BUZZ CHRONICLES > SOCIETY
Saved by @Mollyycolllinss
See On Twitter

Twitter Thread by Billy Bostickson ■■&■ ■

Billy Bostickson ■■&■ ■
@BillyBostickson

1. Why haven't Dr. Alice Latinne @nycbat @peterdaszak @EpsteinJon @HumeField @CarlosTorrelio @linfa_wang of @EcoHealthNYC released the first draft of:
https://t.co/nbZPxmEdja
Why haven't US authorities forced them to?
@USAIDGH @OneHealthUCD @NIHDirector @dylanbgeorge @cmyeaton

Dr. Alice Latinne Alice Latinne sampling a rodent in SE Sulawesi @PREDICTproject in 2017 and 2018 in Indonesia, before her work on bats with Zhengli Shi:
Origin & cross-species transmission of bat coronaviruses in China
Earliest Version: 2. May 31, 2020
https://t.co/vF0tGWDFjv

3. https://t.co/DUCBKIP17R

> 8/End
> \u2022 Are the unreported beta CoVs detected in Tongguan mine samples from 2014-2015 the 78XX group reported in Latinne et al (2020)?
> \u2022 Is it a coincidence that this group seems closely related to RaTG13 and that a 7896 label shows up in RaTG13 amplicons?
>
> h/t @franciscodeasis pic.twitter.com/BnE7xpfFmm
>
> — Ant\xf3nio Duarte (@AntGDuarte) November 18, 2020

4. @franciscodeasis https://t.co/pEHfMHcTr9

> What we know about the 7896 clade? Let's recap:
> 1/ They were published in June 2020 as part of a batch of 630 viruses of Latinne et. (2020). No details were givenhttps://t.co/9r05e9rMKo
>
> — Francisco de Asis (@franciscodeasis) November 18, 2020

5. @MonaRahalkar
https://t.co/cJPncdyqE9

> This is height of limited hangout! Show one and hide 8. Then after the pandemic quietly add these sequences without their exact locations!
> Glad that I asked valid questions in our Frontiers paper! Atleast the Mojiang mineshaft came out as Addendum! https://t.co/F9DD5QPTQp
>
> — Mona (@MonaRahalkar) November 18, 2020

6. @franciscodeasis
https://t.co/0gGQmagLVd

> Just realized: WIV could have been forced to publish 7896-clade because they were already commited by the draft of Latinne sent to Nature in October 2019. That could explain why they published it but with minimum details.
> Nature could be a prosecution witness in this story
>
> — Francisco de Asis (@franciscodeasis) December 1, 2020

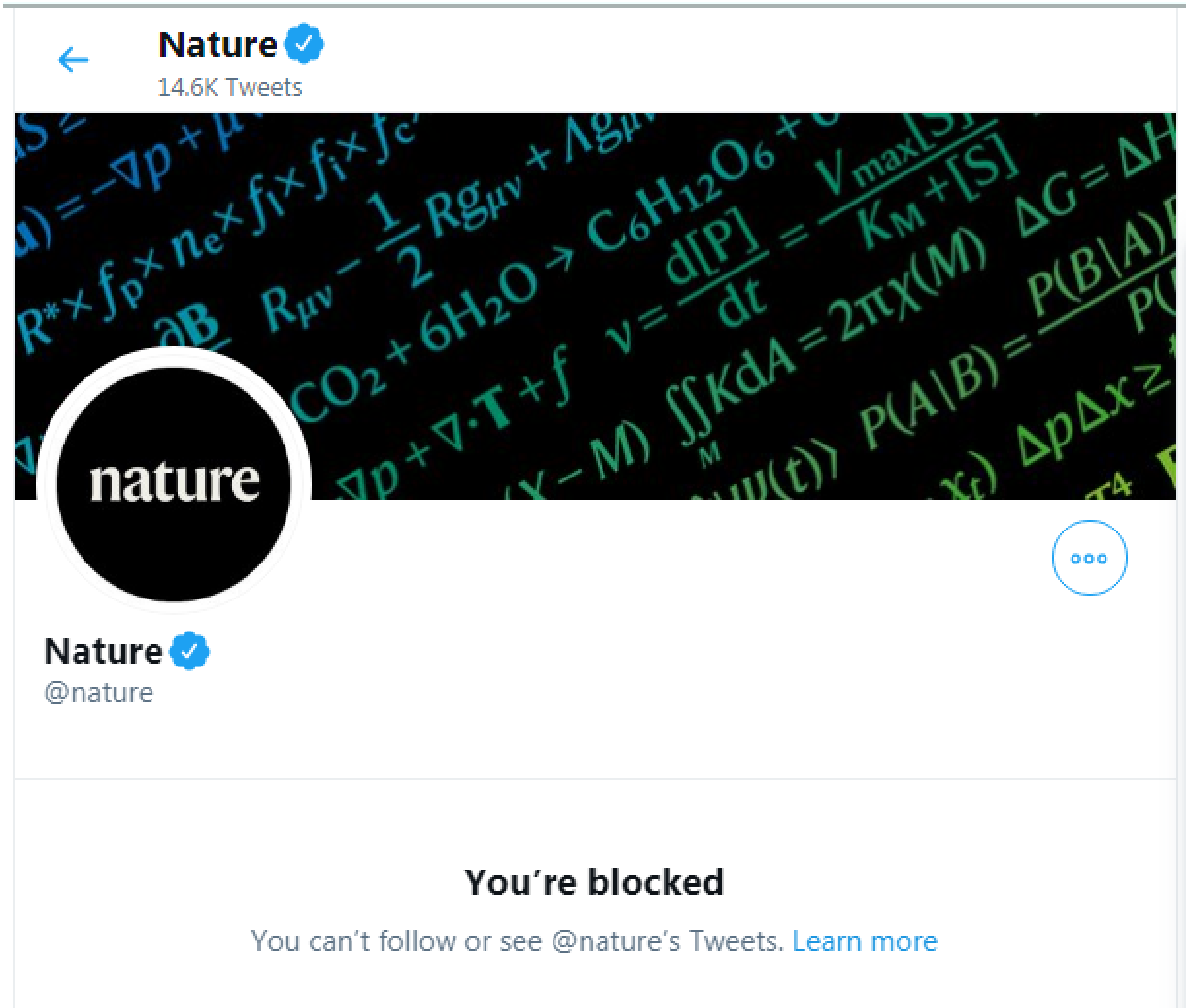
7. @franciscodeasis
https://t.co/8VrlLGgBdd

> A6/ Latinne et al. (2020) was submitted to @Nature for review on October 6th, 2019.
> There is a pre-print on May 31st, 2020, which is essentially the same as the final paper, but there must be a previous version for obvious reasonshttps://t.co/YaEjAlMfVEhttps://t.co/mlQUHYSIEv pic.twitter.com/v0Gd6KJxyH
>
> — Francisco de Asis (@franciscodeasis) November 18, 2020

8. @franciscodeasis @nature @NIHDirector
https://t.co/Ne10WZIqu8

> End/
> - @Nature must provide the scientific community with the first draft of Latinne et al. (2020) dated back in October 2019
> - VIW must open the books, provide further details, share the samples and give full sequencing of 7896-clade viruseshttps://t.co/TYBTVd2CTl
>
> — Francisco de Asis (@franciscodeasis) November 30, 2020

9. Why does @nature hate monkeys?


Nature
14.6K Tweets

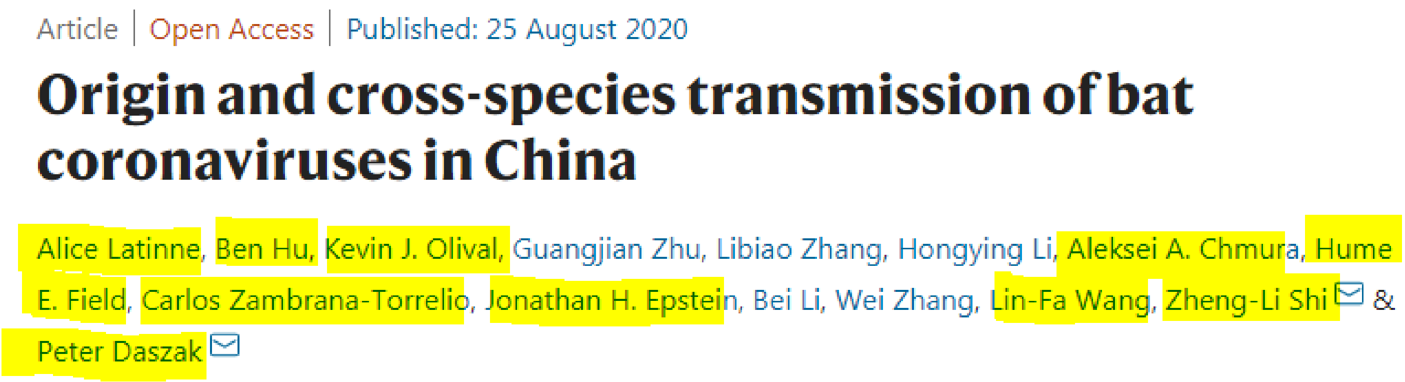
Nature
@nature

You're blocked

You can't follow or see @nature's Tweets. Learn more

10. @Harvard2H
Nature magazine has censored over 1,000 articles at the request of the Chinese State over the past several years, & runs columns sponsored by outside interests.
"The Proximal Origin of SARS-CoV-2"
is just one more example of their influence.
https://t.co/nejos1Ktaq

11. Birds of a feather stick together @nature
https://t.co/nbZPxmmCrC


Article | Open Access | Published: 25 August 2020

Origin and cross-species transmission of bat coronaviruses in China

Alice Latinne, Ben Hu, Kevin J. Olival, Guangjian Zhu, Libiao Zhang, Hongying Li, Aleksei A. Chmura, Hume E. Field, Carlos Zambrana-Torrelio, Jonathan H. Epstein, Bei Li, Wei Zhang, Lin-Fa Wang, Zheng-Li Shi & Peter Daszak

12. One of the good things about @biorxivpreprint is that all the tweets citing the paper are visible at the end of the paper, often to hilarious effect, see here:
https://t.co/rhJtmUNngg

Tweets referencing this article:

@TheSeeker268 @AntGDuarte @BahulikarRahul @luigi_warren @SimonaCCCC @_coltseavers @alimhaider @KevinM…

09 Jul 2020

Billy Bostickson □□ &□ 🆓
@BillyBostickson

RT @BillyBostickson: More shoddy work by EcoHealth Alliance! "Origin & cross-species transmission of bat coronaviruses in China" Duplicate…

09 Jul 2020

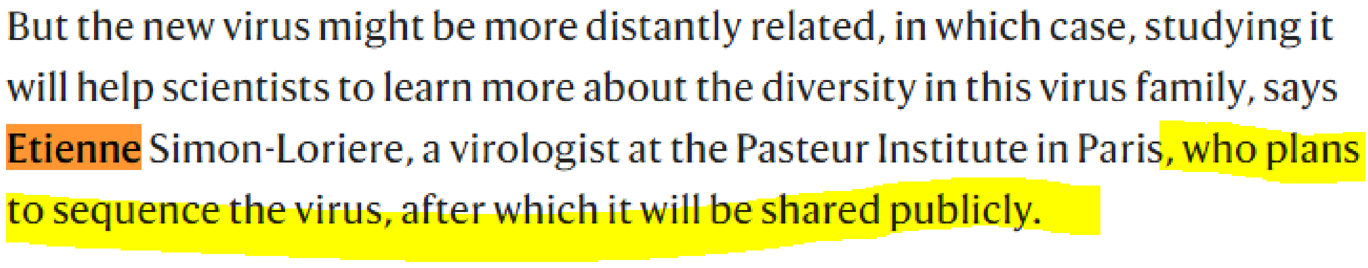
13. Alice Latinne in the News
Coronaviruses closely related to the pandemic virus discovered in Japan and Cambodia
https://t.co/2zIp1CmGan
Scientists call for pandemic investigations to focus on wildlife trade
https://t.co/BqxnE5pfD1

That is the case with the other virus, called Rc-o319, identified in a little Japanese horseshoe bat (*Rhinolophus cornutus*) captured in 2013. That virus shares 81% of its genome with SARS-CoV-2, according to a paper[1] published on 2 November — which makes it too distant to provide insights into the pandemic's origin, says Edward Holmes, a virologist at the University of Sydney in Australia.

No matter what the Cambodian team finds, both discoveries are exciting because they confirm that viruses closely related to SARS-CoV-2 are relatively common in *Rhinolophus* bats, and even in bats found outside China, says Alice Latinne, an evolutionary biologist at the Wildlife Conservation Society Vietnam in Hanoi, who has seen some of the Cambodian team's analysis but was not involved in the investigation.

"This is what we were looking for, and we found it," says Duong. "It was exciting and surprising at the same time."

14. Two Month Old Frozen Cambodian Bat Fudge? @institutpasteur
The new virus might be more distantly related, says Etienne Simon-Loriere, a virologist at Pasteur Institute, who plans to sequence the virus, after which it will be shared publicly (Nov 24th)
https://t.co/2zIp1CmGan



But the new virus might be more distantly related, in which case, studying it will help scientists to learn more about the diversity in this virus family, says Etienne Simon-Loriere, a virologist at the Pasteur Institute in Paris, who plans to sequence the virus, after which it will be shared publicly.

15. Remember, Remember the 24th of November!
https://t.co/Zpg9CDJDIZ

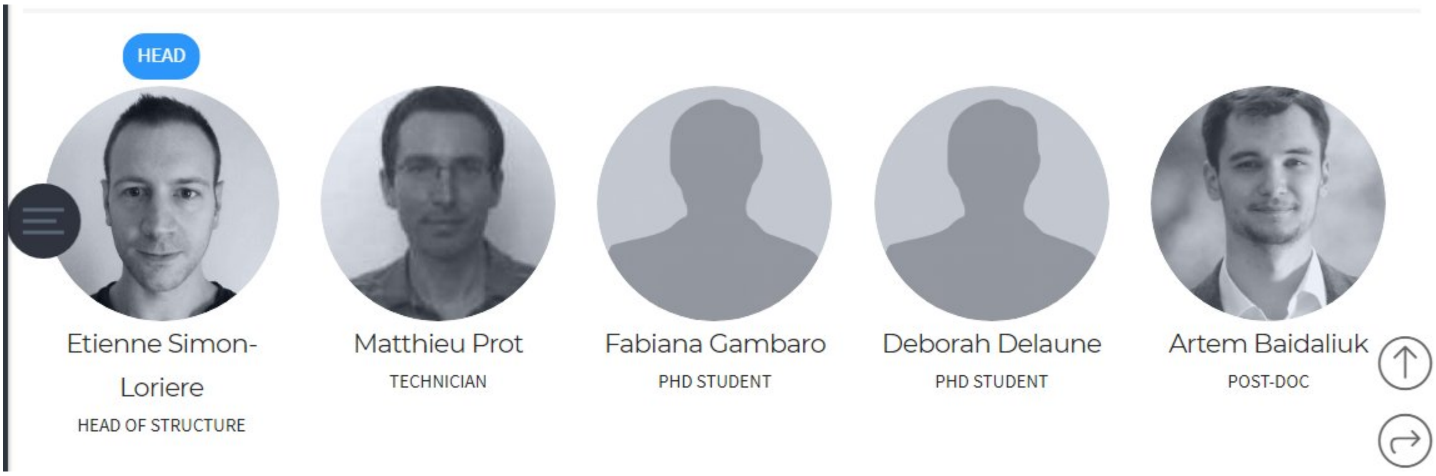
Holmes is "hoping"
Latinne is "concluding"
Goldstein is "plotting"
Etienne is "sequencing"
Institut Pasteur- One Health - UC Davishttps://t.co/2zIp1CEh1V https://t.co/ih4OqwYwHx
pic.twitter.com/PBO1gwnCJg

> — Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) November 23, 2020

16. Was that two month old frozen Cambodian Bat Fudge not as popular as expected?
https://t.co/1w9ktvqIgY

> Keep an eye on these ones!
> Etienne Simon-Loriere https://t.co/t771MVsuoL
> Coronavirus conspiracy claim called 'impossible', 'absurd' Zhang Zhihao - China Daily https://t.co/MOfAOjcPgf
> Virology Unit Team https://t.co/qYHRccnsIl
> Veasna Duong (Local Stooge) https://t.co/2Ef9a1yAiX pic.twitter.com/KNIqIiCtQx
>
> — Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) November 23, 2020

17. Hurry Up with that Sequencing, Laboratory Junior Group (G5)! @institutpasteur @SimonLoriereLab
The world is waiting to taste the Cambodian Bat Fudge!
Evolutionary genomics of RNA viruses
DEPARTMENT OF VIROLOGY
https://t.co/2UUwC8EZ1E



18. Don't be letting "interaction" with #CREID get in the way of publishing that Cambodian Bat Virus sequence
https://t.co/hGNmGjAMsF

EtienneSimon-Loriere
@SimonLoriereLab

Thrilled to be part of #NIAID #CRIED @institutpasteur Center for Emerging Infectious Diseases w/@AnavajS , and colleagues from the #PasteurNetwork in Senegal, Cameroon and Cambodia! Looking forward to interact with them and all the CRIED teams!

NIH establishes Centers for Research in Emerging Infectious Diseases
Global network to focus on spillover potential.
nih.gov

4:19 PM · Aug 28, 2020 · Twitter Web App

> Thrilled to be part of #NIAID #CRIED @institutpasteur Center for Emerging Infectious Diseases w/@AnavajS , and colleagues from the #PasteurNetwork in Senegal, Cameroon and Cambodia! Looking forward to interact with them and all the CRIED teams! https://t.co/NacyJL0071

> — EtienneSimon-Loriere (@SimonLoriereLab) August 28, 2020

19. Don't listen to Metabiota, UC Davis and Ecohealth https://t.co/ifQTmRpqVA

Infect Genet Evol. 2017 Mar; 48: 10–18.
Published online 2016 Dec 6. doi: 10.1016/j.meegid.2016.11.029

PMCID: PMC7106194
PMID: 27932284

Genetic diversity of coronaviruses in bats in Lao PDR and Cambodia

Audrey Lacroix,[a] Veasna Duong,[a] Vibol Hul,[a] Sorn San,[b] Hull Davun,[b] Keo Omaliss,[c] Sokha Chea,[d] Alexandre Hassanin,[e] Watthana Theppangna,[f] Soubanh Silithammavong,[g,h] Kongsy Khammavong,[g] Sinpakone Singhalath,[g] Zoe Greatorex,[g] Amanda E. Fine,[i] Tracey Goldstein,[j] Sarah Olson,[k] Damien O. Joly,[k,l] Lucy Keatts,[d] Philippe Dussart,[a] Aneta Afelt,[m] Roger Frutos,[n,o,⁎] and Philippe Buchy[a,p,⁎⁎]

▾ Author information ▸ Article notes ▸ Copyright and License information Disclaimer

[a]Institut Pasteur du Cambodge, Virology Unit, Phnom Penh, Cambodia
[b]National Veterinary Research Institute, Ministry of Agriculture Forestry and Fisheries, Cambodia
[c]Forest Administration, Ministry of Agriculture Forestry and Fisheries, Cambodia
[d]Wildlife Conservation Society, Cambodia
[e]Muséum national d'Histoire naturelle, Institut de Systématique, Evolution, Biodiversité (ISYEB), UMR 7205 MNHN CNRS UPMC, France
[f]National Animal Health Laboratory, Ministry of Agriculture Forestry and Fisheries, Lao Democratic People's Republic
[g]Wildlife Conservation Society, Lao Democratic People's Republic
[h]Metabiota Inc., Vientiane, Lao Democratic People's Republic
[i]Wildlife Conservation Society, Vietnam Program, Hanoi, Vietnam
[j]One Health Institute, School of Veterinary Medicine, University of California, Davis, USA
[k]Wildlife Conservation Society, Wildlife Health Program, Bronx, New York, USA
[l]Metabiota Inc., Nanaimo, British Columbia, Canada
[m]Institute of Physical Geography, Faculty of Geography and Regional Studies, University of Warsaw, Warsaw, Poland
[n]Cirad, UMR 17, Cirad-Ird, TA-A17/G, Montpellier, France
[o]Université de Montpellier, IES, UMR 5214, CNRS-UM, Montpellier, France
[p]GSK Vaccines R&D, 150 Beach road, # 22-00, 189720, Singapore
Roger Frutos: roger.frutos@ies.univ-montp2.fr; Philippe Buchy: buchyphilippe@hotmail.com
⁎Correspondence to: R. Frutos, Cirad, UMR 17, Cirad-Ird, TA-A17/G, Montpellier, France. roger.frutos@ies.univ-montp2.fr
⁎⁎Correspondence to: P. Buchy, Institut Pasteur du Cambodge, Virology Unit, Phnom Penh, Cambodia. buchyphilippe@hotmail.com

> Metabiota
> UC Davis
> One Health
> Institut pasteur
> Genetic diversity of coronaviruses in bats in Lao PDR and Cambodia (2017)https://t.co/f3DW92j4Bs pic.twitter.com/thHG1xJLtV
>
> — Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) November 23, 2020

20. Our future is in safe hands with #CREID
■ ■ ■■■ ■ ■■■ ■ ■■■ ■ ■ ■ ■ ■https://t.co/Eh8hGP4vDA

> 1. DISTURBING News, Friends!
> Daszak, Fauci, Baric and others are up to no good
> NIAID is funding 10 CREID centers in 28 countries
> CREID (Centers for Research in Emerging Infectious Diseases),https://t.co/BxTGdUbY6k
>
> — Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) October 6, 2020

unroll Dr. Alice Latine's 2 month old frozen Cambodian Bat Fudge @threadreaderapp

https://t.co/X3FP2QrYoO