

LIVEBLOG

NOS NIEUWS · BINNENLAND · BUITENLAND ·
VANDAAG, 05:56

Vanavond persconferentie om 19.00 uur · Mogelijk twaalf besmette personen op Venloos festival

- Welkom in het coronablog van vrijdag 9 juli, we houden je de hele dag op de hoogte van het laatste coronanieuws.
- Het demissionaire kabinet geeft vandaag mogelijk een persconferentie.
- 11.000 meer doden dan verwacht in tweede golf.
- Pfizer wil toestemming van autoriteiten voor derde coronaprik.

LAATSTE UPDATE · 5 MIN GELEDEN



Vanavond persconferentie om 19.00 uur

Demissionair premier Rutte geeft samen met demissionair minister De Jonge (Volksgezondheid) zoals verwacht om 19.00 uur een persconferentie. Mogelijk kondigen ze dan

COVID-19 NIVEL huisarts-peilstations



NIVEL
Kennis voor betere zorg

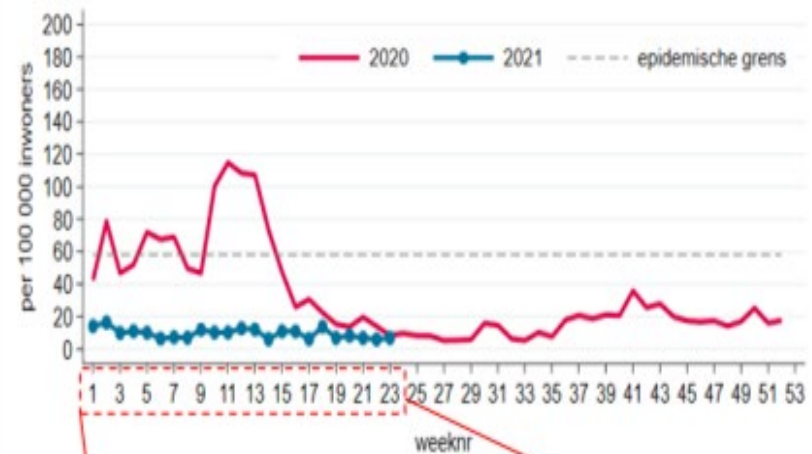
40 Nivel huisartspeilstations - uitbreiding

het aantal patiënten met een influenza-achtig ziektebeeld voor de landelijke griepsurveillance

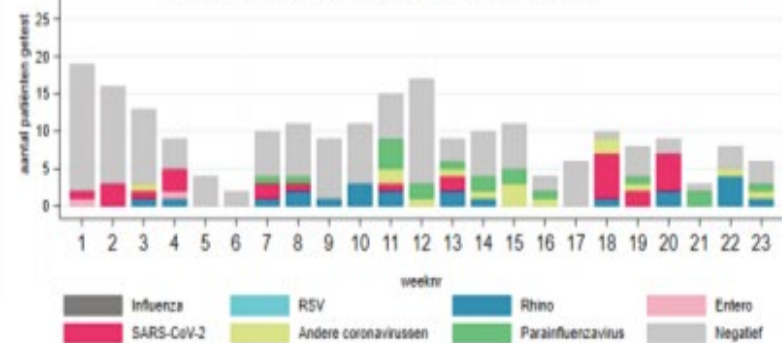
Nu: in aanvulling op teststraten GGD'en



Aantal patiënten met influenza-achtig ziektebeeld, per week per 100.000 inwoners



Respiratoire virussen in monsters afgenomen bij patiënten met griepachtig ziektebeeld of een andere acute luchtweginfectie door Nivel Peilstations, 2020-2021



Lijst A

Pathogenicity and Transmissibility Characteristics of Recently Emerged Viruses in Relation to Outbreak Containment.				
Virus	Case Fatality Rate (%)	Pandemic	Contained	Remarks
2019-nCoV	Unknown*	Unknown	No, efforts ongoing	
pH1N1	0.02–0.4	Yes	No, postpandemic circulation and establishment in human population	
H7N9	39	No	No, eradication efforts in poultry reservoir ongoing	
NL63	Unknown	Unknown	No, endemic in human population	
SARS-CoV	9.5	Yes	Yes, eradicated from intermediate animal reservoir	58% of cases result from nosocomial transmission
MERS-CoV	34.4	No	No, continuous circulation in animal reservoir and zoonotic spillover	70% of cases result from nosocomial transmission
Ebola virus (West Africa)	63	No	Yes	

* Number will most likely continue to change until all infected persons recover.



▲ Bijzondere opsporingsambtenaren gaan deze zomer aan huis controleren of mensen zich wel aan quarantaineplicht houden. © ANP

Boa belt thuis aan voor controle quarantaine, boete kan oplopen tot 20.000 euro

Wie op vakantie gaat in een land waar het coronavirus nog volop rondwaart, kan bij thuiskomst rekenen op bezoek van een boa. Gemeentelijke toezichthouders controleren deze zomer volop of reizigers wel tien dagen verplicht in quarantaine gaan.

Eric Reijnen - Rutten 03-07-21, 07:57 Laatste update: 10:41



Dat moet iedereen die in een hoogrisicoland is geweest, zoals het Verenigd Koninkrijk, Rusland en heel wat landen in Azië, Afrika en Zuid-Amerika. Het zijn landen met veel besmettingen of gevaarlijke varianten van het coronavirus. De

Hugo de Jonge vreest voor reisadvies Nederlanders: 'Kleurcode naar rood'



Foto: A

Wil je nog graag op vakantie, wees je bewust van de veranderende kleurcodes. Demissionair coronaminister Hugo de Jonge vreest dat het reisadvies voor Nederlanders naar rood verandert. Ook dekken sommige verzekeraars helemaal niets als de kleurcode van een land op oranje staat.



Kabinet overweegt clubs te sluiten en
evenementen af te blazen



▲ Bezoekers tonen hun testbewijs bij de toegangspoort van het festivalterrein van Stereo Sunday Festival. Doordat de coronacijfers verbeterd zijn is het weer mogelijk muziekfestivals te bezoeken. © ANP

Feestgangers die misbruik maken van Testen voor Toegang moeten 'strafrechtelijk worden aangepakt'

Feestvierders die moedwillig misbruik maken van Testen voor Toegang om een festival of feest te kunnen bezoeken, moeten strafrechtelijk worden aangepakt. Die oproep doet Robér Willemsen, voorzitter van Koninklijke Horeca Nederland, aan het kabinet en regionale overheden. „Als je doelbewust een testbewijs of identiteitskaart vervalst en daarmee ook de gezondheid in gevaar brengt, dan verdient dat een harde aanpak.”



Kabinet beslist: nachtleven vanaf zaterdag weer op slot tot 13 augustus, grote festivals geschrapt

VIDEO Het kabinet trapt op de rem: om het coronavirus terug te dringen wordt in de horeca vanaf zaterdagnacht de sluitingstijd weer op 24.00 uur gezet. Nachtclubs en discotheken gaan voorlopig dicht, festivals zonder zitplaatsen zijn verboden. Dat bevestigen Haagse bronnen. De maatregelen gelden tot 13 augustus en gaan zaterdagochtend om 06.00 uur in.

Tobias den Hartog, Niels Klaassen 9 jul. 2021
Laatste update: 16:47

deVolkskrant

Het stikstofdossier is een hoofdpijndossier. Vooral omdat er nog steeds weinig wordt gedaan om de uitstoot te verlagen



Foute rekenmethodes en de **verkoop van uitstootrechten**: de aanpak van stikstof loopt op verschillende manieren vast. *De Volkskrant zet de belangrijkste vijf knelpunten op een rij.*

'Basisinkomen invoeren'

Gisteren, 15:30 in WAT U ZEGT



317

 Lees voor



Het initiatief van de Partij van de Arbeid en de ChristenUnie om de komende jaren de armoede onder kinderen te halveren lijkt sympathiek maar gaat helaas niet ver genoeg, vindt Joop Böhm.



Goed dat Wilders veroordeeld is, schrijft Stevo. Maar bizar dat hij in de Tweede Kamer wél alles mag zeggen



Als hij Kaag daar voor **IS-fan** uitmaakt, kan alleen de Kamervoorzitter ingrijpen.
Maar ja, als PVV'er Bosma die rol vervult... **'De PVV is zowel giftig buiten het
parlement als daarbinnen.'**



▲ Rapper Convex Kafka is opgepakt vanwege opruiende teksten op Twitter. © archief Arjan Gofink / Twitter / fotobewerking de Stentor

Rapper Convex Kafka opgepakt vanwege opruiende tweet na aanslag op Peter R. de Vries

Rapper Convex Kafka, de artiestennaam van Bouke van der Vrugt, is gisteravond aangehouden na een opruiende tweet. De controversiële Deventer rapper stelde daarin de vraag of 'Taghi & Co niet beter achter Hugo of Mark aan konden gaan in plaats van Peter R. de Vries.' Vrij snel verwijderde Kafka de tweet. Later op de avond werd hij opgepakt.

Castor van Dillen 07-07-21, 13:11 Laatste update: 07-07-21, 16:40



Klaas Wilting

@wiltingklaas



Willem Engel en andere virusactievoerders opgepakt in Den Haag telegraaf.nl/nieuws/1074538... via [@Telegraaf](https://twitter.com/Telegraaf) Ik weet dat't moeilijk is maar deze dwaas moet langdurig vd straat. Het is gif wat hij verspreidt. Het Corona virus zorgt voor steeds meer slachtoffers. Mede door figuren als Engel

[Translate Tweet](#)



Willem Engel en andere virusactievoerders opgepakt in Den Haag

telegraaf.nl



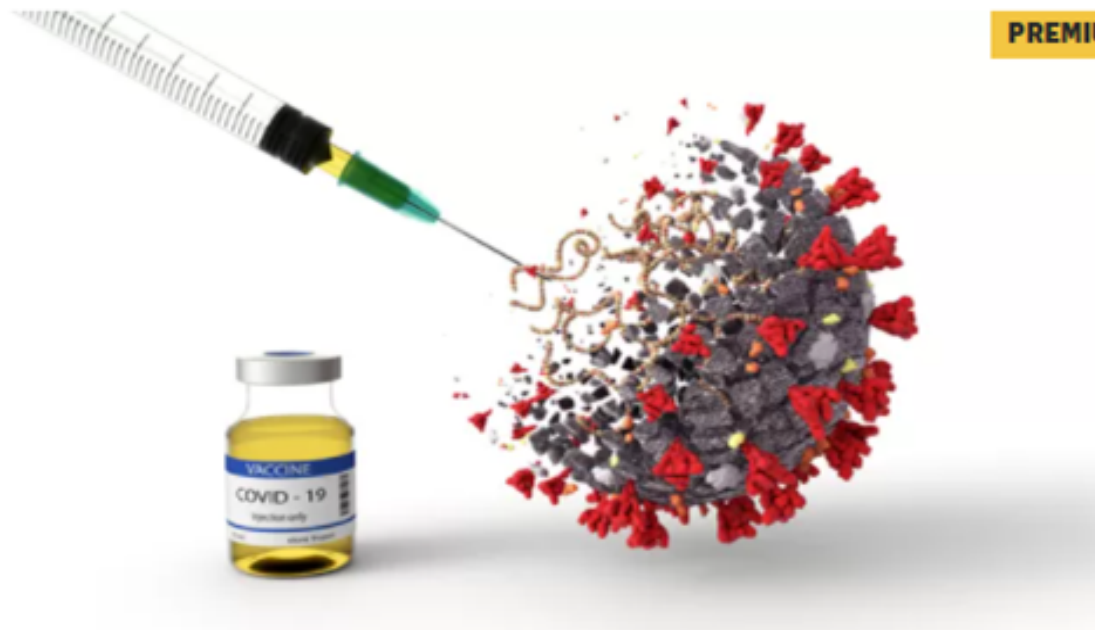
▲ Ziekenhuis Isala in Zwolle boekte in coronajaar 2020 een winst van ruim 20 miljoen euro. © Getty Images

Rode cijfers? Ziekenhuizen in Zwolle, Apeldoorn en Harderwijk maken miljoenenwinst in coronajaar

Drie grote ziekenhuizen in deze regio verdubbelden hun winst in het afgelopen jaar. Isala, in Zwolle en Meppel, spant de kroon met 20,6 miljoen euro. Hoe kan dat in coronatijd?

Jaap Selles 14-06-21, 07:30 Laatste update: 14-06-21, 16:40

PREMIU



▲ © Shutterstock

Bijwerkingen over vijf jaar bij coronavaccin? Dan betaalt Nederland mee aan schadeclaims


Als een coronavaccin in de toekomst onverwachte bijwerkingen veroorzaakt, zal de Nederlandse overheid financieel bijspringen bij eventuele schadeclaims. Dat blijkt uit afspraken die zijn gemaakt tussen lidstaten van de Europese Unie en farmaceuten.

Stephen Friedrichs & Chris van Mersbergen 10-10-20, 03:00 Laatste update: 10-10-20, 13:12

Duizenden Duitsers ziek van corona ondanks prikken

Updated Vandaag, 11:23 Vandaag, 11:22 in BUITENLAND



 Lees voor



BERLIJN - In Duitsland hebben bijna 4000 mensen na volledig te zijn ingeënt tegen het coronavirus toch last gekregen van ziekteverschijnselen. Dat becijferde gezondheidsinstituut RKI, dat benadrukt dat vaccins zeer effectief zijn. Het overgrote deel van de coronapatiënten was de afgelopen maanden niet ingeënt.

piek in de tweede helft van het tweede kwartaal en de eerste helft van het derde kwartaal.

Prognoses leveringen (d.d. 24/2), in miljoenen doses per kwartaal:

	Dec 2020	1Q2021	2Q2021	3Q2021	4Q2021	1Q2022	Totaal
<i>BionTech/ Pfizer</i>	0,165	2,4	7,8	6,8	2,65		19,8
<i>Moderna</i>	0	0,4	1,4	5	7,4	-	14,2
<i>AstraZeneca</i>	0	1,5	4	6,2	-	-	11,7
<i>CureVac</i>	0	0	0,0	5,1	2,8	2,8	10,7
<i>Janssen</i>	0	0	3	6	2,3	-	11,3
<i>Sanofi</i>	0	0	0	0	5,85	5,85	11,7
<i>Novavax</i>	0	0	0,6	1	1,2	1	3,8
<i>Valneva</i>	0	0	0	0	0	1,2	1,2
<i>Totaal</i>	0,165	4,3	16,8	30,1	22,2	10,9	84,5

Actueel > Miljoenen euro's naar rioolwateronderzoek na corona om nieuwe virusuitbraken eerder te ontdekken

Miljoenen euro's naar rioolwateronderzoek na corona om nieuwe virusuitbraken eerder te ontdekken

05-07-2021 07:00 | Binnenland | Auteur: Joost Lammers



Coronavirus

1390 artikelen

Miljoenen euro's naar rioolwateronderzoek na corona om nieuwe virusuitbraken eerder te ontdekken

05-07-2021

Zoveel mensen, zoveel vakantieplannen: hier gaan Annelise heen en zo bereiden zij zich voor

04-07-2021

Raad van Europa: 'Top Nederlandse politiek blijft kwetsbaar voor corruptie'



🏠 / [Europe](#)

Concerns over rule of law as Slovenia takes over EU presidency



Issued on: 01/07/2021 - 00:47



Hoe de Europese instellingen financieel de massamedia ondersteunen



Verzamelde vertalingen van E.J. Bron

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← BREAKING!: “Peter R. de Vries neergeschoten in centrum Amsterdam”

Donderslag in het Europees Parlement: 16 rechtse partijen besluiten samenwerking

Geplaatst op [6 juli 2021](#) door [E.J. Bron](#)



Google Translate

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Twitter Updates

- Aan Peter R. de Vries
ejbron.wordpress.com/2021/07/07/aan... via @EJBron2
5 hours ago
- RECHT IS KROM EN KROM IS WET
ejbron.wordpress.com/2021/07/07/rec... via @EJBron2



WORLD

Covid 19 coronavirus: Ultra-contagious Lambda variant detected in Australia

6 Jul, 2021 08:26 AM

🕒 3 minutes to read

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LIVE BLOG

Follow our live coverage for the latest news on the coronavirus pandemic

COVID-19's delta variant means it's 'absolutely essential' to protect children from infection, experts say

By national medical reporter [Sophie Scott](#) and the Specialist Reporting Team's [Leonie Thorne](#)

Posted 2h ago, updated 46m ago



LIVE BLOG

Follow our live coverage for the latest news on the coronavirus pandemic

COVID live updates: Regional people tip off police about rule breakers fleeing Sydney's lockdown

By [Dannielle Maguire](#) and [Michael Doyle](#)

Posted 22m ago



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transportation support services, import and export, medical examination, treatment, funeral... can continue to operate.

Leaving the house without a valid reason will be fined

When leaving the house, they must wear masks and disinfect; must not gather more than 2 people in public places, outside of offices and hospitals, and must keep a distance of at least 2 meters.

People's Committees of wards, communes and townships organize patrols and surveillance teams, operating 24 hours a day, preventing mass gatherings and strictly handling cases of violations of epidemic prevention and control. ; especially strengthen the sanction of administrative violations for cases where people leave the house not in the cases specified above and without a legitimate reason.

State agencies and units organize for cadres, civil servants and employees to use information technology to work from home; Only really necessary cases come to work at the office.

Stop all meetings at the office (except for anti-epidemic meetings, meetings to handle urgent issues of the unit). When organizing a meeting, it must be approved by the head, make sure not to gather more than 10 people in one room, and strictly comply with the 5K rule of the Ministry of Health.

The City People's Committee assigned the Department of Transport to direct the suspension of public passenger transport by car, except for the cases of official duty, the shuttle bus for workers, experts, quarantined people, vehicles



LATEST NEWS

Haiti rejects COVID-19 vaccine from WHO



BY ONZ CHÉRY
APR. 08, 2021



Home > News > World News

Breaking: President of Haiti assassinated at his home

President Jovenel Moïse has been assassinated during the early hours of Wednesday, and political tensions in Haiti have escalated beyond control.



by **Tom Head** — 07-07-2021 12:29



Photo: Twitter

China collects genetic data from German pregnant women



Photo: Ju Peng / AP

by: **JULIAN RÖPCKE AND PETER TIEDE**
07/09/2021 - 4:56 pm

It sounds like future horror - but it is already reality.

That is why so many rapid tests are false positive



Photo: Marijan Murat / dpa

July 4th, 2021 - 11:22 pm

80 percent of the positive corona rapid tests in Hamburg are wrong. This emerges from a response from the Senate to a request from the CDU parliamentary group.

"We no longer have real democracy"

Marco Bülow is a member of the Bundestag for Die Party. He says: The parliamentary system is dangerously encrusted, MPs no longer act according to their conscience. How does he want to change that?

An interview by [Okan Bellikli](#)

July 4th, 2021, 2.49 p.m.



Covid: Children's extremely low risk confirmed by study

🕒 9 hours ago | 💬 [Comments](#)



Coronavirus pandemic



Ottawa

Heart institute seeing patients with rare condition possibly linked to mRNA vaccines



Myocarditis is an often mild inflammation of the heart muscle

CBC News

Posted: July 05, 2021

Last Updated: July 06, 2021



Boy, 16, had cardiac arrest after exercise following 1st Pfizer vaccine dose



Staff Writer, Singapore · Editorial Team

Mon, 5 July 2021, 1:07 pm · 4-min read



TRENDING

450 domestic doctors file petition to stop vaccination

2021/06/24 19:57

society

#New Corona

#Entertainment feature



“Meeting of doctors and lawmakers who warn the new corona vaccine” (representative: Tokuuji Takahashi) met in the Diet on the 24th, Chiyoda-ku, Tokyo, calling for the discontinuation of vaccination.

A total of 450 doctors nationwide who have raised concerns about the safety of the new coronavirus vaccine submitted a petition to the Ministry of



CORONA
CRISIS

Marc Van Ranst piswoest omwille van deze 'gelekte' informatie (foto's)



Geschreven Door S... — op 5 jul, 2021

Van Ranst

KU LEUVEN

REGA INSTITUTE KU LEUVEN

Naam

(voluit) : **Rega Instituut**

(verkort) :

Rechtsvorm : vzw

Volledig adres v.d. zetel : Herestraat 49 bus 1030, 3000 Leuven

Onderwerp akte : Herbenoeming bestuurders - ontslag - benoeming

Hierbij geef ik graag de volgende functiewissel door :

Debackere Koen, wonende in de Alfons Stesselstraat 8 te 3012 Leuven, geboren te Gent op 14 juli 1961 zetelt niet langer in de Raad van Bestuur Rega vzw in zijn hoedanigheid van algemeen beheerder van de Katholieke Universiteit te Leuven).

Hij blijft echter zetelen als lid KULeuven

De nieuwe algemeen beheerder van de Katholieke Universiteit Leuven is Wim Desmet, wonende in Oude Nethensebaan 26, 3051 Oud-Heverlee, geboren te Waregem op 5 juni 1969 en zetelt in die hoedanigheid in de Raad van Bestuur Rega vzw vanaf 1 november 2020.

Ingevolge het bereiken van de statutair voorziene maximumleeftijd aanvaardt de Algemene Vergadering het ontslag als lid van de Raad van Bestuur van Jozef Van Damme, Merelput 35 te 9080 Lochristi, geboren te Gent op 13 juli 1950.

- Debackere Koen, [redacted] juli 1961
(in zijn hoedanigheid van algemeen beheerder van de Katholieke Universiteit te Leuven)
- Herdewijn Piet, [redacted] september 1954
- Neyts Johan, [redacted] op 21 januari 1966
- Opendakker Ghislain, [redacted] te Dilsen op 23 juni 1956
- Proost Paul, wonende [redacted]
- Schols Dominique, [redacted]
- Van Damme Jozef, [redacted]
- Van Ranst Marc, [redacted] 65
- Van Hulle Cynthia, [redacted]

Johan Neyts



Johan Neyts is hoogleraar aan de KU Leuven, waar hij het vak virologie doceert aan de studenten geneeskunde en tandheelkunde. Neyts groeide op in Blankenberghe, België. Hij liep school aan het Blankenbergse Sint-Pieterscollege in de richting wetenschappen-wiskunde. Wikipedia

Bill Gates bestelt grote coronastudie in Rega-instituut

© 04 maart 2020 door Belga en P.S.



THE BILL & MELINDA GATES FOUNDATION INVESTS \$52M IN CUREVAC FOR VACCINE DEVELOPMENT

[The Bill & Melinda Gates Foundation invests \\$52M in CureVac for vaccine development](#), March 6, 2015. GEN Magazine.

Wie maakt deel uit van het Federaal Platform COVID Testing?

We hebben overeenkomsten gesloten met 8 samenwerkende partners. Elke partner bestaat uit een universitair centrum en een erkend laboratorium voor klinische biologie:

- Universiteit Antwerpen en UZ Antwerpen
- Universiteit Gent en UZ Gent
- KU Leuven en UZ Leuven
- UCL en Hôpital Saint-Luc Bruxelles
- ULB en Institut de Biologie Clinique
- Université de Liège en CHU de Liège
- Université de Namur en CHU-UCL Namur
- Université de Mons en Hôpital de Jolimont

Wat financieren we?

We financieren het platform op 3 niveaus:

- We voorzien een eenmalige opstartkost van maximum 275.000 EUR per site.
- We vergoeden de werkingskosten die noodzakelijk zijn om dagelijks 2.000 testen te kunnen uitvoeren. Dat stemt overeen met een maandelijks bedrag van 720.000 EUR per site.

[Home](#) > [Studeren](#) > [Permanente Vorming](#) > [LIDL](#) > Frank Vandenbroucke (Min. van Staat, Prof. KU Leuven)

FRANK VANDENBROUCKE (MIN. VAN STAAT, PROF. KU LEUVEN)

CV en professionele activiteiten Frank Vandenbroucke

› [Biochem Biophys Res Commun](#). 2004 Oct 8;323(1):264-8. doi: 10.1016/j.bbrc.2004.08.085.

In vitro inhibition of severe acute respiratory syndrome coronavirus by chloroquine

Els Keyaerts ¹, Leen Vijgen, Piet Maes, Johan Neyts, [Marc Van Ranst](#)

Affiliations + expand

PMID: 15351731 PMCID: [PMC7092815](#) DOI: [10.1016/j.bbrc.2004.08.085](#)

[Free PMC article](#)

Abstract

We report on chloroquine, a 4-amino-quinoline, as an effective inhibitor of the replication of the severe acute respiratory syndrome coronavirus (SARS-CoV) in vitro. Chloroquine is a clinically approved drug effective against malaria. We tested chloroquine phosphate for its antiviral potential against SARS-CoV-induced cytopathicity in Vero E6 cell culture. Results indicate that the IC₅₀ of chloroquine for antiviral activity (8.8 +/- 1.2 microM) was significantly lower than its cytostatic activity; CC₅₀ (261.3 +/- 14.5 microM), yielding a selectivity index of 30. The IC₅₀ of chloroquine for inhibition of SARS-CoV in vitro approximates the plasma concentrations of chloroquine reached during treatment of acute malaria. Addition of chloroquine to infected cultures could be delayed for up to 5h postinfection, without an important drop in antiviral activity. Chloroquine, an old antimalarial drug, may be considered for immediate use in the prevention and treatment of SARS-CoV infections.

Copyright 2004 Elsevier Inc.

► [Antimicrob Agents Chemother.](#) 2009 Aug;53(8):3416-21. doi: 10.1128/AAC.01509-08.
Epub 2009 Jun 8.

Antiviral activity of chloroquine against human coronavirus OC43 infection in newborn mice

Els Keyaerts ¹, Sandra Li, Leen Vijgen, Evelien Rysman, Jannick Verbeeck, [Marc Van Ranst](#), Piet Maes

Affiliations + expand

PMID: 19506054 PMCID: [PMC2715625](#) DOI: [10.1128/AAC.01509-08](#)

[Free PMC article](#)

Abstract

Until recently, human coronaviruses (HCoVs), such as HCoV strain OC43 (HCoV-OC43), were mainly known to cause 15 to 30% of mild upper respiratory tract infections. In recent years, the identification of new HCoVs, including severe acute respiratory syndrome coronavirus, revealed that HCoVs can be highly pathogenic and can cause more severe upper and lower respiratory tract infections, including bronchiolitis and pneumonia. To date, no specific antiviral drugs to prevent or treat HCoV infections are available. We demonstrate that chloroquine, a widely used drug with well-known antimalarial effects, inhibits HCoV-OC43 replication in HRT-18 cells, with a 50% effective concentration (+/- standard deviation) of 0.306 +/- 0.0091 microM and a 50% cytotoxic concentration (+/- standard deviation) of 419 +/- 192.5 microM, resulting in a selectivity index of 1,369. Further, we investigated whether chloroquine could prevent HCoV-OC43-induced death in newborn mice. Our results show

> *Antimicrob Agents Chemother.* 2014 Aug;58(8):4875-84. doi: 10.1128/AAC.03011-14.
Epub 2014 May 19.

Screening of an FDA-approved compound library identifies four small-molecule inhibitors of Middle East respiratory syndrome coronavirus replication in cell culture

Adriaan H de Wilde ¹, Dirk Jochmans ², Clara C Posthuma ¹, Jessika C Zevenhoven-Dobbe ¹, Stefan van Nieuwkoop ³, Theo M Bestebroer ³, Bernadette G van den Hoogen ³, Johan Neyts ⁴, Eric J Snijder ⁵

Affiliations + expand

PMID: 24841269 PMID: PMC4136071 DOI: 10.1128/AAC.03011-14

[Free PMC article](#)

Abstract

Coronaviruses can cause respiratory and enteric disease in a wide variety of human and animal hosts. The 2003 outbreak of severe acute respiratory syndrome (SARS) first demonstrated the potentially lethal consequences of zoonotic coronavirus infections in humans. In 2012, a similar previously unknown coronavirus emerged, Middle East respiratory syndrome coronavirus (MERS-CoV), thus far causing over 650 laboratory-confirmed infections, with an unexplained steep rise in the number of cases being recorded over recent months. The human MERS fatality rate of ~ 30% is alarmingly high, even though many deaths were associated with underlying medical conditions. Registered therapeutics for the treatment of coronavirus infections are not available. Moreover, the pace of drug development and registration for human use is generally incompatible with strategies to combat emerging infectious diseases. Therefore, we have screened a library of 348 FDA-approved drugs for

Substituted nucleosides, nucleotides and analogs thereof

Abstract

Disclosed herein are nucleosides, nucleotides and nucleotide analogs, methods of synthesizing the same and methods of treating diseases and/or conditions such as a Coronaviridae virus, a Togaviridae virus, a Hepeviridae virus and/or a Bunyaviridae virus infection with one or more nucleosides, nucleotides and nucleotide analogs.

Images (1)



Classifications

- [A61K31/708](#) Compounds having saccharide radicals and heterocyclic rings having nitrogen as a ring hetero atom, e.g. nucleosides, nucleotides containing six-membered rings with nitrogen as a ring hetero atom containing condensed or non-condensed pyrimidines containing purines, e.g. adenosine, adenylic acid having oxo groups directly attached to the purine ring system, e.g. guanosine, guanylic acid

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US9603864B2

United States

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Inventor: Lawrence M. Blatt, Leonid Beigelman, Julian Alexander Symons, David Bernard Smith

Current Assignee : Janssen Biopharma Inc

Worldwide applications

2015 • [JP](#) [WO](#) [DK](#) [EA](#) [EP](#) [SG](#) [LT](#) [US](#) [AU](#) [MX](#) [EP](#) [CN](#) [SI](#) [CA](#) [HU](#) [TW](#)
2016 • [IL](#) [PH](#) 2017 • [US](#) 2020 • [JP](#) [HR](#)

Application US14/746,500 events

2014-06-24 • Priority to US201462016232P

2015-06-22 • Application filed by Alios Biopharma Inc

2015-12-24 • Publication of US20150366888A1

2017-03-28 • Application granted

2017-03-28 • Publication of US9603864B2

Status • Active

2035-06-22 • Anticipated expiration

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WHO

Therapeutics and COVID-19

LIVING GUIDELINE
6 JULY 2021



Ongoing uncertainties and opportunities for future research

IL-6 receptor blockers (despite the strong recommendation, there are a number of uncertainties that persist):

- long-term mortality and functional outcomes in COVID-19 survivors;
- safety data in terms of nosocomial infections
- data in children, pregnant patients and those that are already immunocompromised
- patients with non-severe COVID-19
- immunity and the risk of a subsequent infection, which may impact the risk of death after 28 days;
- outcomes by different IL-6 receptor blocker dosing and optimal timing of drug initiation.

Ivermectin

Given the very low certainty in estimates for most critical outcomes of interest, the GDG felt that further high-quality clinical trials examining this drug would be essential before any recommendation for use as part of clinical care. This includes further RCTs examining both inpatients and outpatients and those with varying disease severities and using different ivermectin dosing regimens. The focus of these studies should be on outcomes important to patients such as mortality, quality of life, need for hospitalization, need for invasive mechanical ventilation and time to clinical or symptom improvement. Also, a better characterization of potential harms with ivermectin in patients with COVID-19 would be important.

Hydroxychloroquine

Although some uncertainty remains, the GDG panel felt that further research was unlikely to uncover a subgroup of patients that benefit from hydroxychloroquine on the most important outcomes (mortality, mechanical ventilation) given the consistent results in trials across disease severity and location.

Lopinavir/ritonavir

Although some uncertainty remains, the GDG panel felt that further research was unlikely to uncover a subgroup of patients that

Sjoemelen met wetenschap komt vaak voor in Nederland, blijkt uit integriteitsenquête

Wetenschap Een op de twee wetenschappers in Nederland heeft wel eens gesjoemeld met onderzoeksresultaten.

✍ Bart Funnekotter ⌚ 8 juli 2021 om 22:30 ⌚ Leestijd 2 minuten



Infectious Disease > COVID-19

Did Fecal Transplant Stop COVID in Its Track

— Two Polish patients co-infected with *C difficile* saw improvements


by [Zaina Hamza](#), Staff Writer, MedPage Today July 6, 2021

ADVERT



Commentary | [Open Access](#) | Published: 31 May 2021

Potential adverse events in Japanese women who received tozinameran (BNT162b2, Pfizer-BioNTech)

[Rumiko Shimazawa](#) & [Masayuki Ikeda](#) 

Journal of Pharmaceutical Policy and Practice **14**, Article number: 46 (2021) | [Cite this article](#)

47k Accesses | **1021** Altmetric | [Metrics](#)

Abstract

Reports of cerebral venous sinus thrombosis and intracranial hemorrhage (ICH) following the administration of coronavirus vaccines have raised concerns regarding their safety. Although no regulatory authority has recognized ICH as an adverse event associated with tozinameran (BNT162b2, Pfizer-BioNTech), fatal and non-fatal cases have been reported. In Japan, 10 fatal cases (five men and women) have been reported to date. Four of the five women died of ICH and the other died of aspiration pneumonia, whereas all five men died of causes other than stroke. This imbalance is incompatible with the mortality data on cardiovascular diseases in the National Statistics, which show no apparent disparity between sexes or between hemorrhagic and ischemic stroke. Cumulatively, our analysis reveals a disproportionately high incidence of death by ICH in Japanese women who received tozinameran, suggesting a potential association of ICH with the vaccine. Although we understand that the benefits of tozinameran still outweigh the risks, we believe that a causal link with the vaccine is not proven but possible and warrants further analysis.

Investigation of Long COVID Prevalence and Its Relationship to Epstein-Barr Virus Reactivation

by  Jeffrey E. Gold ^{1,*} ,  Ramazan A. Okyay ² ,  Warren E. Licht ³  and  David J. Hurley ⁴ 

¹ World Organization, Watkinsville, GA 30677, USA

² Department of Public Health, Kahramanmaraş Sütçü İmam University, Kahramanmaraş 46040, Turkey

³ Warren Alpert Medical School of Brown University, Providence, RI 02903, USA

⁴ College of Veterinary Medicine, University of Georgia, Athens, GA 30602, USA

* Author to whom correspondence should be addressed.

Academic Editor: Lisa Gralinski

Pathogens **2021**, *10*(6), 763; <https://doi.org/10.3390/pathogens10060763>

Received: 26 May 2021 / Revised: 10 June 2021 / Accepted: 12 June 2021 / Published: 17 June 2021

(This article belongs to the Collection **SARS-CoV Infections**)

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Abstract

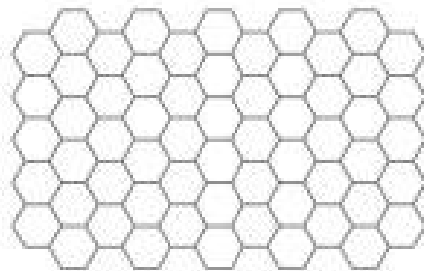
Coronavirus disease 2019 (COVID-19) patients sometimes experience long-term symptoms following resolution of acute disease, including fatigue, brain fog, and rashes. Collectively these have become known as long COVID. Our aim was to first determine long COVID prevalence in 185 randomly surveyed COVID-19 patients and, subsequently, to determine if there was an association between

graphene oxide

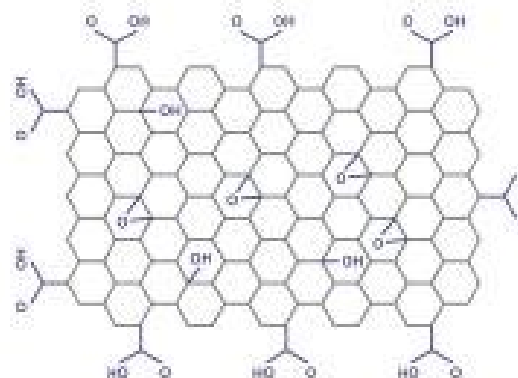
CONCLUSIES EN AANBEVELINGEN

- 1 Microscopisch onderzoek van het monster levert **sterke aanwijzingen op voor de waarschijnlijke aanwezigheid van grafeenderivaten, hoewel microscopie geen sluitend bewijs levert**. De definitieve identificatie van grafeen, geoxideerd grafeen (GO) of gereduceerd geoxideerd grafeen (rGO) in het RD1 monster vereist de **STRUCTURELE CHARACTERISATIE** door de analyse van specifieke spectrale patronen vergelijkbaar met die gepubliceerd in de literatuur en met die verkregen uit het standaard monster, verkregen met spectroscopische technieken zoals XPS, EDS, NMR, FTIR of Raman, onder andere.

De analyses in dit verslag hebben betrekking op EEN **ENKELE SAMPEL, waarvan het totale voor verwerking beschikbare volume beperkt is**. Daarom moet een significante bemonstering van soortgelijke flacons worden uitgevoerd om conclusies te kunnen trekken die kunnen worden veralgemeend naar vergelijkbare monsters, waarbij de herkomst, de traceerbaarheid en de kwaliteitscontrole tijdens de opslag en het vervoer vóór de analyse worden geregistreerd.



Graphene



Graphene Oxide

Overview

Symptoms

Treatment

Severe acute respiratory syndrome (SARS) is a viral respiratory disease caused by a SARS-associated coronavirus. It was first identified at the end of February 2003 during an outbreak that emerged in China and spread to 4 other countries. WHO co-ordinated the international investigation with the assistance of [the Global Outbreak Alert and Response Network \(GOARN\)](#) and worked closely with health authorities in affected countries to provide epidemiological, clinical and logistical support and to bring the outbreak under control.

SARS is an airborne virus and can spread through small droplets of saliva in a similar way to the cold and influenza. It was the first severe and readily transmissible new disease to emerge in the 21st century and showed a clear capacity to spread along the routes of international air travel.

SARS can also be spread indirectly via surfaces that have been touched by someone who is infected with the virus.

Most patients identified with SARS were previously healthy adults aged 25–70 years. A few suspected cases of SARS have been reported among children under 15 years. The case fatality among persons with illness meeting the current WHO case definition for probable and suspected cases of SARS is around 3%.

2-7 days
incubation period

The incubation period of SARS is usually 2-7



The Fauci/COVID-19 Dossier

This document is prepared for humanity by Dr. David E. Martin.



- 1986-1990 NIAID Grant AI 23946 leading to patent U.S. 7,279,327 "Methods for Producing Recombinant Coronavirus" Filed 2002 and issued 2007 <https://patents.google.com/patent/US7279327B2/ru>
- The paper first published from the NIAID grant is
<https://europepmc.org/backend/ptpmcrender.fcgi?accid=PMC7109931&blobtype=pdf>
- 1990 Pfizer files U.S. Patent 6,372,224 on a vaccine for the S-protein on coronavirus November 14, 2000 which was abandoned April 2010 making it public domain.
- 1990s Work focused on CoV association with cardiomyopathy (see above)
- Early reference to the "emergence" of CoV as a *respiratory pathogen* in
https://link.springer.com/content/pdf/10.1007%2F978-1-4615-1899-0_91.pdf
- 2000 Ralph Baric AI23946 and GM63228 from the National Institutes of Health actively working recombinant CoV
- 2001 National Institute of Health, Allergy and Infectious diseases. "Reverse Genetics with a Coronavirus Infectious cDNA Construct." 4/1/2001-3/31/005 \$1.0 million total costs/yr. RS Baric, PI
- 2002 Asia CoV SARS outbreak
- 2003 April 25, 2003 CDC Patent filed and ultimately becomes US7,220,852 (the patent on the RNA sequence) and 7,776,521 (the patent on the testing methodology. These patents give the U.S. Department of Health and Human Services the ability to control the commercial exploitation of SARS coronavirus.
- Dr. Anthony Fauci appointed to the Bill and Melinda Gates Foundation's Global Grand Challenges Scientific Advisory Board (served through 2010).
- April 28, 2003 Sequoia Pharmaceuticals \$953K for pathogen response and patent US7,151,163
<https://www.sbir.gov/node/305319>
- July 21, 2003 Ralph Baric's team (using AI23946 and GM63228) file U.S. Patent 7,618,802 which issued on November 17, 2009. <https://patents.google.com/patent/US7618802B2>

NIAID-Moderna vaccin deal

p. 105

"Jointly-owned by NIAID and Moderna"

PUBLIC HEALTH SERVICE

MATERIAL TRANSFER AGREEMENT

This Material Transfer Agreement ("MTA") has been adopted for use by the National Institutes of Health, the Food and Drug Administration and the Centers for Disease Control and Prevention, collectively referred to herein as the Public Health Service ("PHS") in all transfers of research material (Research Material) whether PHS is identified below as its Provider or Recipient.

Providers: *National Institute of Allergy and Infectious Diseases, National Institutes of Health ("NIAID")*
ModernaTX, Inc ("Moderna")

Recipient: The University of North Carolina at Chapel Hill

1. Provider agrees to transfer to Recipient's Investigator the following Research Material:

mRNA coronavirus vaccine candidates developed and jointly-owned by NIAID and Moderna.

Annotated by Bob Herman, Axios

be used for commercial purposes such as screening, production or sale, for which a commercialization license may be required. Recipient agrees to comply with all Federal rules and regulations applicable to the Research Project and the handling of the Research Material.

- a. Are the Research Materials of human origin?

Yes No

- b. If Yes in 2a, were Research Materials collected according to 45 CFR Part 46, "Protection of Human Subjects"?

Yes Please provide Assurance Number: _____
 No

3. This Research Material will be used by Recipient's Investigator solely in connection with the following research project ("Research Project") described with specificity as follows (use an attachment page if necessary):

Perform challenge studies with the mRNA vaccine in a Proprietary Info model as described on Exhibit A.

4. Upon a Provider's reasonable request, Recipient will furnish a status report to such Provider regarding the use of the Research Materials and any data or results generated therefore. In all oral presentations or written

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Collaborative research and licensing opportunity: Prefusion coronavirus spike proteins and their use

Inventors at the Vaccine Research Center of the National Institute of Allergy and Infectious Diseases have developed a novel CoV S protein vaccine antigen. This technology employs protein engineering to stabilize S in its prefusion conformation, preventing structural rearrangement, and exposing antigenically preferable surfaces. The technology has been applied to several CoV spikes, including those from human-relevant viruses, such as HKU1-CoV, SARS-CoV, and MERS-CoV. Particularly for MERS-COV, stabilized S proteins have been shown to elicit superior neutralizing antibody responses up to 10-fold higher in animal models and protect mice against lethal MERS-CoV infection.

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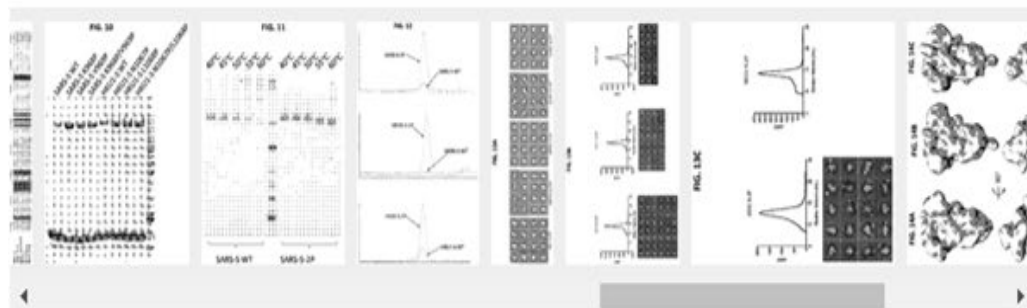


Prefusion coronavirus spike proteins and their use

Abstract

Coronavirus S ectodomain trimers stabilized in a prefusion conformation, nucleic acid molecules and vectors encoding these proteins, and methods of their use and production are disclosed. In several embodiments, the coronavirus S ectodomain trimers and/or nucleic acid molecules can be used to generate an immune response to coronavirus in a subject. In additional embodiments, the therapeutically effective amount of the coronavirus S ectodomain trimers and/or nucleic acid molecules can be administered to a subject in a method of treating or preventing coronavirus infection.

Images (24)



Classifications

■ **A61K39/12** Viral antigens

[View 7 more classifications](#)

US10960070B2

United States

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Inventor: Barney Graham, Jason McLellan, Andrew Ward, Robert Kirchdoerfer, Christopher Cottrell, Michael Gordon Joyce, Masaru Kanekiyo, Nianshuang Wang, Jesper Pallesen, Hadi Yassine, Hannah Turner, Kizzmekia Corbett

Current Assignee : Dartmouth College , US Department of Health and Human Services , Scripps Research Institute

Worldwide applications

2017 · [US](#) [WO](#) [EP](#)

Application US16/344,774 events

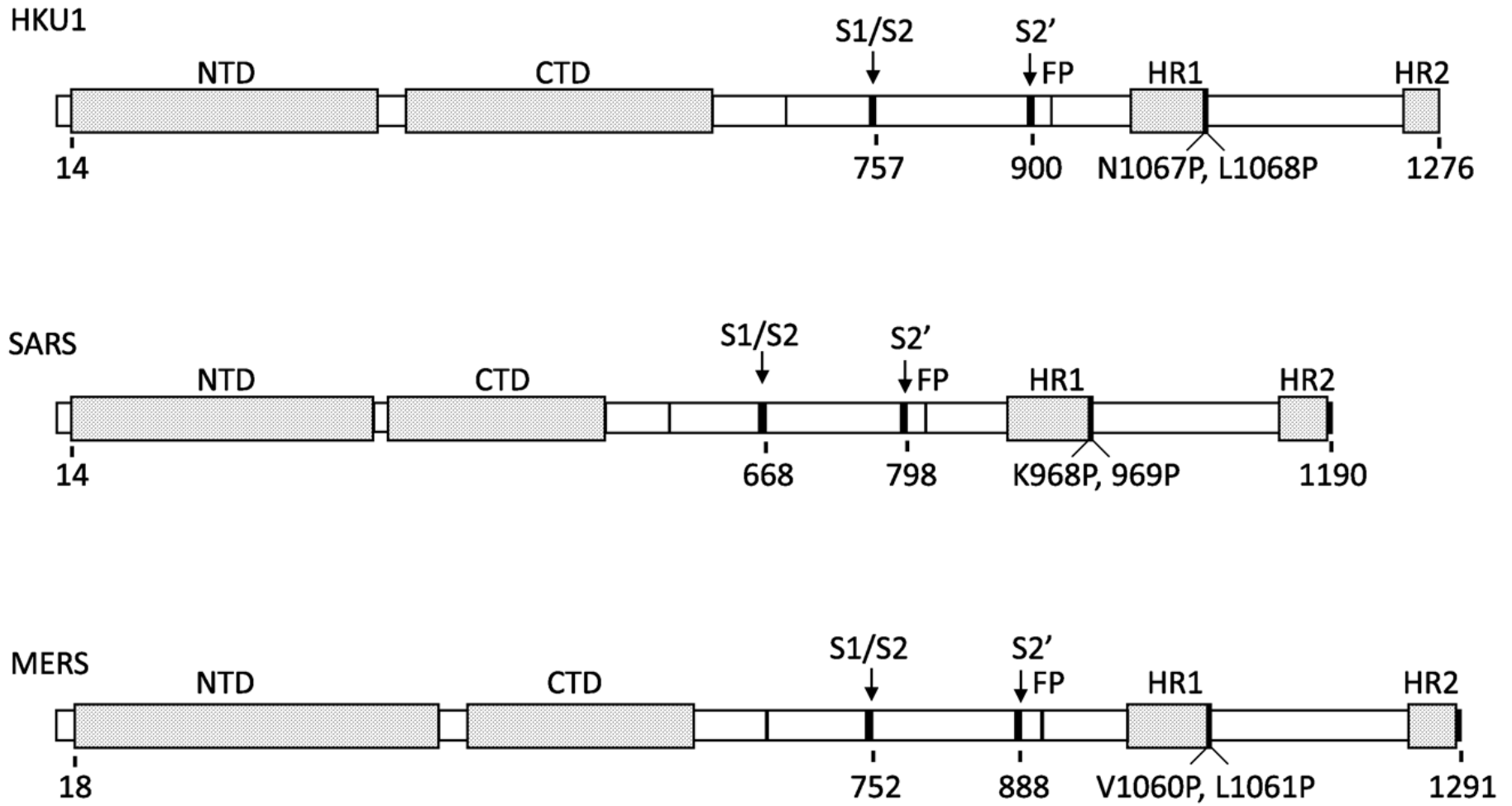
2016-10-25 • Priority to US201662412703P

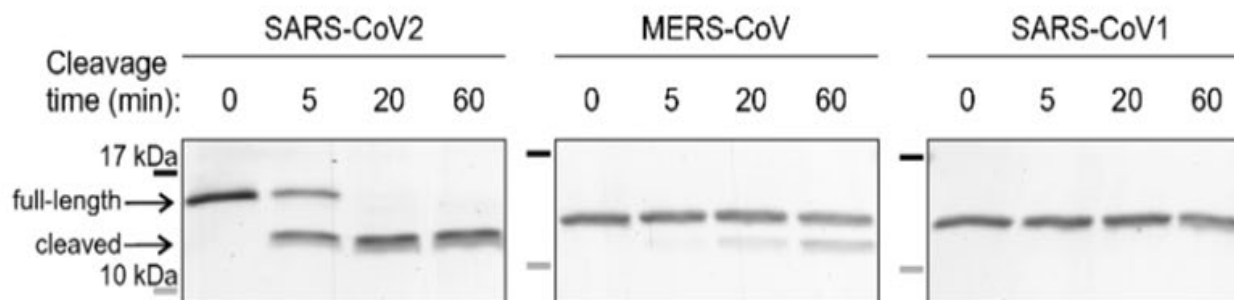
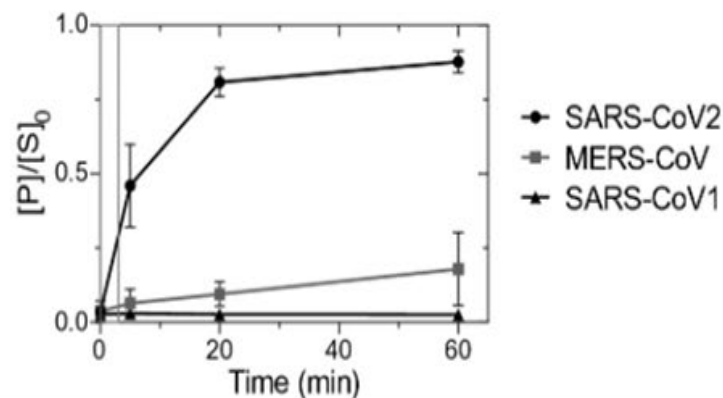
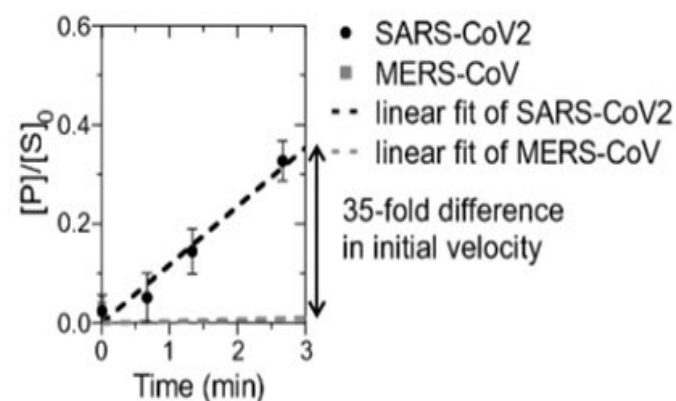
2017-10-25 • Application filed by Dartmouth College, Scripps Research Institute, US Department of Health and Human Services

2020-02-27 • Publication of US20200061185A1

2021-03-30 • Publication of US10960070B2

FIG. 8



d**e****f**

An insertion to the S1/S2 proteolytic cleavage site of SARS-CoV2 Spike protein introduces a furin site. (a) A structural model of SARS-CoV2 Spike protein¹⁵. Spike protein S1 (residue 1–685) is colored blue, Spike protein S2 (residue 686–1273) is colored brown and the intrinsically disordered S1/S2 proteolytic cleavage site is shown in red. The structure lacks the C-terminal residues 1148–1273. (b) Scheme of the constructs used to examine furin specificity. A 20-residue segment around the S1/S2 site was fused with a linker ELQGGGGG to the Streptococcal protein G B1 domain (GB1) and a C-terminal 6xHis tag. (c) Sequence alignment of the S1/S2 region in SARS-CoV, MERS-CoV, SARS-CoV2, and bat virus SARSr-CoV RaTG13, which is closely related to SARS-CoV2¹⁶. (d) Coomassie-stained SDS-PAGE gels showing the proteolytic cleavage of the GB1-fused reporter constructs. Furin activity towards the S1/S2 region of SARS-CoV2, MERS-CoV, and SARS-CoV1 was measured in vitro using the GB1 reporter constructs shown in 'b'. The MW of SARS-CoV2 GB1 reporter protein is 10.9 kDa, which is cleaved by furin to 9.2 kDa and 1.7 kDa fragments. Uncropped images are shown in Supplementary Fig. S1. (e) Quantified data from the furin cleavage assay. The plot shows the relative amount of cleaved product compared to amount of uncleaved substrate at $t = 0$ min. Error bars show

FIG. 12

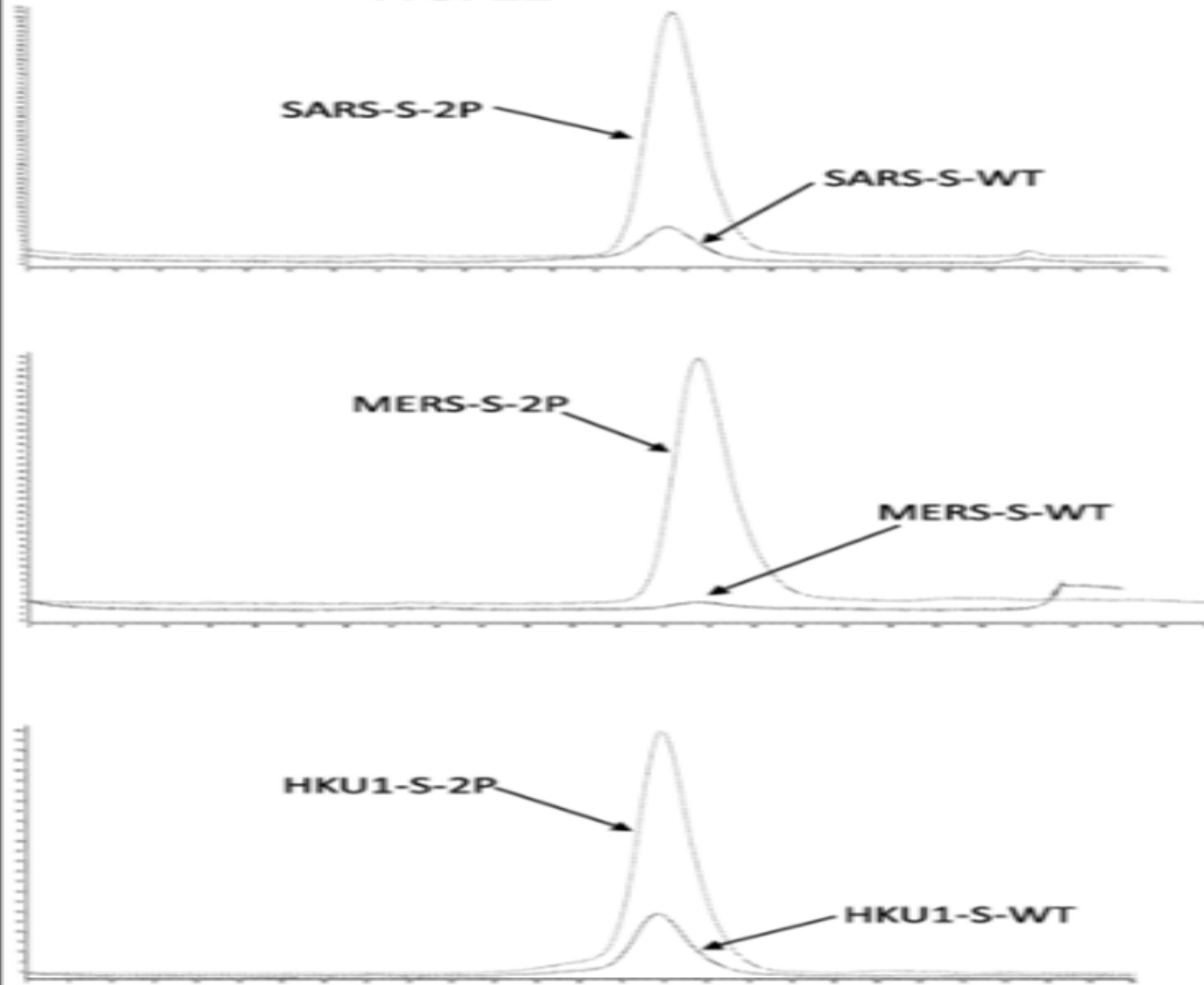


FIG. 14A

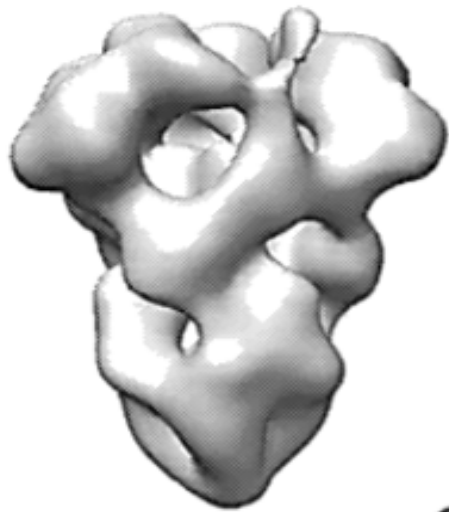


FIG. 14B

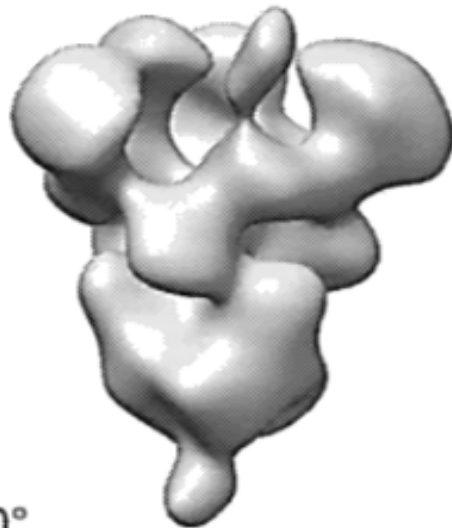
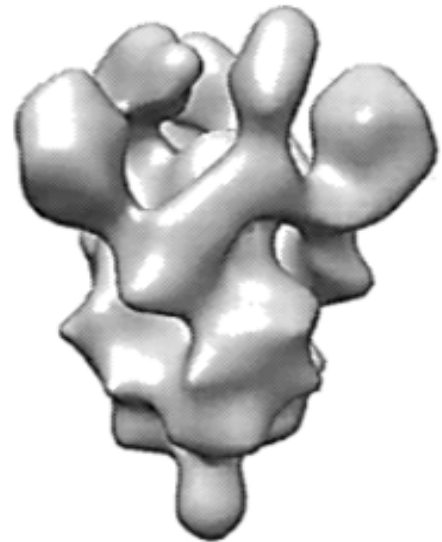
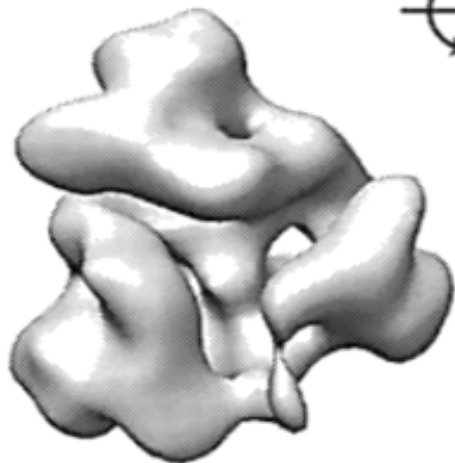


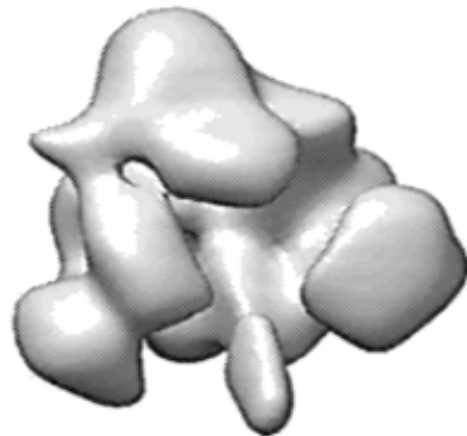
FIG. 14C



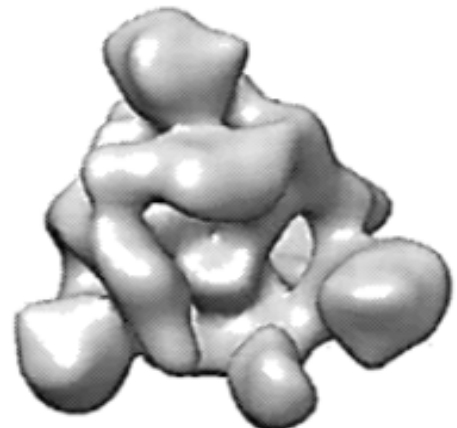
 90°



HKU1 S 2P



MERS S 2P



SARS S 2P

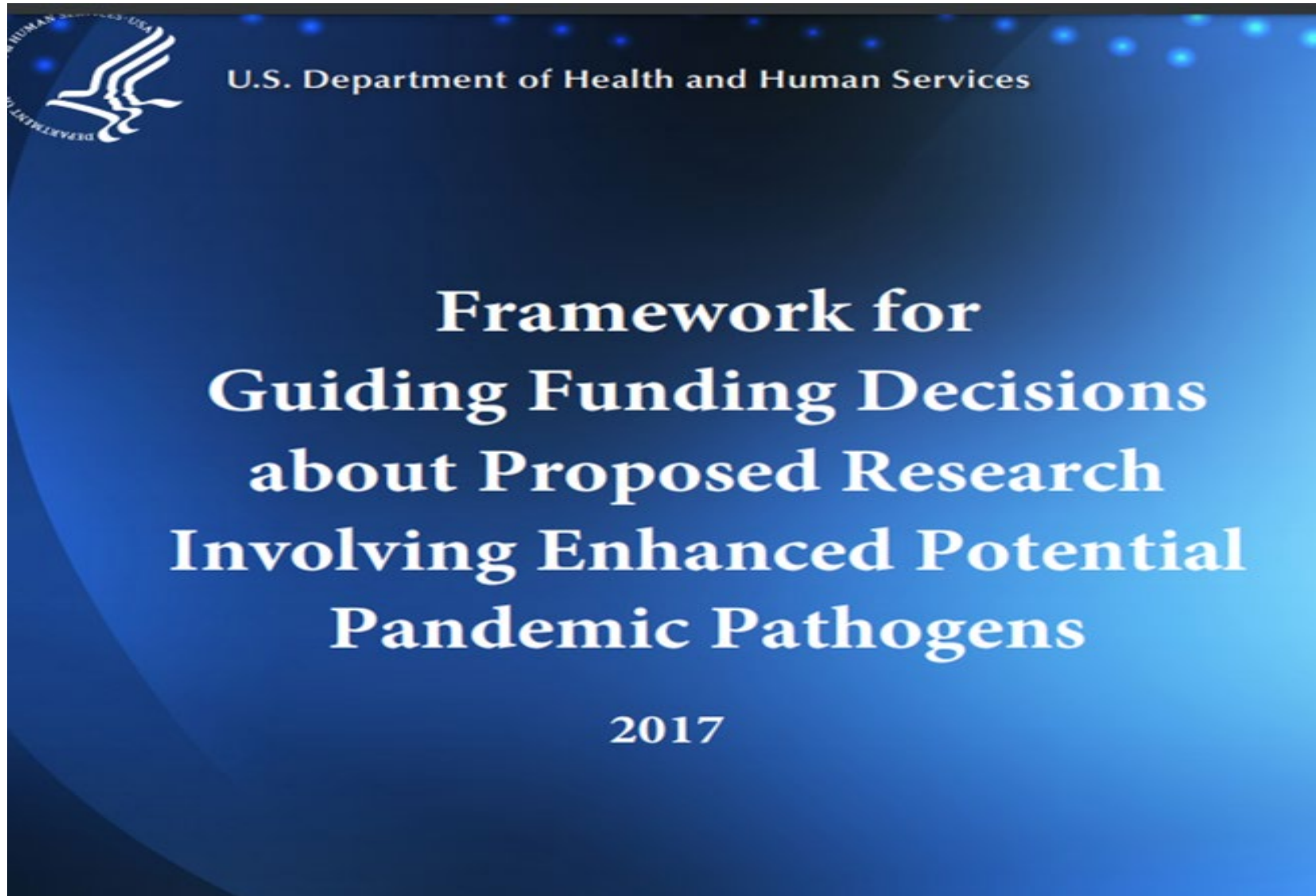
U.S. Government Gain-of-Function Deliberative Process and Research Funding Pause on Selected Gain-of-Function Research Involving Influenza, MERS, and SARS Viruses

studies may entail biosafety and biosecurity risks; therefore, the risks and benefits of gain-of-function research must be evaluated, both in the context of recent U.S. biosafety incidents and to keep pace with new technological developments, in order to determine which types of studies should go forward and under what conditions.

In light of recent concerns regarding biosafety and biosecurity, effective immediately, the U.S. Government (USG) will pause new USG funding for gain-of-function research on influenza, MERS or SARS viruses, as defined below. This research funding pause will be effective until a robust and broad deliberative process is completed that results in the adoption of a new USG gain-of-function research policy¹. Restrictions on new funding will apply as follows:

New USG funding will not be released for gain-of-function research projects that may be reasonably anticipated to confer attributes to influenza, MERS, or SARS viruses such that the virus would have enhanced pathogenicity and/or transmissibility in mammals via the respiratory route. The research funding pause would not apply to characterization or testing of naturally occurring influenza, MERS, and SARS viruses, unless the tests are reasonably anticipated to increase transmissibility and/or pathogenicity.

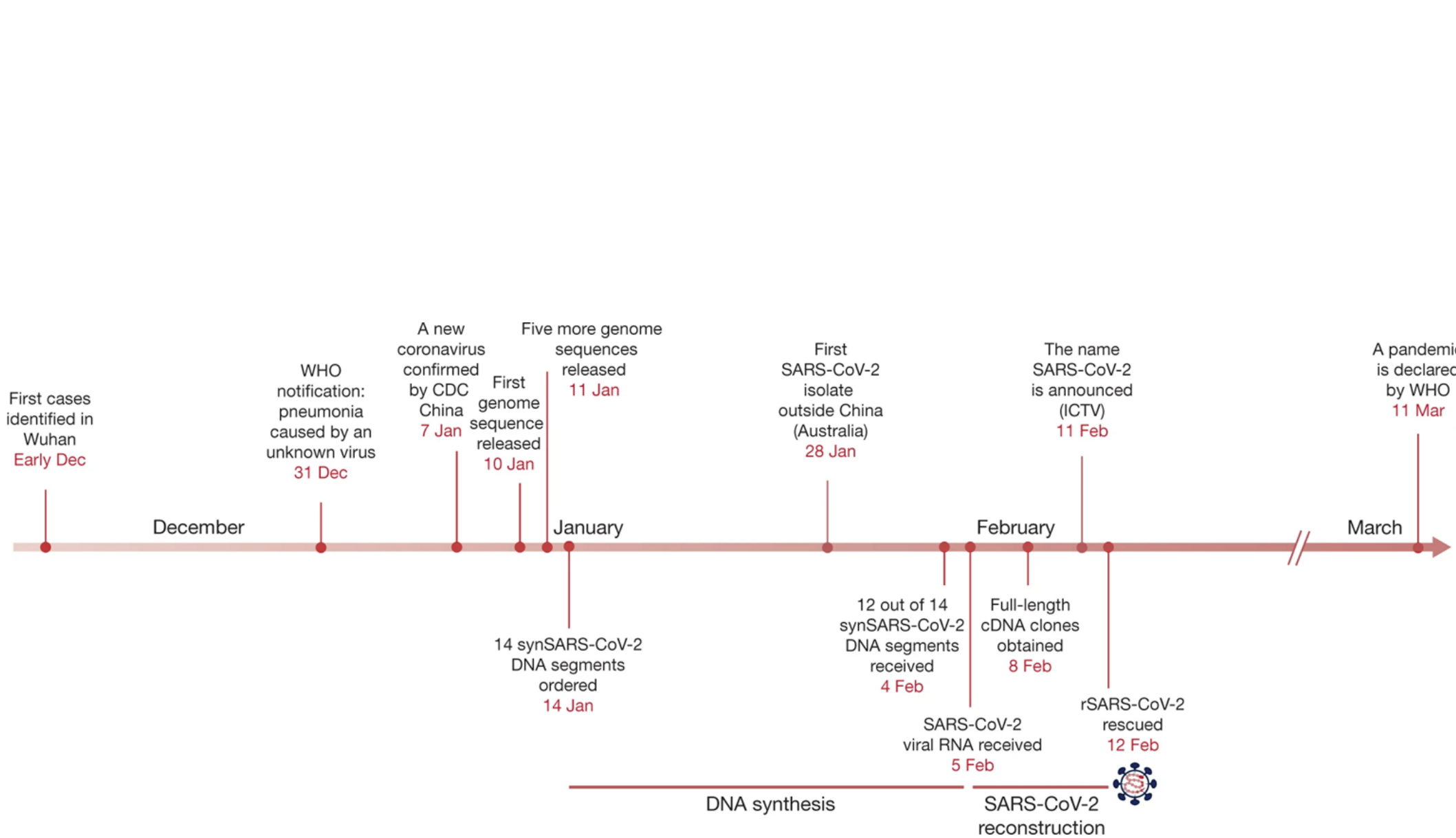
P3CO



U.S. Department of Health and Human Services

**Framework for
Guiding Funding Decisions
about Proposed Research
Involving Enhanced Potential
Pandemic Pathogens**

2017



From: Degrace, Marciela (NIH/NIAID) [E]

Sent: Thursday, January 9, 2020 2:11 PM

To: Webby, Richard <Richard.Webby@STJUDE.ORG>; malik <malik@hku.hk>; Ghazi Kayali <ghazi@human-link.org>; Yoshi Kawaoka <kawaokay@vetmed.wisc.edu>; R.A.M. Fouchier <r.fouchier@erasmusmc.nl>; adolfo.garcia-sastre@mssm.edu; Richard Rothman <rrothma1@jhmi.edu>; Pekosz, Andrew S. (apekosz@jhsph.edu) <apekosz@jhsph.edu>; Schultz-Cherry, Stacey <Stacey.Schultz-Cherry@STJUDE.ORG>; david_topham@urmc.rochester.edu; Orenstein, Walter <worenst@emory.edu>; Lowen, Anice <anice.lowen@emory.edu>

Cc: ryan.camping@mssm.edu; Melissa Uccellini <melissa.uccellini@mssm.edu>; McKenzie, Pamela <Pamela.McKenzie@STJUDE.ORG>; Neu, Donna <Donna_Neu@URMC.Rochester.edu>; Kathryn Shaw-Saliba <kshaw15@jhu.edu>; Collins, Erin-Joi <emcneal@emory.edu>; Stemmy, Erik (NIH/NIAID) [E] <erik.stemmy@nih.gov>; Lampley, Rebecca (NIH/VRC) [F] <rebecca.lampley@nih.gov>

Subject: Wuhan Pneumonia response - setting up a call

Importance: High

Hi all,

As you all have heard, China is reporting a novel coronavirus is causing viral pneumonia in Wuhan. While we have very little information at this point, NIAID leadership would like to begin thinking about how we would perform a research response should the outbreak continue and we get access to samples. We would like to hear what you think would be important research directions to pursue to start as well as the capabilities your groups may have given what is known at the moment. We can also discuss potential resources needed from NIAID by your groups so that we can prepare on this end to help you all if needed.

We will look to add some additional coronavirus experts to the call, and if there's anyone I haven't copied here from CEIRS that you think should be involved, please let me know. We need to move quickly, so the goal is to have a call next week at the time when most people are available.

Below is a doodle poll to find a time. Please fill out by the **end of the day tomorrow** so we can schedule a time accordingly.

I know it is already such a busy time – but I'm hopeful since we know the drill for these sorts of things that preparing now will help us.

Novel 2019 coronavirus genome

SARS-CoV-2 coronavirus



edward_holmes

6  Jan '20

10th January 2020

This posting is communicated by Edward C. Holmes, University of Sydney on behalf of the consortium led by Professor Yong-Zhen Zhang, Fudan University, Shanghai

The Shanghai Public Health Clinical Center & School of Public Health, in collaboration with the Central Hospital of Wuhan, Huazhong University of Science and Technology, the Wuhan Center for Disease Control and Prevention, the National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control, and the University of Sydney, Sydney, Australia is releasing a coronavirus genome from a case of a respiratory disease from the Wuhan outbreak. The sequence has also been deposited on GenBank ([accession MN908947](#) 31.0k) and will be released as soon as possible.

Update: [This genome is now available on GenBank and an updated version has been posted](#) 31.0k.

Disclaimer:

Please feel free to download, share, use, and analyze this data. We ask that you communicate with us if you wish to publish results that use these data in a journal. If you have any other questions –then please also contact us directly.

Professor Yong-Zhen Zhang,
Shanghai Public Health Clinical Center & School of Public Health,
Fudan University,
Shanghai, China.

Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete g

GenBank: MN908947.1

⚠ This sequence has been updated. [See current version.](#)

[FASTA](#) [Graphics](#)

Go to: 

LOCUS MN908947 30473 bp ss-RNA linear VRL 12-JAN-2020
DEFINITION Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete genome.
ACCESSION MN908947
VERSION MN908947.1
KEYWORDS .
SOURCE Wuhan seafood market pneumonia virus
ORGANISM [Wuhan seafood market pneumonia virus](#)
Viruses; Riboviria; Nidovirales; Coronaviridae; Orthocoronavirinae; Betacoronavirus; unclassified Betacoronavirus.
REFERENCE 1 (bases 1 to 30473)
AUTHORS Zhang,Y.-Z., Wu,F., Chen,Y.-M., Pei,Y.-Y., Xu,L., Wang,W., Zhao,S., Yu,B., Hu,Y., Tao,Z.-W., Song,Z.-G., Tian,J.-H., Zhang,Y.-L., Liu,Y., Zheng,J.-J., Dai,F.-H., Wang,Q.-M., She,J.-L. and Zhu,T.-Y.
TITLE A novel coronavirus associated with a respiratory disease in Wuhan of Hubei province, China
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 30473)
AUTHORS Zhang,Y.-Z., Wu,F., Chen,Y.-M., Pei,Y.-Y., Xu,L., Wang,W., Zhao,S., Yu,B., Hu,Y., Tao,Z.-W., Song,Z.-G., Tian,J.-H., Zhang,Y.-L., Liu,Y., Zheng,J.-J., Dai,F.-H., Wang,Q.-M., She,J.-L. and Zhu,T.-Y.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-2020) Department of Zoonoses, National Institute of Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Changping Liuzi 5, Beijing 102206, China
COMMENT [WARNING] On Jan 14, 2020 this sequence was replaced by [MN908947.2](#).

##Assembly-Data-START##
Assembly Method :: Megahit v. V1.1.3
Sequencing Technology :: Illumina
##Assembly-Data-END##
FEATURES Location/Qualifiers
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/organism="Wuhan seafood market pneumonia virus"
/mol_type="genomic RNA"

Recovery of deleted deep sequencing data sheds more light on the early Wuhan SARS-CoV-2 epidemic

Jesse D. Bloom

Fred Hutchinson Cancer Research Center

Howard Hughes Medical Institute



Seattle, WA, USA

ABSTRACT The origin and early spread of SARS-CoV-2 remains shrouded in mystery. Here I identify a data set containing SARS-CoV-2 sequences from early in the Wuhan epidemic that has been deleted from the NIH's Sequence Read Archive. I recover the deleted files from the Google Cloud, and reconstruct partial sequences of 13 early epidemic viruses. Phylogenetic analysis of these sequences in the context of carefully annotated existing data suggests that the Huanan Seafood Market sequences that are the focus of the joint WHO-China report are not fully representative of the viruses in Wuhan early in the epidemic. Instead, the progenitor of known SARS-CoV-2 sequences likely contained three mutations relative to the market viruses that made it more similar to SARS-CoV-2's bat coronavirus relatives.

[nature](#) > [articles](#) > [article](#)

Article | Published: 04 May 2020

Rapid reconstruction of SARS-CoV-2 using a synthetic genomics platform

Tran Thi Nhu Thao, Fabien Labrousseau, Nadine Ebert, Philip V'kovski, Hanspeter Stalder, Jasmine Portmann, Jenna Kelly, Silvio Steiner, Melle Holwerda, Annika Kratzel, Mitra Gultom, Kimberly Schmied, Laura Laloli, Linda Hüsser, Manon Wider, Stephanie Pfaender, Dagny Hirt, Valentina Cippà, Silvia Crespo-Pomar, Simon Schröder, Doreen Muth, Daniela Niemeyer, Victor M. Corman, Marcel A. Müller, [Christian Drosten](#), Ronald Dijkman, Joerg Jores  & Volker Thiel  -Show fewer authors

Nature **582**, 561–565 (2020) | [Cite this article](#)

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Abstract

Reverse genetics has been an indispensable tool to gain insights into viral pathogenesis and vaccine development. The genomes of large RNA viruses, such as those from coronaviruses, are cumbersome to clone and manipulate in *Escherichia coli* owing to the size and occasional instability of the genome^{1,2,3}. Therefore, an alternative rapid and robust reverse-genetics platform for RNA viruses would benefit the research community. Here we show the [4-9#author-information](#) fidelity of a yeast-based synthetic genomics platform to genetically reconstruct

<https://www.ncbi.nlm.nih.gov/nuccore/MN481979>

[FASTA](#) [Graphics](#) [PopSet](#)

Go to:

LOCUS MN481979 29918 bp RNA linear VRL 01-MAY-2020

DEFINITION Middle East respiratory syndrome-related coronavirus isolate
Riyadh_1734_2015, partial genome.

ACCESSION MN481979

VERSION MN481979.1

KEYWORDS .

SOURCE Middle East respiratory syndrome-related coronavirus (MERS-CoV)

ORGANISM [Middle East respiratory syndrome-related coronavirus](#)

Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes;
Nidovirales; Coronidovirineae; Coronaviridae; Orthocoronavirinae;
Betacoronavirus; Merbecovirus.

REFERENCE 1 (bases 1 to 29918)

AUTHORS Schroeder,S., Drosten,C., Corman,V.M., Muth,D. and Muller,M.A.

TITLE Direct Submission

JOURNAL Submitted (12-SEP-2019) Institute of Virology, Charite Berlin,
Campus Charite Mitte Chariteplatz 1, Berlin, Berlin 10117, Germany

COMMENT ##Assembly-Data-START##

Assembly Method :: Geneious v. 9.1.8

Sequencing Technology :: Illumina

##Assembly-Data-END##

FEATURES Location/Qualifiers

source

1..29918

/organism="Middle East respiratory syndrome-related
coronavirus"

/mol_type="genomic RNA"

/isolate="Riyadh_1734_2015"

/isolation_source="cell culture"

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/db_xref="taxon:1222600"

Links to pubmed

Human respiratory syncytial virus B isolate HRSV/B/Bern/2019, complete

GenBank: MT107528.1

[FASTA](#) [Graphics](#)

[Go to:](#)

LOCUS MT107528 15311 bp cRNA linear VRL 16-APR-2020

DEFINITION Human respiratory syncytial virus B isolate HRSV/B/Bern/2019, complete genome.

ACCESSION MT107528

VERSION MT107528.1

KEYWORDS .

SOURCE Human respiratory syncytial virus B

ORGANISM [Human respiratory syncytial virus B](#)

Viruses; Riboviria; Orthornavirae; Negarnaviricota; Haploviricotina; Monjiviricetes; Mononegavirales; Pneumoviridae; Orthopneumovirus.

REFERENCE 1 (bases 1 to 15311)

AUTHORS Thao,T.T.N., Labroussaa,F., Ebert,N., Stalder,H., Dijkman,R., Jores,J., Thiel,V., Bittel,P., Suter-Riniker,F. and Kelly,J.

TITLE Rapid reconstruction of SARS-CoV-2 using a synthetic genomics platform

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 15311)

AUTHORS Thao,T.T.N., Labroussaa,F., Ebert,N., Stalder,H., Dijkman,R., Jores,J., Thiel,V., Bittel,P., Suter-Riniker,F. and Kelly,J.

TITLE Direct Submission

JOURNAL Submitted (19-FEB-2020) Department of Infectious Diseases and Pathobiology, Institute of Virology and Immunology (IVI), Laenggassstrasse 122, Bern, BE 3001, Switzerland

COMMENT ##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

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/mol_type="viral cRNA"
/isolate="HRSV/B/Bern/2019"
/host="Homo sapiens"
/db_xref="taxon:208895"
/country="Switzerland"
/collection_date="2019"
gene 125..544

Synthetic construct ORF1ab, spike, ORF3, E, M, ORF6, ORF8, and N gene complete cds

GenBank: MT108784.1

[FASTA](#) [Graphics](#)

Go to:

LOCUS MT108784 29891 bp DNA linear SYN 17-APR-2020 ←

DEFINITION Synthetic construct ORF1ab, spike, ORF3, E, M, ORF6, ORF8, and N genes, complete cds.

ACCESSION MT108784

VERSION MT108784.1

KEYWORDS .

SOURCE synthetic construct

ORGANISM [synthetic construct](#)

other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 29891)

AUTHORS Thao,T.N., Labroussaa,F., Ebert,N., Portmann,J., Stalder,H., Gultom,M.L., V'kovski,P., Cippa,V., Crespo-Pomar,S., Kratzel,A., Laloli,L., Steiner,S., Holwerda,M., Huesser,L., Kelly,J., Pfaender,S., Hirt,D., Schroeder,S., Muth,D., Niemeyer,D., Mueller,M.A., Drosten,C., Wider,M., Stuermer,I., Dijkman,R., Jores,J. and Thiel,V.

TITLE Rapid reconstruction of SARS-CoV-2 using a synthetic genomics platform

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 29891)

AUTHORS Thao,T.N., Labroussaa,F., Ebert,N., Portmann,J., Stalder,H., Gultom,M.L., V'kovski,P., Cippa,V., Crespo-Pomar,S., Kratzel,A., Laloli,L., Steiner,S., Holwerda,M., Huesser,L., Kelly,J., Pfaender,S., Hirt,D., Schroeder,S., Muth,D., Niemeyer,D., Mueller,M.A., Drosten,C., Wider,M., Stuermer,I., Dijkman,R., Jores,J. and Thiel,V. ←

TITLE Direct Submission ←

JOURNAL Submitted (18-FEB-2020) Department of Infectious Diseases and Pathobiology, Institute of Virology and Immunology (IVI), Laenggassstrasse 122, Bern, BE 3001, Switzerland

COMMENT ##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..29891

spike [synthetic construct]

GenBank: QIG55857.1

[Identical Proteins](#) [FASTA](#) [Graphics](#)

Go to:

LOCUS QIG55857 1273 aa linear SYN 17-APR-2020
DEFINITION spike [synthetic construct].
ACCESSION QIG55857
VERSION QIG55857.1
DBSOURCE accession [MT108784.1](#)
KEYWORDS .
SOURCE synthetic construct
ORGANISM [synthetic construct](#)
other sequences; artificial sequences.
REFERENCE 1 (residues 1 to 1273)
AUTHORS Thao,T.N., Labroussaa,F., Ebert,N., Portmann,J., Stalder,H., Gultom,M.L., V'kovski,P., Cippa,V., Crespo-Pomar,S., Kratzel,A., Laloli,L., Steiner,S., Holwerda,M., Huesser,L., Kelly,J., Pfaender,S., Hirt,D., Schroeder,S., Muth,D., Niemeyer,D., Mueller,M.A., Drosten,C., Wider,M., Stuermer,I., Dijkman,R., Jores,J. and Thiel,V.
TITLE Rapid reconstruction of SARS-CoV-2 using a synthetic genomics platform
JOURNAL Unpublished
REFERENCE 2 (residues 1 to 1273)
AUTHORS Thao,T.N., Labroussaa,F., Ebert,N., Portmann,J., Stalder,H., Gultom,M.L., V'kovski,P., Cippa,V., Crespo-Pomar,S., Kratzel,A., Laloli,L., Steiner,S., Holwerda,M., Huesser,L., Kelly,J., Pfaender,S., Hirt,D., Schroeder,S., Muth,D., Niemeyer,D., Mueller,M.A., Drosten,C., Wider,M., Stuermer,I., Dijkman,R., Jores,J. and Thiel,V.
TITLE Direct Submission
JOURNAL Submitted (18-FEB-2020) Department of Infectious Diseases and Pathobiology, Institute of Virology and Immunology (IVI), Laenggassstrasse 122, Bern, BE 3001, Switzerland
FEATURES
source Location/Qualifiers
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/note="derived from Severe acute respiratory syndrome coronavirus 2 BetaCoV/Wuhan/IVDC-HB-01/2019"

https://www.ncbi.nlm.nih.gov/protein/QJS57327.1

surface glycoprotein [synthetic construct]

GenBank: QJS57327.1

[Identical Proteins](#) [FASTA](#) [Graphics](#)

Go to:

LOCUS QJS57327 1273 aa linear SYN 13-MAY-2020
DEFINITION surface glycoprotein [synthetic construct].
ACCESSION QJS57327
VERSION QJS57327.1
DBSOURCE accession [MT461669.1](#)
KEYWORDS .
SOURCE synthetic construct
ORGANISM [synthetic construct](#)
other sequences; artificial sequences.
REFERENCE 1 (residues 1 to 1273)
AUTHORS Hou,Y.J., Okuda,K., Edwards,C.E., Martinez,D.R., Asakura,T.,
Dinnon,K.H. III, Kato,T., Lee,R.E., Yount,B.L., Mascenik,T.M.,
Chen,G., Olivier,K.N., Ghio,A., Tse,L.V., Leist,S.R.,
Gralinski,L.E., Schaefer,A., Dang,H., Gilmore,R., Nakano,S.,
Fulcher,M.L., Livraghi-Butrico,A., Nicely,N.I., Cameron,M.,
Cameron,C., Kelvin,D.J., de Silva,A., Margolis,D.M., Markmann,A.,
Bartelt,L., Zumwalt,R., Martinez,F.J., Salvatore,S.P., Borczuk,A.,
Tata,P.R., Sontake,V., Kimple,A., Jaspers,I., O'Neal,W.K.,
Randell,S.H., Boucher,R.C. and Baric,R.S.
TITLE SARS-CoV-2 Genetics Reveals a Variable Infection Gradient in the
Respiratory Tract
JOURNAL Unpublished
REFERENCE 2 (residues 1 to 1273)
AUTHORS Hou,Y.J., Okuda,K., Edwards,C.E., Martinez,D.R., Asakura,T.,
Dinnon,K.H. III, Kato,T., Lee,R.E., Yount,B.L., Mascenik,T.M.,
Chen,G., Olivier,K.N., Ghio,A., Tse,L.V., Leist,S.R.,
Gralinski,L.E., Schaefer,A., Dang,H., Gilmore,R., Nakano,S.,
Fulcher,M.L., Livraghi-Butrico,A., Nicely,N.I., Cameron,M.,
Cameron,C., Kelvin,D.J., de Silva,A., Margolis,D.M., Markmann,A.,
Bartelt,L., Zumwalt,R., Martinez,F.J., Salvatore,S.P., Borczuk,A.,
Tata,P.R., Sontake,V., Kimple,A., Jaspers,I., O'Neal,W.K.,
Randell,S.H., Boucher,R.C. and Baric,R.S.
TITLE Direct Submission



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Law for the prevention and control of infectious diseases in humans (Infection Protection Law - IfSG)

§ 21 Vaccines

In the case of a protective vaccination ordered on the basis of this law or one publicly recommended by the highest state health authority or a vaccination according to § 17a paragraph 2 of the Soldiers Act, vaccines may be used that contain microorganisms that can be excreted by the vaccinated and absorbed by other people. The basic right to physical integrity (Article 2, Paragraph 2, Clause 1 of the Basic Law) is restricted in this respect.

		compensation law of December 12, 2019 (Federal Law Gazette I p. 2652)
11/01/2021	(not yet in force)	Article 1 Measles Protection Act of February 10, 2020 (Federal Law Gazette I p. 148)
10/01/2021	(not yet in force)	Article 4 Act to update the structural reform of the federal fee law of July 18, 2016 (Federal Law Gazette I p. 1666)

past and consolidated changes (change missed? [Subscribe to IfSG!](#))

06/01/2021	Synopsis as a whole or individually for Section 5 , Section 5b (new) , Section 22 , Section 25 , Section 28c , Section 36 , Section 74 , Section 75a (new) , Annex (new)	Article 1 Second law amending the Infection Protection Act and other laws of May 28, 2021 (Federal Law Gazette I p. 1174)
05/04/2021 (05/31/2021)	§ 28b	Article 1 Second law amending the Infection Protection Act and other laws of May 28, 2021 (Federal Law Gazette I p. 1174)
04/23/2021 (05/31/2021)	Section 56	Article 1 Second law amending the Infection Protection Act and other laws of May 28, 2021 (Federal Law Gazette I p. 1174)

<https://www.ncbi.nlm.nih.gov/protein/QOT47607.1>

LOCUS QOT47607 1273 aa linear SYN 02-NOV-2020
DEFINITION synthetic SARS-CoV-2 spike glycoprotein [Measles morbillivirus].
ACCESSION QOT47607
VERSION QOT47607.1
DBSOURCE accession [MW090971.1](#)
KEYWORDS .
SOURCE Measles morbillivirus
ORGANISM [Measles morbillivirus](#)
Viruses; Riboviria; Orthornavirae; Negarnaviricota;
Haploviricotina; Monjviricetes; Mononegavirales; Paramyxoviridae;
Orthoparamyxovirinae; Morbillivirus.
REFERENCE 1 (residues 1 to 1273)
AUTHORS Hoerner,C., Schuermann,C., Auste,A., Ebenig,A., Muraleedharan,S.,
Dinnon,K.H. III, Scholz,T., Herrmann,M., Schnierle,B., Baric,R.S.
and Muehlebach,M.D.
TITLE A Highly Immunogenic and Effective Measles Virus-based Th1-biased
COVID-19 Vaccine
JOURNAL Unpublished
REFERENCE 2 (residues 1 to 1273)
AUTHORS Hoerner,C., Schuermann,C., Auste,A., Ebenig,A., Muraleedharan,S.,
Dinnon,K.H. III, Scholz,T., Herrmann,M., Schnierle,B., Baric,R.S.
and Muehlebach,M.D.
TITLE Direct Submission
JOURNAL Submitted (09-OCT-2020) Abteilung Veterinaermedizin,
Paul-Ehrlich-Institut, Paul-Ehrlich-Str. 51-59, Langen, Hessia
63225, Germany
FEATURES Location/Qualifiers
source 1..1273
/organism="Measles morbillivirus"
/strain="MeVvac2-SARS2-S(H)"
/db_xref="taxon:[11234](#)"
/country="Germany"
/note="recombinant measles virus strain expressing the
SARS-CoV-2 spike glycoprotein (S); designed for vaccine
production; derived from measles virus vaccine strain
Edmonston B/Moraten"
Protein 1..1273
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/name="codon-optimized for Homo sapiens"
CDS 1..1273
/gene="S"



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