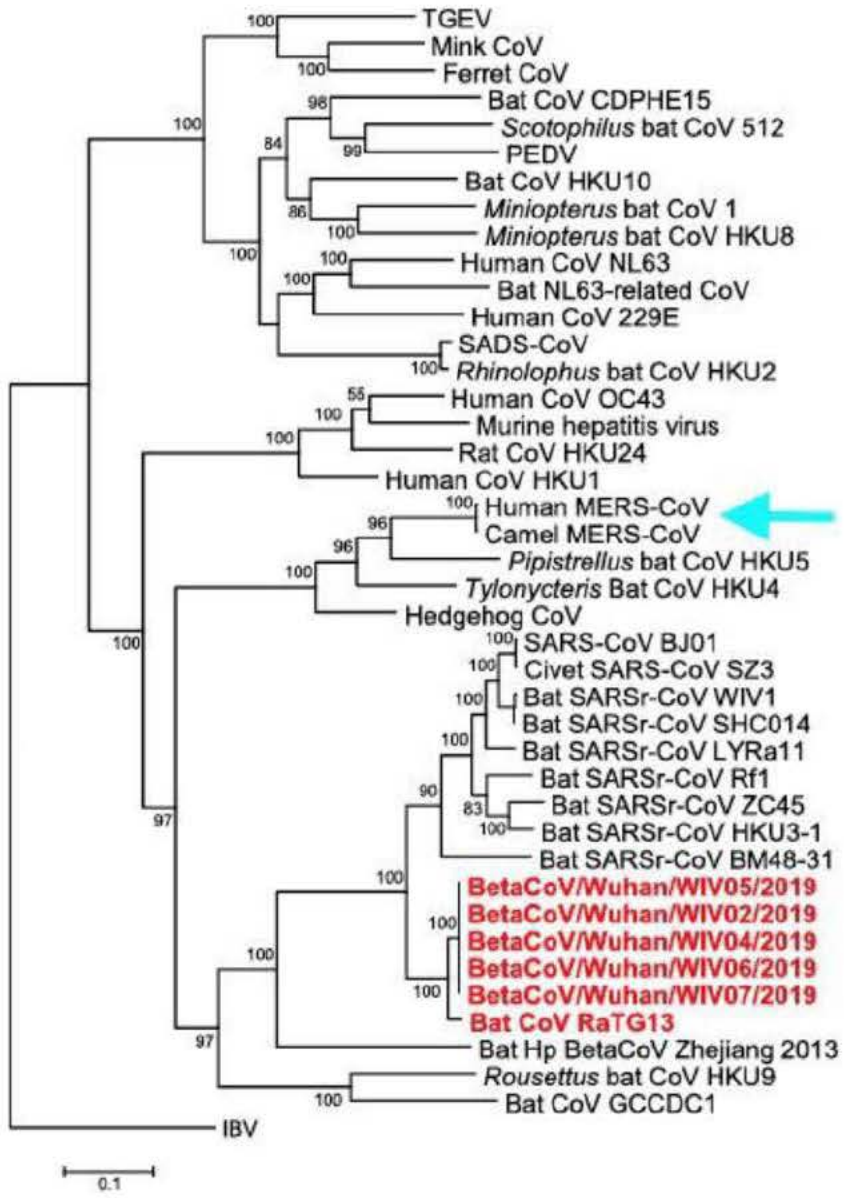
When the first 2019-nCoV sequence became available, researchers placed it on a family tree of known coronaviruses—which are abundant and infect many species—and found that it was most closely related to relatives found in bats. A team led by Shi Zheng-Li, a coronavirus specialist at the Wuhan Institute of Virology, reported on 23 January on bioRxiv that 2019-nCoV's sequence was 96.2% similar to a bat virus and had 79.5% similarity to the coronavirus that causes severe acute respiratory syndrome (SARS), a disease whose initial outbreak was also in China more than 15 years ago. But the SARS coronavirus has a similarly close relationship to bat viruses, and sequence data make a powerful case that it jumped into people from a coronavirus in civets that differed from human SARS viruses by as few as 10 nucleotides. That's one reason why many scientists suspect there's an "intermediary" host species—or several—between bats and 2019-nCoV.

According to Bedford's analysis, the bat coronavirus sequence that Shi Zheng-Li's team highlighted, dubbed RaTG13, differs from 2019-nCoV by nearly 1100 nucleotides. On nextstrain.org, a site he co-founded, Bedford has created coronavirus family trees (example below) that include bat, civet, SARS, and 2019-nCoV sequences. (The trees are interactive—by dragging a computer mouse over them, it's easy to see the differences and similarities between the sequences.)



Bedford's analyses of RaTG13 and 2019-nCoV suggest that the two viruses shared a common ancestor 25 to 65 years ago, an estimate he arrived at by combining the difference in nucleotides between the viruses with the presumed rates of mutation in other coronaviruses. So it likely took decades for RaTG13-like viruses to mutate into 2019-nCoV.

Middle East respiratory syndrome (MERS), another human disease caused by a coronavirus, similarly has a link to bat viruses. But studies have built a compelling case it jumped to humans from camels. And the phylogenetic tree from Shi's bioRxiv paper (below) makes the camel-MERS link easy to see.



The longer a virus circulates in a human populations, the more time it has to develop mutations that differentiate strains in infected people, and given that the 2019-nCoV sequences analyzed to date differ from each other by seven nucleotides at most, this suggests it jumped into humans very recently. But it remains a mystery which animal spread the virus to humans. "There's a very large gray area between viruses detected in bats and the virus now isolated in humans," says Vincent Munster, a virologist at the U.S. National Institute of Allergy and Infectious Diseases who studies coronaviruses in bats, camels, and others species.

Strong evidence suggests the marketplace played an early role in spreading 2019-nCoV, but whether it was the origin of the outbreak remains uncertain. Many of the initially confirmed 2019-nCoV cases—27 of the first 41 in one report, 26 of 47 in another—were connected to the Wuhan market, but up to 45%, including the earliest handful, were not. This raises the possibility that the initial jump into people happened elsewhere.

According to Xinhua, the state-run news agency, "environmental sampling" of the Wuhan seafood market has found evidence of 2019-nCoV. Of the 585 samples tested, 33 were positive for 2019-nCoV and all were in the huge market's western portion, which is where wildlife were sold. "The positive tests from the wet market are hugely important," says Edward Holmes, an evolutionary biologist at the University of Sydney who collaborated with the first group to publicly release a 2019-nCoV sequence. "Such a high rate of positive tests would strongly imply that animals in the market played a key role in the emergence of the virus."

Yet there have been no preprints or official scientific reports on the sampling, so it's not clear which, if any, animals tested positive. "Until you consistently isolate the virus out of a single species, it's really, really difficult to try and determine what the natural host is," says Kristian Andersen, an evolutionary biologist at Scripps Research.

One possible explanation for the confusion about where the virus first entered humans is if there was a batch of recently infected animals sold at different marketplaces. Or an infected animal trader could have transmitted the virus to different people at different markets. Or, Bedford suggests, those early cases could have been infected by viruses that didn't easily transmit and sputtered out. "It would be hugely helpful to have just a sequence or two from the marketplace [environmental sampling] that could illuminate how many zoonoses occurred and when they occurred," Bedford says.



A research group sent fecal and other bodily samples from bats they trapped in caves to the Wuhan Institute of Virology to search for coronaviruses.

EcoHealth Alliance

In the absence of clear conclusions about the outbreak's origin, theories thrive, and some have been scientifically shaky. A sequence analysis led by Wei Ji of Peking University and published online by the *Journal of Medical Virology* received substantial press coverage when it suggested that "snake is the most probable wildlife animal reservoir for the 2019-nCoV." Sequence specialists, however, pilloried it.

Conspiracy theories also abound. A CBC News report about the Canadian government deporting Chinese scientists who worked in a Winnipeg lab that studies dangerous pathogens was distorted on social media to suggest that they were spies who had smuggled out coronaviruses. The Wuhan Institute of Virology, which is the premier lab in China that studies bat and human coronaviruses, has also come under fire. "Experts debunk fringe theory linking China's coronavirus to weapons research," read a headline on a story in *The Washington Post* that focused on the facility.

Concerns about the institute predate this outbreak. *Nature* ran a story in 2017 about it building a new biosafety level 4 lab and included molecular biologist Richard Ebright of Rutgers University, Piscataway, expressing concerns about accidental infections, which he noted repeatedly happened

with lab workers handling SARS in Beijing. Ebright, who has a long history of raising red flags about studies with dangerous pathogens, also in 2015 criticized an experiment in which modifications were made to a SARS-like virus circulating in Chinese bats to see whether it had the potential to cause disease in humans. Earlier this week, Ebright questioned the accuracy of Bedford's calculation that there are at least 25 years of evolutionary distance between RaTG13—the virus held in the Wuhan virology institute—and 2019-nCoV, arguing that the mutation rate may have been different as it passed through different hosts before humans. Ebright tells *Science*Insider that the 2019-nCoV data are "consistent with entry into the human population as a natural accident."

Shi did not reply to emails from *Science*, but her longtime collaborator, disease ecologist Peter Daszak of the EcoHealth Alliance, dismissed Ebright's conjecture. "Every time there's an emerging disease, a new virus, the same story comes out: This is a spillover or the release of an agent or a bioengineered virus," Daszak says. "It's just a shame. It seems humans can't resist controversy and these myths, yet it's staring us right in the face. There's this incredible diversity of viruses in wildlife and we've just scratched the surface. Within that diversity, there will be some that can infect people and within that group will be some that cause illness."



A team of researchers from the Wuhan Institute of Virology and the EcoHealth Alliance have trapped bats in caves all over China, like this one in Guangdong, to sample them for coronaviruses.
EcoHealth Alliance

Daszak and Shi's group have for 8 years been trapping bats in caves around China to sample their feces and blood for viruses. He says they have sampled more than 10,000 bats and 2000 other species. They have found some 500 novel coronaviruses, about 50 of which fall relatively close to the SARS virus on the family tree, including RaTG13—it was fished out of a bat fecal sample they collected in 2013 from a cave in Moglang in Yunnan province. "We cannot assume that just because this virus from Yunnan has high sequence identity with the new one that that's the origin," Daszak says, noting that only a tiny fraction of coronaviruses that infect bats have been discovered. "I expect that once we've sampled and sampled and sampled across southern China and central China that we're going to find many other viruses and some of them will be closer [to 2019-nCoV]."

It's not just a "curious interest" to figure out what sparked the current outbreak, Daszak says. "If we don't find the origin, it could still be a raging infection at a farm somewhere, and once this outbreak dies, there could be a continued spillover that's really hard to stop. But the jury is still out on what the real origins of this are."

Posted in:

- Asia/Pacific

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 18:34:43 +0000
To: Tabak, Lawrence (NIH/OD) [E]
Subject: FW: Teleconference
Attachments: Coronavirus sequence comparison[1].pdf

FYI

From: Jeremy Farrar (b) (6)>
Sent: Saturday, February 1, 2020 1:13 PM
To: Fauci, Anthony (NIH/NIAID) [E] (b) (6)>; Patrick Vallance (b) (6)
Cc: Drosten, Christian (b) (6); Marion Koopmans (b) (6)>; R.A.M. Fouchier (b) (6); Edward Holmes (b) (6) Andrew Rambaut (b) (6) Kristian G. Andersen (b) (6); Paul Schreier (b) (6); (b) (6); Ferguson, Mike (b) (6); Collins, Francis (NIH/OD) [E] (b) (6)
Subject: Re: Teleconference

Kristen and Eddie have shared this and will talk through it on the call. Thank you.

Hope it will help frame the discussions.

From: Jeremy Farrar (b) (6)
Date: Saturday, 1 February 2020 at 15:34

1st February (2nd Feb for Eddie)
Information and discussion is shared in total confidence and not to be shared until agreement on next steps.

Dial in details attached.
Please mute phones.
I will be on email throughout – email Paul or I Paul if any problems
If you cannot make it, I will phone you afterwards to update.

One Hour

6am Sydney
8pm CET

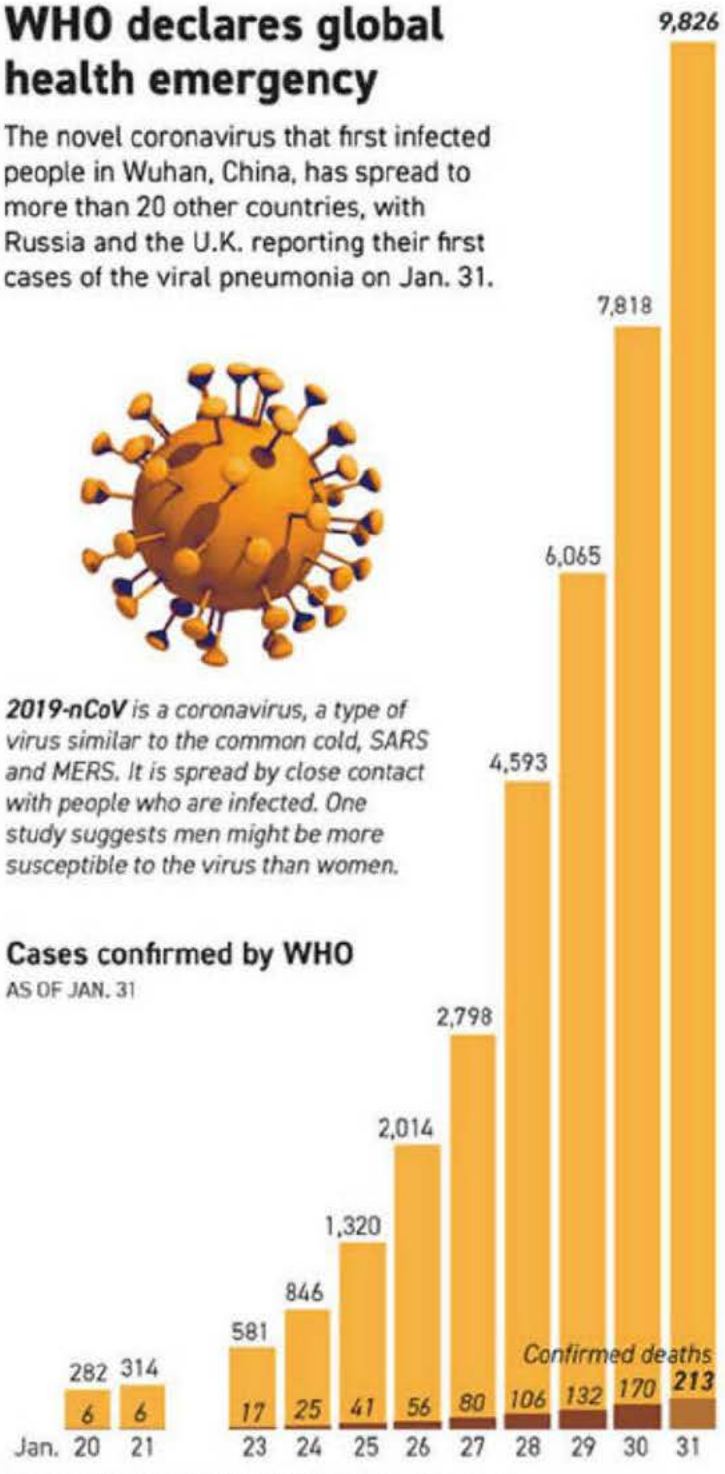
7pm GMT
2pm EST
11am PST
(Hope I have the times right!)

Thank you for the series of calls and for agreeing to join this call.

Agenda

- Introduction, focus and desired outcomes - JF
- Summary – KA
- Comments – EH
- Q&A – All
- Summary and next steps - JF

Kristian Anderson
Bob Garry - I have not been able to contact Bob. Please forward if you can.
Christian Drosten
Tony Fauci
Mike Ferguson
Ron Fouchier
Eddie Holmes
Marion Koopmans
Stefan Pohlmann
Andrew Rambaut
Paul Schreier
Patrick Vallance



Patterson Clark/POLITICO Pro DataPoint

"There is a compelling reason that the American people want us to consider this and so we're going to have to figure this one out and balance both of those issues," Hahn said, referring to safety and affordability.

The FDA for years has mostly stayed out of the debate around drug prices; the agency doesn't regulate the cost of medicines or health insurance coverage. But Hahn talked up FDA's role in getting prices down by approving more generics, acknowledging that "the American people are expecting us to do more." Trump has touted the FDA's record on boosting competition via generic approvals.

As FDA works on finalizing the importation rule, Hahn said the agency will be open to addressing criticism that states can't save money bringing in drugs from Canada if the pathway is too burdensome. But he stressed safety is tantamount. "Our primary concern is the protection of the drug supply," he said.

Hahn said he has also talked with CMS Administrator Seema Verma about addressing costs of new brand-name products that are approved with limited data sets, similar to the way CMS decides to cover some medical devices. That approach — known as coverage with evidence development — lets CMS cover a new product on the condition that manufacturers keep providing data.

FDA has not done that, but new medicines are increasingly being approved on smaller clinical trials without hard data on clinical benefits — and can come with six-figure price tags.

As an academic, Hahn had co-written an editorial suggesting that payments for newly approved radiation oncology devices could be linked to older products until enough evidence builds up to show that the new products are superior. Only then would manufacturers have more pricing leeway.

"It's a CMS call about coverage with evidence development, but I do think in this world where we are concerned, and rightfully so, about the cost of medicine and health et cetera, that we should be looking at all avenues to approach that," he told POLITICO.

Over the last few years, some critics have said the FDA is overcorrecting and moving too quickly to approve drugs without adequate evidence. But Hahn did not indicate he would put the brakes on.

"At the end of the day there is this balance between the gold standard and being efficient and getting things in people's hands I'm totally confident in the agency's ability to do that."

Hahn must balance all that while leading the FDA's response to the Wuhan crisis, which has heightened some lawmakers' concern about U.S. reliance on Chinese drug manufacturing after incidents of contamination with carcinogens.

"We have to be concerned about the supply chain to make sure that we have enough of what we need if there are any potential outbreaks here," Rep. Susan Brooks (R-Ind.) said after a closed-door briefing Thursday for Energy and Commerce committee members with top health officials. The fact that China manufactures much of the protective medical gear used in U.S. hospitals and clinics "should cause us to be reexamining what we're doing in China versus what should be brought back to this country." she said.

Outside of the coronavirus, a host of thorny regulatory issues await Hahn. Industry and lawmakers have pressed for a clear FDA framework on selling cannabidiol, the popular hemp and marijuana byproduct decriminalized by the 2018 farm bill — and since sold as medicine, dietary supplements and infused in food, cosmetics and skincare products.

"You cannot walk down the street without seeing the products" but there is a dearth of solid data on how safe and effective CBD actually is, said Hahn.

Those CBD challenges have fueled larger discussions about how to better regulate the vast dietary supplement market, where manufacturers often push legal boundaries by making unverified claims about how herbal or homeopathic products can help people.

"It will be something else next," said Hahn. We don't want to overstep our bounds but we want to make sure that safe and effective products are in the hands of people."

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From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 17:51:31 +0000
To: Auchincloss, Hugh (NIH/NIAID) [E]
Subject: RE: Continued

OK. Stay tuned.

-----Original Message-----
From: Auchincloss, Hugh (NIH/NIAID) [E] (b) (6)>
Sent: Saturday, February 1, 2020 11:47 AM
To: Fauci, Anthony (NIH/NIAID) [E] <(b) (6)>
Subject: Continued

The paper you sent me says the experiments were performed before the gain of function pause but have since been reviewed and approved by NIH. Not sure what that means since Emily is sure that no Coronavirus work has gone through the P3 framework. She will try to determine if we have any distant ties to this work abroad.

Sent from my iPad

From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 13:19:06 +0000
To: Tabak, Lawrence (NIH/OD) [E]
Subject: FW: IMPORTANT
Attachments: Baric, Shi et al - Nature medicine - SARS Gain of function.pdf

Here it is

Anthony S. Fauci, MD
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From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 12:29:01 +0000
To: Auchincloss, Hugh (NIH/NIAID) [C] (b) (6)
Cc: (b) (6)
Subject: IMPORTANT
Attachments: Baric, Shi et al - Nature medicine - SARS Gain of function.pdf

Hugh:

It is essential that we speak this AM. Keep your cell phone on. I have a conference call at 7:45 AM with Azar. It likely will be over at 8:45 AM. Read this paper as well as the e-mail that I will forward to you now. You will have tasks today that must be done.

Thanks,

Tony

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From: Fauci, Anthony (NIH/NIAID) [E]
Sent: Sat, 1 Feb 2020 02:48:59 +0000
To: Kadlec, Robert (OS/ASPR/IO)
Cc: (b) (6)
Subject: FW: Science: Mining coronavirus genomes for clues to the outbreak's origins

Bob:
This just came out today. Gives a balanced view.
Best,
Tony

From: Folkers, Greg (NIH/NIAID) [E] (b) (6)>
Sent: Friday, January 31, 2020 8:43 PM
Subject: Science: Mining coronavirus genomes for clues to the outbreak's origins



As part of a long-running effort to see what viruses bats harbor, researchers in China collect one from a cave in Guandong.
EcoHealth Alliance

Mining coronavirus genomes for clues to the outbreak's origins

By Jon CohenJan. 31, 2020 , 6:20 PM
attaaaggtt tataccttcc caggtaacaa accaaccaac tttcgatctc ttgtagatct ...
That string of apparent gibberish is anything but: It's a snippet of a DNA sequence from the viral pathogen, dubbed 2019 novel coronavirus (2019-nCoV), that is overwhelming China and frightening the entire world. Scientists are publicly sharing an ever-growing number of full sequences of the virus from patients—53 at last count in the Global Initiative on Sharing All Influenza Data database. These viral genomes are being intensely studied to try to understand the origin of 2019-nCoV and how it fits on the family tree of related viruses found in bats and other species. They have also given glimpses into what this newly discovered virus physically looks like, how it's changing, and how it might be stopped.