

← **Collectie**



**AlleBurgers**  
@AlleBurgers



1\n

Tijdlijn: Dichtbij de oorsprong van SARS-CoV-2:  
De doos van Pandora is open.



@emilykopp, 12 september 2022



usrtk.org

Timeline: The proximal origin of SARS-CoV-2 - U.S. Right to Know

Read our timeline of evidence surrounding the Proximal Origin of SARS-CoV-2, one of the most influential scientific articles in history.

10:36 p.m. · 26 nov. 2022 · Twitter for Android

7 Retweets   3 Geciteerde Tweets   18 Vind-ik-leuks



Je antwoord tweeten

Beantwoorden



**AlleBurgers** @AlleBurgers · 26 nov.  
Als antwoord op @AlleBurgers



2\

22-11-2022 Geredigeerde emails komen nu volledig beschikbaar via USRTK.

De rol van Koopmans en Fouchier blijkt de kathalisator te zijn in gesprekken begin 2020 olv Fauci over de positie van overheden/WHO, financiers, media en wetenschappers voor #OriginOfCovid.

**From:** Fauci, Anthony (NIH/NIAID) [E]  
**Sent:** Sat, 1 Feb 2020 00:38:35 +0000  
**To:** Jeremy Farrar  
**Cc:** Kristian G. Andersen  
**Bcc:** Conrad, Patricia (NIH/NIAID) [E];Mascola, John (NIH/VRC) [E];Conrad, Patricia (NIH/NIAID) [E]  
**Subject:** RE: Phone call

Jeremy:  
 I just got off the phone with Kristian Anderson and he related to me his concern about the Furine site mutation in the spike protein of the currently circulating 2019-nCoV. I told him that as soon as possible he and Eddie Holmes should get a group of evolutionary biologists together to examine carefully the data to determine if his concerns are validated. He should do this very quickly and if everyone agrees with this concern, they should report it to the appropriate authorities. I would imagine that in the USA this would be the FBI and in the UK it would be MIS. It would be important to quickly get confirmation of the cause of his concern by experts in the field of coronaviruses and evolutionary biology. In the meantime, I will alert my US. Government official colleagues of my conversation with you and Kristian and determine what further investigation they recommend. Let us stay in touch.  
 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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**From:** Jeremy Farrar (b) (6)  
**Sent:** Friday, January 31, 2020 5:57 PM



AlleBurgers @AlleBurgers · 26 nov.



3a\

Wat zien we?

1 feb 2020 telcon van Fauci: er zijn grote zorgen over de 'furine-splitsingsplaats' van SARS2.

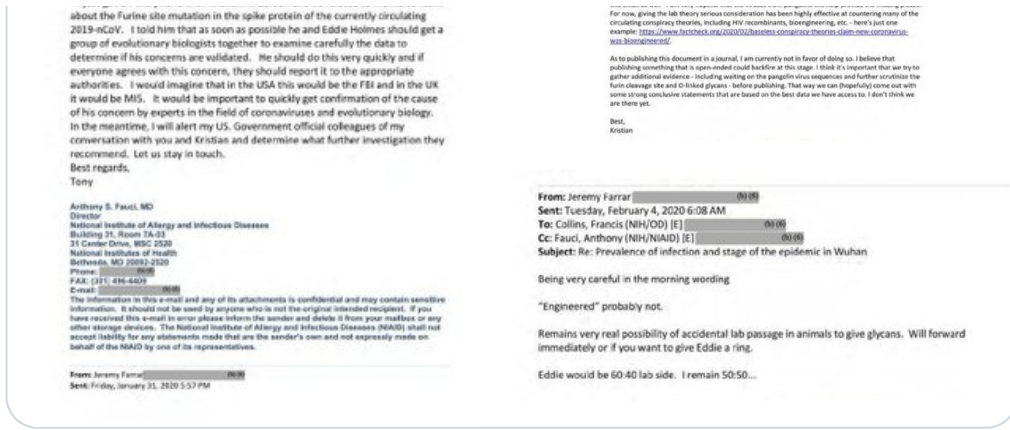
Besluit: brief "Proximal Origin", publiceren en lab-oorsprong weg zetten als complot.

Echter Fauci, Farrar, Holmes, Andersen dachten privé meer aan lab-oorsprong.

**From:** Fauci, Anthony (NIH/NIAID) [E]  
**Sent:** Sat, 1 Feb 2020 00:38:35 +0000  
**To:** Jeremy Farrar  
**Cc:** Kristian G. Andersen  
**Bcc:** Conrad, Patricia (NIH/NIAID) [E];Mascola, John (NIH/VRC) [E];Conrad, Patricia (NIH/NIAID) [E]  
**Subject:** RE: Phone call

Jeremy:  
 I just got off the phone with Kristian Anderson and he related to me his concern

On 8 Feb 2020, at 22:15, Kristian G. Andersen <[redacted]> wrote:  
 A lot of good discussion here, so I just wanted to add a couple of things for context that I think are important - and why what we're considering is far from "another conspiracy theory", but rather is taking a valid scientific approach to a question that is increasingly being asked by the public, media, scientists, and politicians (i.e., I have been contacted by Science, NYU, and many other news outlets over the last couple of days about this exact question).  
 To Ron's question, passage of SARS-like CoVs has been ongoing for several years, and more specifically in Wuhan under BSL-2 conditions - see references 12-13 in the document for a few examples. The fact that Wuhan became the epicenter of the ongoing epidemic caused by nCoV is likely an unfortunate coincidence, but it raises questions that would be wrong to dismiss out of hand. Our main work over the last couple of weeks has been focused on trying to disprove any type of lab theory, but we are at a crossroad where the scientific evidence isn't conclusive enough to say that we have high confidence in any of the three main theories considered, like fiddle - and I believe Rob, Andrew, and everybody on this email as well - I am very hopeful that the viruses from samoa will help provide the missing pieces.



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**AlleBurgers** @AlleBurgers · 26 nov.

3b\  
Veel betrokkenen bij Proximal Origin zijn afkomstig van Oxford Zoology Department, oa Holmes, Rambaut, Worobey en Pybus.

Ze werken al bijna 30 jaar samen om een theorie over kunstmatige oorsprong van HIV te 'ontkrachten'.

ht [@breakfast\\_dogs](#)

**Dog's Breakfast** @breakfast\_dogs · 23 nov.

Many figures involved in the efforts to show a natural origin of Covid are linked to Oxford Zoology department including Holmes, Rambaut, Worobey and Pybus. They've worked together for nearly 30 years to "debunk" a theory of an artificial origin of HIV.

[aidsorigins.com](http://aidsorigins.com)  
Deze collectie weergeven

Many readers of my book "The River" (Penguin/Allen Lane; 1999; 2000) will recognise the Department of Zoology at Oxford as the academic home of Professor William Hamilton, who wrote the powerful Foreword to "The River", and who from 1993 up to his untimely death in 2000 was my mentor and main scientific supporter. Several members or former members of the Department of Zoology, including Andrew Rambaut, Oliver Pybus and Michael Worobey have been promoting the bushmeat hypothesis since around the time of Hamilton's death, and one of them, Eddie Holmes, from some years before that. Two of them (Rambaut and Pybus) are co-authors of the present article, and their style and prejudices are clearly visible in its content.

Again, this was one of the tactics used by opponents of the OPV theory both before and after the Royal Society (RS) meeting. Articles and letters that supported the OPV hypothesis were routinely rejected by journals such as Nature and Science, while dozens of submissions in support of the bushmeat hypothesis were published. And nowhere was the OPV theory described, save in passing in reviews of my book *The River* by commentators such as Weiss and Wain-Hobson. Both their reviews, in Science and Nature Medicine, were essentially fair, but they led to later statements by the same men which prematurely declared the theory to have been disproved, and which were based more on assertion than on sound and balanced scientific reasoning. I have been told by several sources that by 2000 Robin Weiss held an unofficial role of special advisor on AIDS for Nature and to a lesser extent Science. He and a Science journalist, Jon Cohen, effectively decided what was published on AIDS in these leading journals, and what wasn't.

Latham identifies seven individual members of the so-called OPV1 team. As I have pointed out in previous posts, four of these seven have a great history in that they have previously played leading roles in attempts to debunk the OPV theory of how AIDS began. I had discussions with all four men in 2000 and the year immediately following, when I suspected (and now firmly believe) that their opposition to OPV/AIDS was based on erroneous analysis. They are Eddie Holmes, Andrew Rambaut, Michael Worobey and Robert Garry. At the start of the millennium the first three were all members of the Department of Zoology at the University of Oxford, where they effectively established an informal coalition in opposition to the OPV theory. This happened shortly after the death in March 2000 of Bill Hamilton, from the same Oxford department, who was my mentor and one of the leading proponents of the OPV theory. The fourth man, Robert Garry, is an American researcher who

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**AlleBurgers** @AlleBurgers · 26 nov. ...

4a\

Voorstanders van natuurlijke oorsprong waren bezorgd over het risicovol werk aan SARS in Wuhan in BSL-2 lab (laag veiligheidsniveau)

Dit gold ook voor de financiers, die dit onderzoek bij Wuhan Institute of Virology hadden gefinancierd: Farrar/Wellcome; het "Wilde Westen".

**From:** Jeremy Farrar  
**Sent:** Tue, 4 Feb 2020 20:26:23 +0000  
**To:** Collins, Francis (NIH/OD) [E];Fauci, Anthony (NIH/NIAID) [E]  
**Subject:** Re: Prevalence of infection and stage of the epidemic in Wuhan

Wild West....

**From:** Francis Collins (b) (6)  
**Date:** Tuesday, 4 February 2020 at 20:23  
**To:** Jeremy Farrar (b) (6), "Fauci, Anthony (NIH/NIAID) [E]" (b) (6)  
**Subject:** RE: Prevalence of infection and stage of the epidemic in Wuhan

Surely that wouldn't be done in a BSL-2 lab?

**From:** Jeremy Farrar (b) (6)  
**Sent:** Tuesday, February 4, 2020 9:03 AM  
**To:** Fauci, Anthony (NIH/NIAID) [E] <(b) (6)> Collins, Francis (NIH/OD) [E] <(b) (6)>  
**Subject:** Re: Prevalence of infection and stage of the epidemic in Wuhan

Exactly!

**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

?? Serial passage in ACE2-transgenic mice

**AlleBurgers** @AlleBurgers · 26 nov. ...

4b\

Farrar/Wellcome verandert de discussie compleet. Waarschijnlijk doelt hij op de WHO die gemakkelijk manipuleerbaar is voor betrokkenen zoals bleek bij Covid/Airborne.

[drive.google.com/file/d/17jJZ2d...](https://drive.google.com/file/d/17jJZ2d...)

**AlleBurgers** @AlleBurgers · 26 nov. ...

5\

Zorgen in de goep over lab-oorsprong werd met de term "chagrijn" weggezet.

Desondanks werd gedacht aan het verkrijgen van de furine-splitsingsplaats via seriële passage (snel ernstig/gevaarlijk maken van virussen door infectie in dierpopulaties); Fouchier's deskundigheid.

**From:** Jeremy Farrar  
**Sent:** Wed, 5 Feb 2020 06:57:54 +0000  
**To:** Collins, Francis (NIH/OD) [E];Fauci, Anthony (NIH/NIAID) [E];Edward Holmes  
**Subject:** FW: Origins  
**Attachments:** Summary.pdf

Tony and Francis

The revised draft from Eddie, copied here.

I asked Eddie about the addition of the glycans and where these could be added accidentally by passage in lab animals or of course in the wild – the reply from Bob and Kristian

?Kristian that's correct about everything he said for the P residue. It's what's shifted me to thinking that the insert of the furin site is the result of cell culture passage [or less likely intense transmission in a nonbat host]. Really need to see the data from Ron about generating the furin cleavage site on in vitro passage. Really!

CoV come with or without a furin site. CoV without a furin site are said to be non-cleaved and rely on endosomal proteases like cathepsin for entry. However if you infect a virus like SARS in culture in the presence of exogenous protease like trypsin its 100X more effective at entering because the spike gets cleaved and it can enter at the cell surface.

You have to infect flu viruses (the ones without the multibasic cleavage site) in the presence of trypsin, and include trypsin in the overlay if you want to get virus spread aka plaques.

This also contributes to the pathogenicity of - well - highly pathogenic flu virus – different tissues have different proteases and are able to “activate” flu to different extents - if the flu v has a furin cleavage site it has a lot more choices and can more easily go systemic.

This is an excellent review on CoV fusion – deals with all the complexities:

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3397359/>

Bottom line – I think that if you put selection pressure on a Cov without a furin cleavage site in cell culture you could well generate a furin cleavage site after a number of passages (but let's see the data Ron!). It will infect a lot better if it can effectively fuse at the cell surface and doesn't have to rely on endosomal cleavage and receptor mediated endocytosis..?

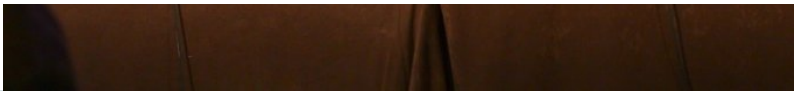


**AlleBurgers** @AlleBurgers · 26 nov. ⋮

6\

Fouchier (ErasmusMC) is bekend om zijn wisselende verklaringen over het risico en het onderschatten van de kans op een lab-ongeval bij functie-aanpassing van virussen. De meest beruchte controverses in de virologie, tot de [#OriginOfCovid](#).





usrtk.org

Paper critical of 'lab leak theory' cribbed ideas from controversial gain...  
The virologist behind the most notorious lab-generated virus in history played an undisclosed role in persuading the world that the COVID-19 ...



**AlleBurgers** @AlleBurgers · 26 nov.



7\

Een concept van "Proximal Origin" spreekt nog van 'seriële passage' doelend op een geconstrueerd virus.

Fauci en Collins maakten zich er grote zorgen om.

From: Jeremy Farrar  
Sent: Fri, 7 Feb 2020 18:54:20 +0000  
To: Collins, Francis (NIH/OD) [E]; Fauci, Anthony (NIH/NIAID) [E]  
Cc: Tabak, Lawrence (NIH/OD) [E]  
Subject: Re: Revised draft

I do not think so yet but ...chasing!

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From: Francis Collins (b) (6)  
Date: Friday, 7 February 2020 at 12:17  
To: Jeremy Farrar (b) (6) >, "Fauci, Anthony (NIH/NIAID) [E]" (b) (6)  
Cc: "Tabak, Lawrence (NIH/OD) [E]" (b) (6)  
Subject: RE: Revised draft

Has the actual sequence of the pangolin coronavirus isolate been released? That will be VERY interesting. Does it have the furin cleavage site?

Francis

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From: Jeremy Farrar (b) (6)  
Sent: Friday, February 7, 2020 1:21 AM  
To: Collins, Francis (NIH/OD) [E] (b) (6); Fauci, Anthony (NIH/NIAID) [E] (b) (6)  
Subject: Re: Revised draft

Plus two updates

- Reports coming out overnight that Chinese group have pangolin viruses that are 99% similar. This would be a crucially important finding and if true could be the 'missing link' and explain a natural evolutionary link.

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From: Jeremy Farrar  
Sent: Tue, 4 Feb 2020 20:26:23 +0000  
To: Collins, Francis (NIH/OD) [E]; Fauci, Anthony (NIH/NIAID) [E]  
Subject: Re: Prevalence of infection and stage of the epidemic in Wuhan

Wild West....

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Subject: RE: Prevalence of infection and stage of the epidemic in Wuhan

?? Serial passage in ACE2-transgenic mice



**AlleBurgers** @AlleBurgers · 26 nov.



8a\

(Ongeziene) informatie over corona bij schubdieren (pangolins) doet de discussie kantelen van lab naar natuurlijk. Holmes publiceert hier al op 7 februari over.

Later ontstond een bizar probleem; schubdieren werden niet verkocht op de Wuhan Market.

On 8 Feb 2020, at 22:15, Kristian G. Andersen (b) (6) > wrote:

A lot of good discussion here, so I just wanted to add a couple of things for context that I think are important - and why what we're considering is far from "another conspiracy theory", but rather is taking a valid scientific approach to a question that is increasingly being asked by the public, media, scientists, and politicians (e.g., I have been contacted by Science, NYT, and many other news outlets over the last couple of days about this exact question).

To Ron's question, passage of SARS-like CoVs have been ongoing for several years, and more specifically in Wuhan under BSL-2 conditions - see references 12-15 in the document for a few examples. The fact that Wuhan became the epicenter of the ongoing epidemic caused by nCoV is likely an unfortunate coincidence, but it raises questions that would be wrong to dismiss out of hand. Our main work over the last couple of weeks has been focused on trying to *disprove* any type of lab theory, but we are at a crossroad where the scientific evidence isn't conclusive enough to say that we have high confidence in any of the three main theories considered. Like Eddie - and I believe Bob, Andrew, and everybody on this email as well - I am very hopeful that the viruses from pangolins will help provide the missing pieces. For now, giving the lab theory serious consideration has been highly effective at countering many of the circulating conspiracy theories, including HIV recombinants, bioengineering, etc. - here's just one example: <https://www.factcheck.org/2020/02/baseless-conspiracy-theories-claim-new-coronavirus-was-bioengineered/>.

As to publishing this document in a journal, I am currently not in favor of doing so. I believe that publishing something that is open-ended could backfire at this stage. I think it's important that we try to gather additional evidence - including waiting on the pangolin virus sequences and further scrutinize the furin cleavage site and O-linked glycans - before publishing. That way we can (hopefully) come out with some strong conclusive statements that are based on the best data we have access to. I don't think we are there yet.

Best,  
Kristian



**AlleBurgers** @AlleBurgers · 26 nov. ...

8b\

4 februari 2020: het is dezelfde tijd dat hoofdauteur Andersen de National Academy of Sciences informeert dat lab-oorsprong een idiote samenzweringstheorie was.



**AlleBurgers** @AlleBurgers · 26 nov. ...

8c\

Echter, veel betrokkenen zetten in op een lab-incident. 🙄

Maar draaien bij, reden: angst voor GOF-moratorium en strenge regelgeving.

ht @Rosanna38510044



**Rossana Segreto** @Rossana38510044 · 23 nov.

Als antwoord op @HansMahncke

He probably had very good reasons to do so.

[science.org/content/articl...](https://www.factcheck.org/content/article...)

2/2019: "Controversial lab studies that modify bird flu viruses in ways that could make them more risky to humans will soon resume after being on hold for more than 4 years."



**AlleBurgers** @AlleBurgers · 26 nov. ...

8d\


22-11-22. Die zorg blijkt terecht. De VS-Senaat doet een oproep aan het congres om een moratorium in te stellen voor riskant (GOF)onderzoek.

Tevens wil de Senaat onderzoek naar EcoHealth Alliance, partner van Koopmans' Viroscience ErasmusMC (Kuipers)

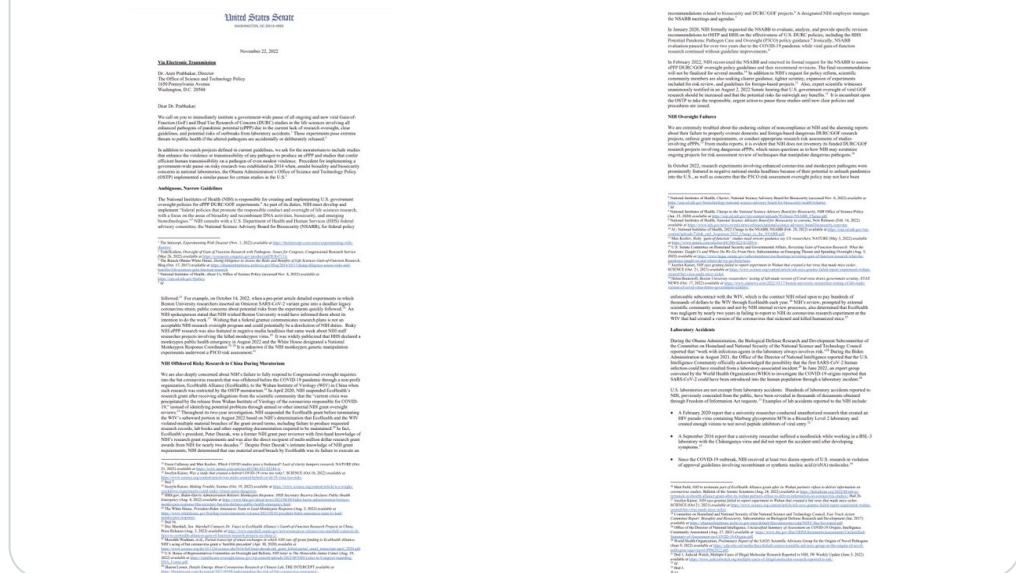
 **AlleBurgers @AlleBurgers** · 26 nov.

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US Congress call on a moratorium on risky (GOF) research.

In NL ErasmusUMC, Viroscience with Marion Koopmans, Fouchier incl management of Kuipers, today Min. of Health, partnered with EcoHealth in the coverup of sound #OriginOfCovid research, and presumably GOF research.  [twitter.com/R\\_H\\_Ebright/st...](https://twitter.com/R_H_Ebright/st...)

Deze collectie weergeven



The screenshot shows a tweet from AlleBurgers @AlleBurgers dated November 26, 2022. The tweet text is: "US Congress call on a moratorium on risky (GOF) research." Below the text is a link to a PDF document titled "United States Senate" with the subtitle "Introduction, Background, Recommendations". The document appears to be a report or hearing transcript regarding research, specifically mentioning "GOF" (Gain-of-Function) research and "risky" research. The document is partially visible, showing sections like "Introduction", "Background", and "Recommendations".

1 1 4 



**AlleBurgers @AlleBurgers** · 26 nov.

8e\

Andersen accepteert het halfzachte argument van Fouchier over een bestaande backbone. Maar dat werd 4 februari al weer losgelaten.

Niet bekend was dat er al een voorstel lag om backbones door WIV te laten construeren (DEFUSE).

 **Louis R Nemzer @BiophysicsFL** · 23 nov.

This whole "see, they totally considered a lab leak" is not really true at all for the possibility of an engineered origin. KGA allowed Fouchier's lame argument about using an existing backbone to scratch it out by



Feb 4.

They didn't even know about DEFUSE or unpublished seqs!  
Deze collectie weergeven



AlleBurgers @AlleBurgers · 26 nov.



8f\

Fouchier somt een reeks argumenten tegen een lab-oorsprong, veelal uitgaande van dubieuze inschattingen van kansen. Ze worden klaarblijkelijk geaccepteerd.

Bespreking, zie bijlagen en ht @WashburneAlex



On 2 Feb 2020, at 09:30, R.A.M. Fouchier  **NOT** :

Dear Jeremy and others,

This was a very useful teleconference. Given the evidence presented and the discussions around it, I would conclude that a follow-up discussion on the possible origin of 2019-nCoV would be of much interest. However, I doubt if it needs to be done on very short terms, given the importance of other activities of the scientific community, WHO and other stakeholders at present. It is my opinion that a non-natural origin of 2019-nCoV is highly unlikely at present. Any conspiracy theory can be approached with factual information. I have written down some of the counter-arguments. It is a bit long (below) but wanted to share it with you anyway.

Thanks for organizing this on such short notice,  
Kind regards  
Ron

Ron's notes:

An accusation that nCoV-2019 might have been engineered and released into the environment by humans (accidental or intentional) would need to be supported by strong data, beyond reasonable doubt. It is good that this possibility was discussed in detail with a team of experts. However, further debate about such accusations would unnecessarily distract top researchers from their active duties and do unnecessary harm to science in general and science in China in particular. At present, the arguments that nCoV-2019 could have emerged from an animal source is much stronger than other possibilities.

Observations about the genome that were inferred to be suggestive for a non-animal origin:

1. HIV-like sequences in the spike protein.
2. Level of mutations in the spike protein region.

3. Presence of a furin cleavage site in the middle of spike

4. BamHI1 restriction site at the end of the spike sequence

5. An F-to-Y substitution in the receptor-binding domain of spike

6. Potential O-linked glycan sites protecting the cleavage site of spike

1. The basic publication by Prokhorov and colleagues from July 2019 (Genome stability of influenza B in the 2019-2020 winter season in 2019) and the fact that the amino acid sequence of the spike protein is highly conserved. The amino acid sequence of the spike protein is highly conserved. There are no other known sequences that are highly similar to the spike protein. Such conservation is especially true for the spike protein.

2. Amino acid conservation in the furin cleavage site in the spike protein. The furin cleavage site is a highly conserved site in the spike protein. The furin cleavage site is a highly conserved site in the spike protein. The furin cleavage site is a highly conserved site in the spike protein.

3. The BamHI1 restriction site is a highly conserved site in the spike protein. The BamHI1 restriction site is a highly conserved site in the spike protein. The BamHI1 restriction site is a highly conserved site in the spike protein.

4. The F-to-Y substitution in the receptor-binding domain of spike is a highly conserved site in the spike protein. The F-to-Y substitution in the receptor-binding domain of spike is a highly conserved site in the spike protein. The F-to-Y substitution in the receptor-binding domain of spike is a highly conserved site in the spike protein.

5. The potential O-linked glycan sites in the spike protein are a highly conserved site in the spike protein. The potential O-linked glycan sites in the spike protein are a highly conserved site in the spike protein. The potential O-linked glycan sites in the spike protein are a highly conserved site in the spike protein.

Additional arguments:

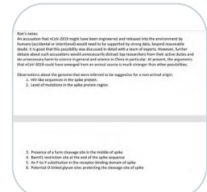
A. Influenza virus spike is a highly variable protein in general, useful for host adaptation and other strong natural selection.

B. The furin cleavage site is a highly conserved site in the spike protein. The furin cleavage site is a highly conserved site in the spike protein. The furin cleavage site is a highly conserved site in the spike protein.

C. The patterns of mutations we observe in the receptor-binding domain and the protease cleavage sites of spike are typical for host-switched naturally evolving viruses. We can infer it for the naturally evolved human coronaviruses, we have seen it for the natural zoonoses of SARS-CoV and HKU22-CoV. Convergent (parallel) evolutionary events are common in virology. Also for influenza, we see the same mutations emerge during the pandemics of 1918 (H1N1), 1957 (H2N2) and 1968 (H3N2), in the 2013 zoonotic H7N9 virus and e.g. an epizootic in seals in 2014 (H10N7). Regardless of the divergent subtype, we see identical substitutions in the receptor-binding domains, identical substitutions in polymerase, and non-identical substitutions with identical phenotypic consequences (e.g. stability) in the genome. The fact that we (think we) see recognizable traits in spike does not mean it must be man-made.

D. We do not know the source of 2019-nCoV. There is ~30 years of evolutionary gap between 2019-nCoV and the closest bat virus relative. These 30 years may have been in any host. We have no idea what might have happened (in evolutionary sense) between BatCoV/NATG13 and 2019-nCoV. We should rest our case until we have a close relative of 2019-nCoV.

 Alex Washburne @WashburneAlex · 22 nov.



We now have access to Ron Fouchier's notes from the call. He starts with a strong zoonotic prior & fleshes out the evidence for non-animal origin they were considering at the time.

...  
Deze collectie weergeven

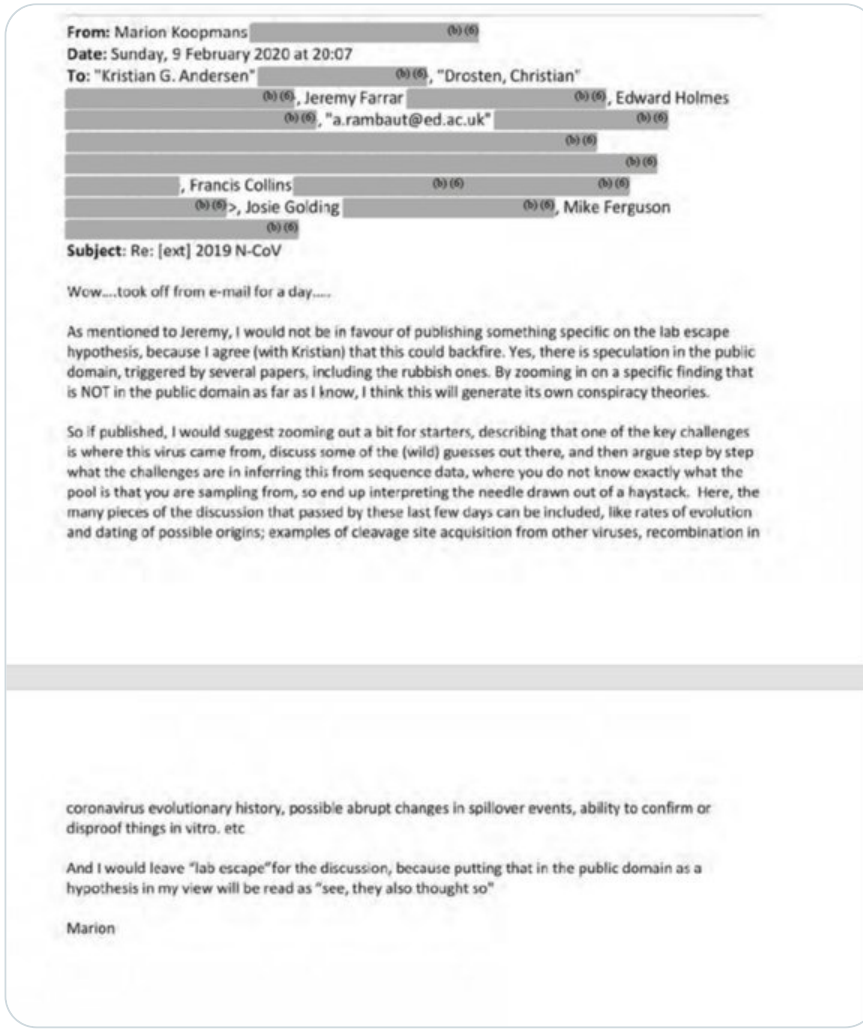


AlleBurgers @AlleBurgers · 26 nov.



9\

Koopmans argumenteert onwetenschappelijk en onethisch dat de verschillende artikelen over lab-oorsprong niet in het publieke domein zijn. En dat daarom er geen aandacht aan moet worden besteed. "Het geeft aanleiding tot complottheorieën" (sic, AB).



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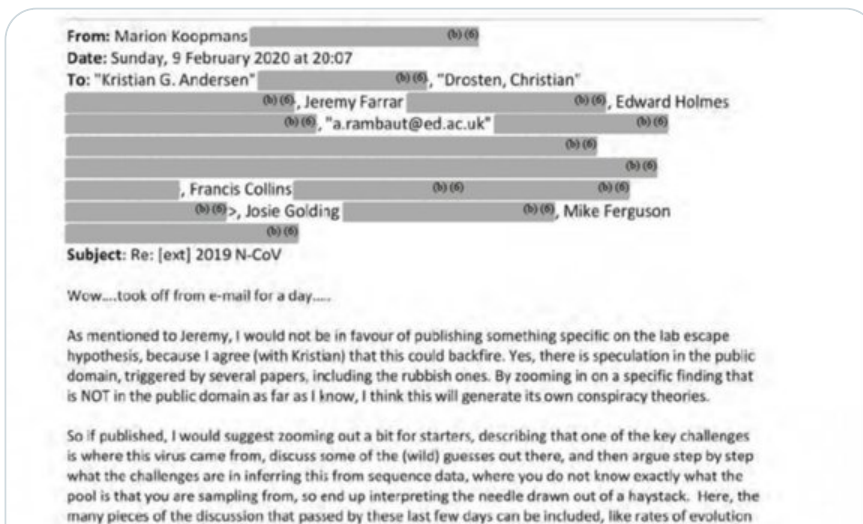
**AlleBurgers** @AlleBurgers · 26 nov.

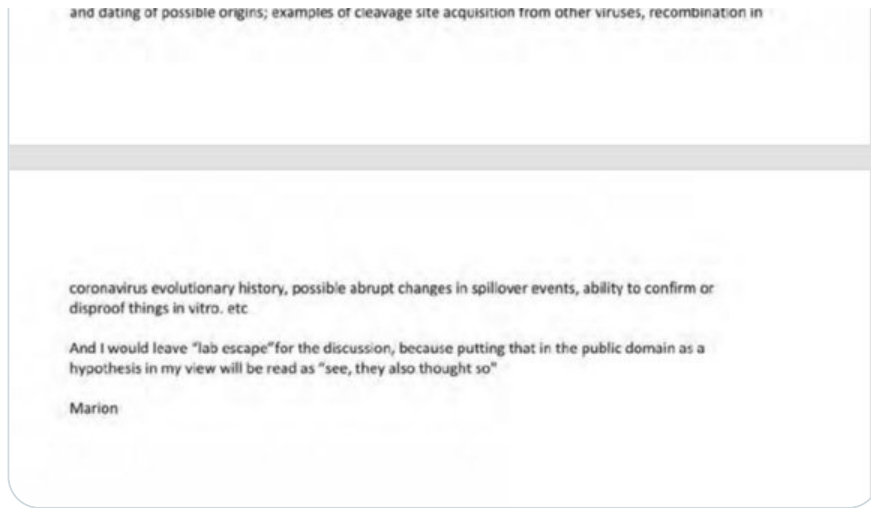


10\

Koopmans pleit ook voor een benadering van de verschillende mogelijkheden, die "... end up interpreting the needle drawn out of a haystack".

Nooit eerder zo'n onwetenschappelijke benadering gezien, met zo'n sterke taal en zo weinig bewijs. 😞





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**AlleBurgers** @AlleBurgers · 26 nov.



11\

April 2020: Fauci citeert Proximal Origin aan de media, en hoopt vragen over lab-oorsprong weg te nemen.

Onderzoekers (oa Koopmans/ Fouchier) en financiers verhullen onethisch/onwetenschappelijk betrokkenheid bij de brief

Ze kunnen niet meer terug.



**Alina Chan** @Ajchan · 23 nov.

By April, the Proximal Origin letter was being cited by Fauci to the media to shut down questions about an accidental lab leak #OriginOfCovid - without revealing their involvement in the genesis of the letter.

[twitter.com/Ayjchan/status...](https://twitter.com/Ayjchan/status...)

Deze collectie weergeven



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12\

Conclusies

Ht @AlexWashburne geeft hierboven een mooie inhoudelijke samenvatting, met name over de co-incidenties en kansbenaderingen van Fouchier, maar komt nog niet toe aan de achterliggende redenen. Een eerste poging [↓](#)



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13\

1. We zien dat virologen/veterinairen als Koopmans, Fouchier ea hegemonisch koninkrijkjes hebben gebouwd, met groepsdruk en bedrog. Ze pronken met hun status.

ht [@moos\\_tbe](#) [@trishgreenhalgh](#) The Lancet



**Alex Washburne** @WashburneAlex · 22 nov.

Reading through these emails & sharing observations in this thread.

1/ [twitter.com/JamesCTobias/s...](https://twitter.com/JamesCTobias/s...)

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14\

2. De emails laten een doelbewuste cover-up zien. Veel voorbeelden zijn hierboven genoemd.

Drijfveren zijn budget, grants, status, reputatie, paralleliteit van belangen met financiers, geo- en nationale politiek, big farma/vaccins.



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15\

3. De virologen hebben een duidelijk, maar dubieuze agenda. Andersens verwoordt die als volgt: "Ons belangrijkste werk van de afgelopen weken was gericht op het \*weerleggen\* van \*elk\* type laboratoriumtheorie..."

Koopmans/Fouchier komen met een soortgelijke argumenten.



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16\

...Geen oog voor consequenties als risicomitigering; tijdigheid juiste maatregelen, kans lab-incidenten (hoog), impact (extreem hoog).

Niets over de enormiteit van public health/sociaal-economische consequenties; géén woord in de email-wisseling, géén agenda-onderwerp.



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17\

Kennelijk moest er een case worden gebouwd voor de perceptie van burgers en politiek (oa Koopmans): geen betrokkenheid lab, virusmanipulatie etc.

Allemaal voor de onderzoeksbudgetten en het voorkomen van strengere regulering of moratoria...



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18\

4. We zien flagrante onwetenschappelijkheid, concluderend:

- Bewijslast dierlijke/markt-oorsprong: lage standaard.
- Bewijslast lab-oorsprong/incident: hoge standaarden.



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19\

5. Financiers willen de discussie over de oorsprong bij een "vertrouwde internationale instantie" (WHO) brengen; voor uitoefenen invloed, bepalen agenda, verdelen budgetten, en het verhullen van de waarheid.

En de wetenschappers? Die zijn naïeve instrumenten in het spel.



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**AlleBurgers** @AlleBurgers · 26 nov. ...

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[#OriginOfCovid](#)

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[@Nieuwsuur](#) [@RTLnieuws](#) [@HartvNL](#) [@NU.nl](#) [@NPORadio1](#) [@EenVandaag](#)  
[@HumbertoRTL](#) [@Jinek\\_RTL](#) [@AD.nl](#)



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**AlleBurgers** @AlleBurgers · 26 nov. ...

[@\\_investico](#) [@2eKamertweets](#)



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3





**AlleBurgers** @AlleBurgers · 27 nov. ...

Drosten DLD ook in de problemen. Mogelijk meened in zaak Wiesedanger-Drosten.

**AlleBurgers** @AlleBurgers · 25 nov.

NIEUWE Corona déconfiture. #Drosten (vergl Marion Koopmans, DLD) heeft waarschijnlijk valse beëdigde verklaring afgelegd om het Wiesedanger-proces (3x beste wetenschapper EUR) te winnen.

Drosten ontkent betrokkenheid doofpot Lab-#OriginOfCovid (en GoF-onderzoek).

[twitter.com/holmenkollin/s...](https://twitter.com/holmenkollin/s...)

Deze collectie weergeven

Eidestättliche Versicherung

Belehrt über die Bedeutung einer eidestättlichen Versicherung, insbesondere über den Umstand, dass die Abgabe einer falschen oder unvollständigen eidestättlichen Versicherung mit erheblicher Strafe beledet ist, und über den Umstand, dass diese Erklärung zur Vorlage bei Gericht bestimmt ist, erkläre ich, Prof. Dr. Christian Drosten, c/o Charité – Universitätsmedizin Berlin, Charitéplatz 1, 10117 Berlin, an Eider Saat, dass der nachfolgende Sachverhalt zutrifft:

Ich nahm am 01.02.2020 an einer Telefonkonferenz mit mehreren Wissenschaftlern teil, zu der Jeremy Farrar auf Bitte von Anthony Fauci eingeladen hatte. Ich nahm an dieser Telefonkonferenz über einen längeren Zeitraum teil. An dem letzten Teil der Telefonkonferenz konnte ich nicht teilnehmen. In dieser Telefonkonferenz wurde die u.a. von Kristian Andersen zur Diskussion gestellte These einer möglichen gentechnischen Veränderung des Virus und damit ein vielleicht denkbarer Ursprung des SARS-CoV-2-Virus aus dem Labor erörtert.

Die Diskussion führte zu dem Ergebnis, dass die These aus mehreren wissenschaftlich-technischen Gründen unwahrscheinlich und in jedem Fall nicht belegbar sei. Die möglichen Begründungen für die These wurden in einem kollegialen Gespräch wissenschaftlich „zerpfückt“. Während meiner Teilnahme wurde keine Vereinbarung getroffen, die Möglichkeit einer Laborherkunft in der Öffentlichkeit zu veröffentlichen. Mir ist auch nicht bekannt, dass eine solche Vereinbarung zu einem späteren Zeitpunkt getroffen wurde.

An dem offenen Brief (Correspondence) „The proximal origin of SARS-CoV-2“, der in Nature Medicine veröffentlicht wurde, war ich nicht beteiligt. Mir war diese Veröffentlichung vor Einreichung nicht bekannt. Ich verteidigte diese Veröffentlichung zu keinem Zeitpunkt.

Ich betreibt keine „gain-of-function-Experimente“ im Sinne der Theorien um einen Laborsprung von SARS-CoV-2, also Experimente, in denen Viren entstehen, die so in der Natur nicht existieren und absehbar eine erhöhte Gefährlichkeit für den Menschen beinhalten.

Ich habe kein Interesse, den Verdacht über den Ursprung des SARS-CoV-2-Virus in eine bestimmte Richtung zu lenken.

Insbesondere hatte und habe ich kein persönliches Interesse, die sog. Laborthese als Ursprung des Virus auszuschließen. Gäbe es Anhaltspunkte für die Richtigkeit der Laborthese, würde ich dies mit Nachdruck in der wissenschaftlichen und öffentlichen Diskussion vertreten.

Berlin, den 02.03.2022

Prof. Dr. med. Christian Drosten

On 9 Feb 2020, at 6:52 am, Drosten, Christian wrote:

Dear All,

I am overloaded with nCoV patient-related work and will need a few days before I can work on this text.

Can someone help me with one question: didn't we congregate to challenge a certain theory, and if we could, drop it? This whole text reads as if the hypothesis was obvious, or was brought up by some external source, forcing us to respond. Is this the case? It does not seem as if this was linked to the HIV nonsense.

Who came up with this story in the beginning? Are we working on debunking our own conspiracy theory?

Christian

Prof. Christian Drosten  
Director, Institute of Virology  
Scientific Director, Charité Global Health

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**Joop - #AlleHandenSamen #Alleburgers #zer...** @joopdel... · 5 u ...

Als antwoord op @AlleBurgers en @EmilyKopp  
[@threadreaderapp](#) Please unroll

Deze Tweet is verwijderd door de auteur van de Tweet. Meer informatie



**Thread Reader Unroll Helper** @UnrollHelper · 1 u ...

Als antwoord op @DlrEijnde  
Hola, the unroll you asked for: [threadreaderapp.com/thread/1596618...](https://threadreaderapp.com/thread/1596618...)  
Talk to you soon.

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