

Biomarker Identification / Therapeutics Development from Proteomics and Metabolomics Studies of COVID-19 Patients

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School of Biochemistry and Immunology

Protein Folding and Biomolecular NMR Spectroscopy Lab / TBSI NMR Facility

Dublin 2, Ireland

3rd June 2020 (Wed)

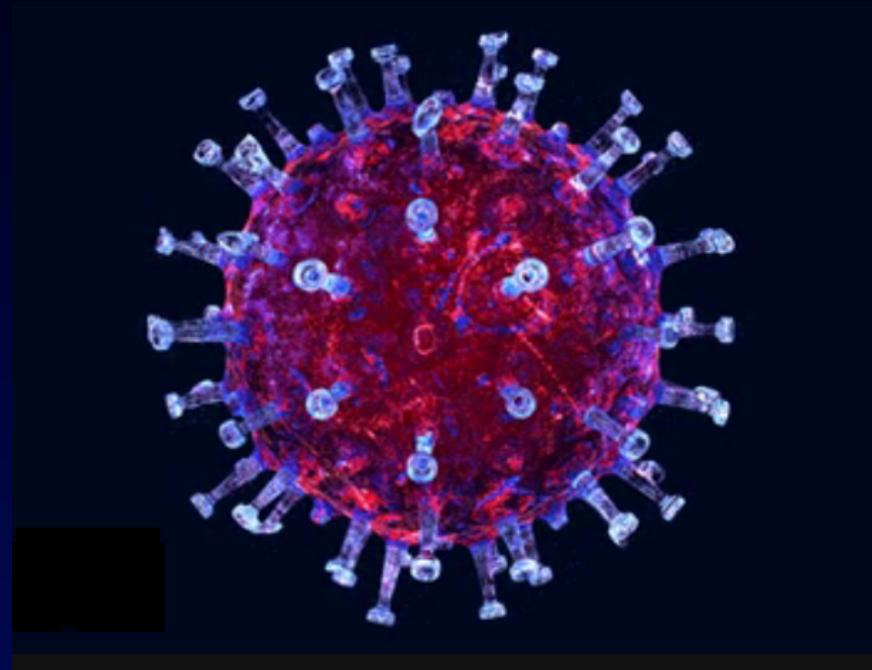
**International Trends in Pandemic Quarantine and the Development of
Vaccines / Therapeutics**

KOFST – KSEAs Online Forum

Seoul - Dublin



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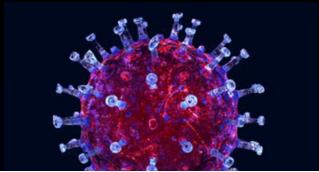
SARS-CoV-2

(The Epidemic: COVID-19)



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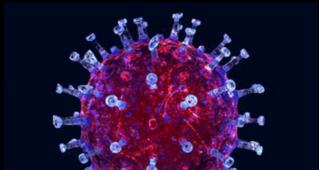
RNA Viruses



Virus Family	Examples (common names)	Capsid naked/enveloped	Capsid Symmetry	Nucleic acid type	Group
1. <i>Reoviridae</i>	Reovirus, rotavirus	Naked	Icosahedral	ds	III
2. <i>Picornaviridae</i>	Enterovirus, rhinovirus, hepatovirus, cardiovirus, aphthovirus, poliovirus, parechovirus, erbovirus, kobuvirus, teschovirus, coxsackie	Naked	Icosahedral	ss	IV
3. <i>Caliciviridae</i>	Norwalk virus	Naked	Icosahedral	ss	IV
4. <i>Togaviridae</i>	Eastern equine encephalitis	Enveloped	Icosahedral	ss	IV
5. <i>Arenaviridae</i>	Lymphocytic choriomeningitis virus, Lassa fever	Enveloped	Complex	ss(-)	V
6. <i>Flaviviridae</i>	Dengue virus, hepatitis C virus, yellow fever virus, Zika virus	Enveloped	Icosahedral	ss	IV
7. <i>Orthomyxoviridae</i>	Influenzavirus A, influenza virus B, influenza virus C, isavirus, thogotovirus	Enveloped	Helical	ss(-)	V
8. <i>Paramyxoviridae</i>	Measles virus, mumps virus, respiratory syncytial virus, Rinderpest virus, canine distemper virus	Enveloped	Helical	ss(-)	V
9. <i>Bunyaviridae</i>	California encephalitis virus, Sin nombre virus	Enveloped	Helical	ss(-)	V
10. <i>Rhabdoviridae</i>	Rabies virus, Vesicular stomatitis	Enveloped	Helical	ss(-)	V
11. <i>Filoviridae</i>	Ebola virus, Marburg virus	Enveloped	Helical	ss(-)	V
12. <i>Coronaviridae</i>	SARS-CoV-2, MERS	Enveloped	Helical	ss	IV
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14. <i>Bornaviridae</i>	Borna disease virus	Enveloped	Helical	ss(-)	V
15. <i>Arteriviridae</i>	Arterivirus, equine arteritis virus	Enveloped	Icosahedral	ss	IV
16. <i>Hepeviridae</i>	Hepatitis E virus	Naked	Icosahedral	ss	IV



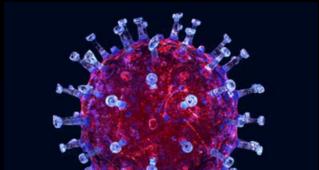
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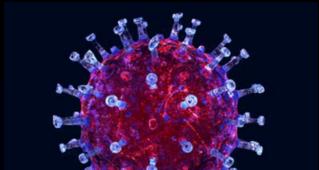
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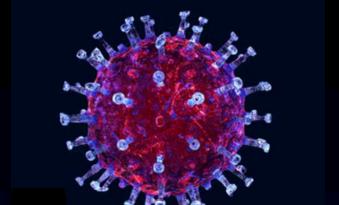


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RNA Polymerase



Remdesivir : An Inhibitor of RNA Polymerase



The NEW ENGLAND JOURNAL of MEDICINE
ORIGINAL ARTICLE

Remdesivir for the Treatment of Covid-19 — Preliminary Report

J.H. Beigel, K.M. Tomashek, L.E. Dodd, A.K. Mehta, B.S. Zingman, A.C. Kalil, E. Hohmann, H.Y. Chu, A. Luetkemeyer, S. Kline, D. Lopez de Castilla, R.W. Finberg, K. Dierberg, V. Tapson, L. Hsieh, T.F. Patterson, R. Paredes, D.A. Sweeney, W.R. Short, G. Touloumi, D.C. Lye, N. Ohmagari, M. Oh, G.M. Ruiz-Palacios, T. Benfield, G. Fätkenheuer, M.G. Kortepeter, R.L. Atmar, C.B. Creech, J. Lundgren, A.G. Babiker, S. Pett, J.D. Neaton, T.H. Burgess, T. Bennett, M. Green, M. Makowski, A. Osinusi, S. Nayak, and H.C. Lane, for the ACTT-1 Study Group Members*

ABSTRACT

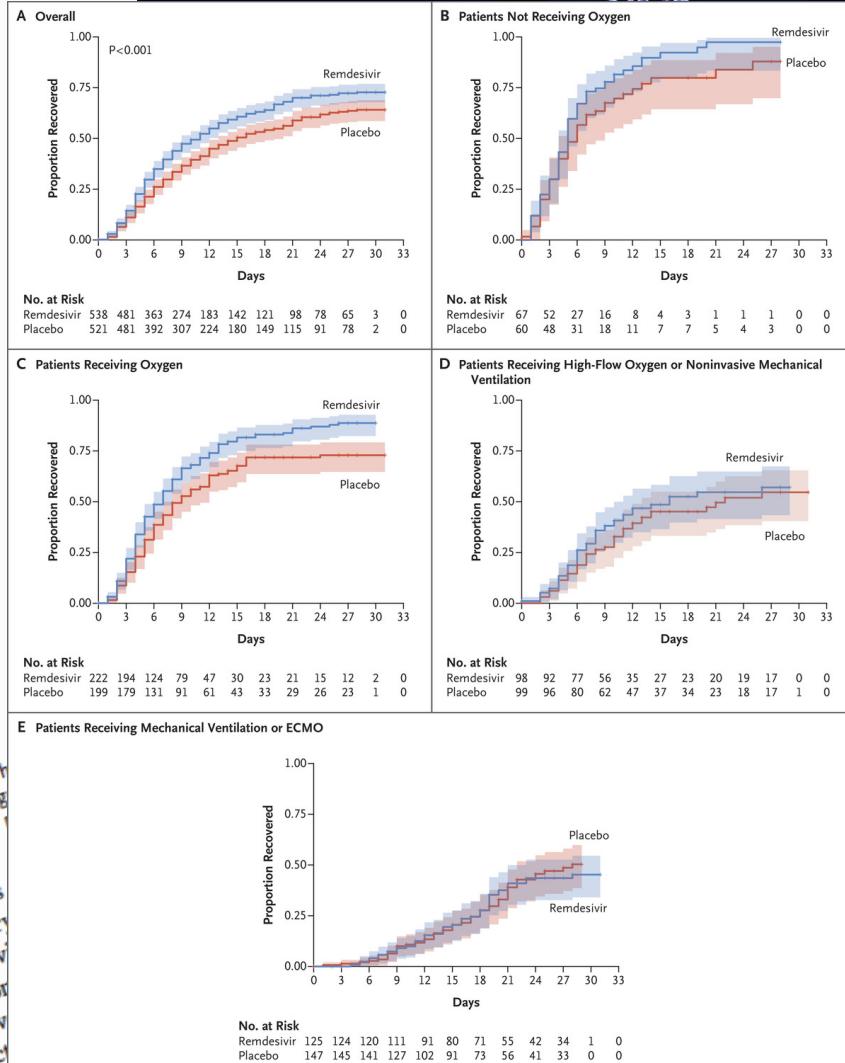
BACKGROUND
Although several therapeutic agents have been evaluated for the treatment of coronavirus disease 2019 (Covid-19), none have yet been shown to be efficacious.

METHODS

We conducted a double-blind, randomized, placebo-controlled trial of intravenous remdesivir in adults hospitalized with Covid-19 with evidence of lower respiratory tract involvement. Patients were randomly assigned to receive either remdesivir (200 mg loading dose on day 1, followed by 100 mg daily for up to 9 additional days) or placebo for up to 10 days. The primary outcome was the time to recovery (either discharge from the hospital or hospitalization for infection).

The data and safety monitoring board evaluated the results on the basis of findings from the first 521 patients assigned to the remdesivir group. Pre-

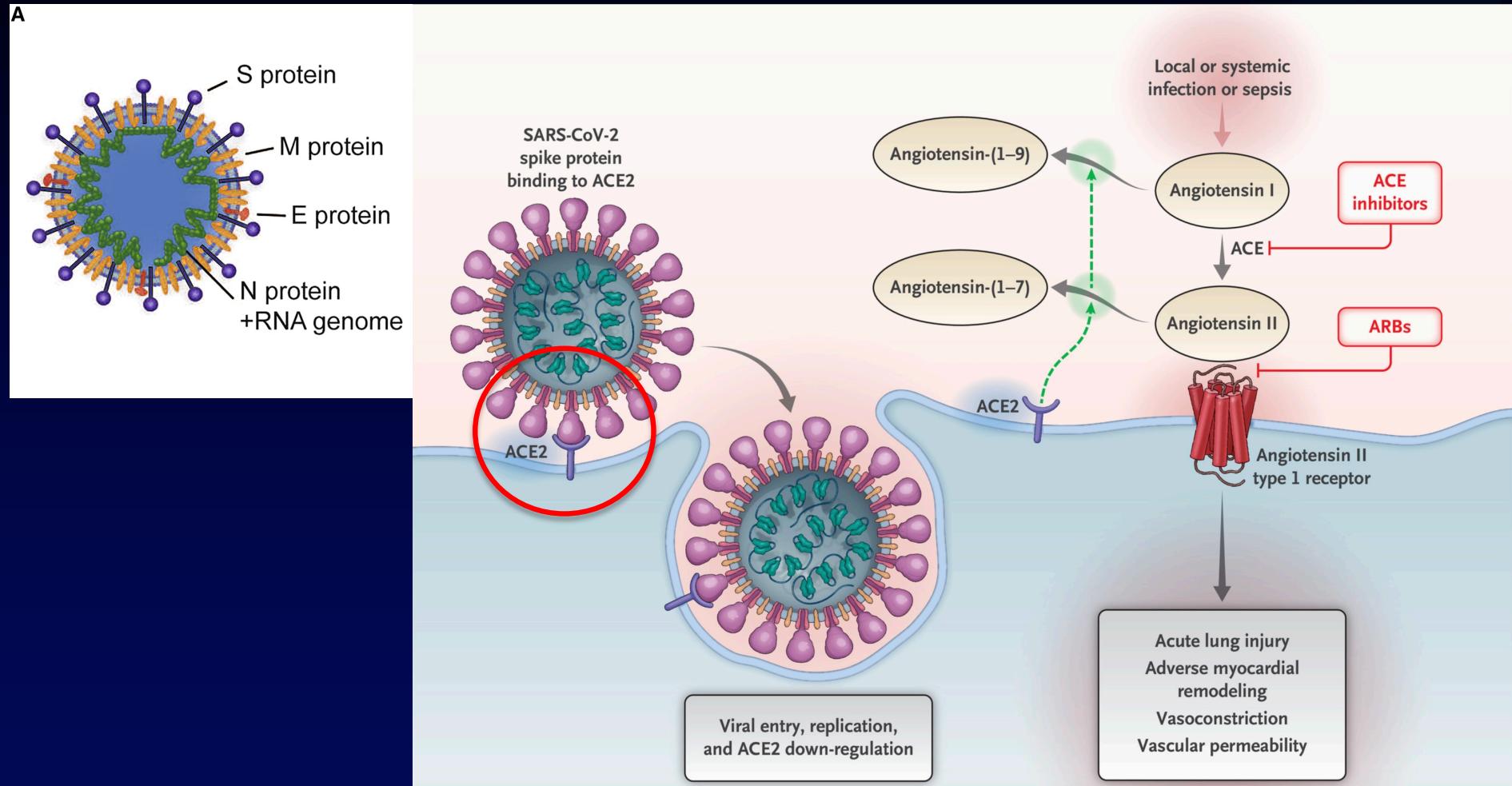
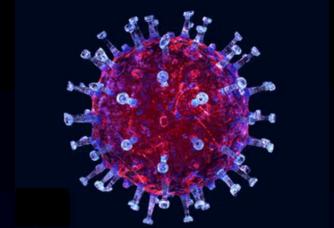
2020.5.22.



2020, 382: 1413-1421
DOI: 10.1056/NEJMoa2020333
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The Cellular Entry Path of SARS-CoV-2



- **The S (Spike) Protein** selectively binds to ACE2, then the complex enters via endocytosis
- As a result, ACE2 is unable to carry out its inherent function of vascular relaxation and protection of the heart.



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Renin–Angiotensin–Aldosterone System Inhibitors in Patients with Covid-19

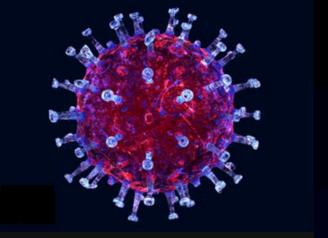
Muthiah Vaduganathan, M.D., M.P.H., John J.V. McMurray, M.D.,

Orly Vardeny, Pharm.D., Marc A. Pfeffer, M.D., Ph.D., Thomas Michel, M.D., Ph.D., and Scott D. Solomon, M.D.

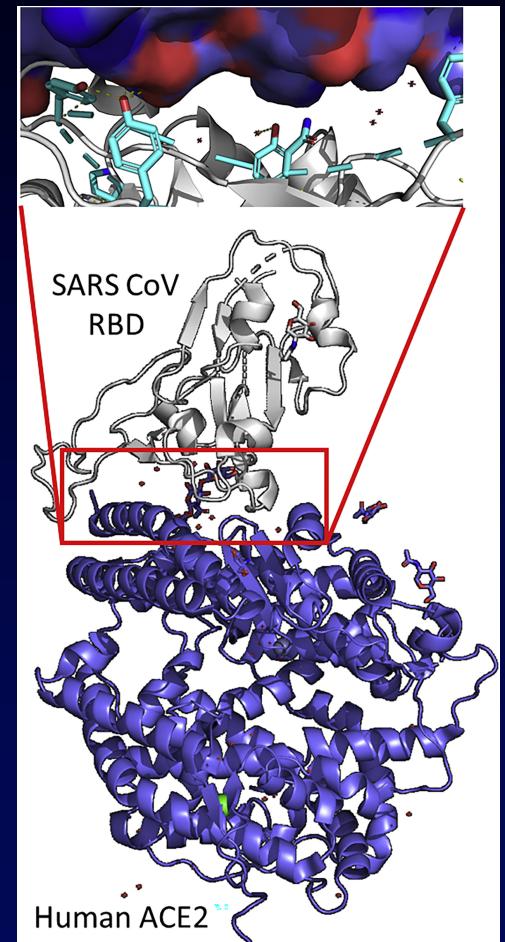
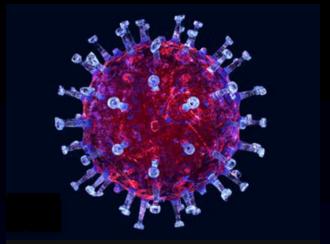
The renin–angiotensin–aldosterone system (RAAS) is an elegant cascade of vasoactive peptides that orchestrate key processes in human physiology. Severe acute respiratory syndrome coronavirus 1 (SARS-CoV-1) and SARS-CoV-2, which have been responsible for the SARS epidemic in 2002 to 2004 (Covid-19) pandemic, respectively, interface with the RAAS through angiotensin-converting enzyme (ACE2), an enzyme that physiologically counters activation but also functions as a receptor for viruses.^{1,2} The interaction between ACE2 has been proposed as

Initial reports⁵⁻⁸ have called attention to the potential overrepresentation of hypertension among patients with Covid-19. In the largest of several case series from China that have been released during the Covid-19 pandemic (Table S1 in the Supplementary Appendix, available with the full text of this article at NEJM.org), hypertension was the most frequent coexisting condition in 1099 patients, with an estimated prevalence of 15%⁹; however, this estimate appears to be lower than

2020.3.30.



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- A strategy:
Diluting the
endocytosis of
SARS-CoV-2

Cell

Article
**Inhibition of SARS-CoV-2 Infections
in Engineered Human Tissues Using
Clinical-Grade Soluble Human ACE2**

Vanessa Montell,¹ Hyesoo Kwon,² Patricia Prado,³ Astrid Hagelkötüs,⁴ Reiner A. Wimmer,⁴ Martin Stahl,⁵ Alexandra Leopoldi,¹ Elena Garreta,³ Carmen Hurtado del Pozo,³ Felipe Prosper,⁶ Juan Pablo Romero,⁶ Gerald Wimsberger,⁷ Haibo Zhang,⁸ Arthur S. Slutsky,⁸ Ryan Conder,⁵ Nuria Montserrat,^{9,10,*} Ali Mirazimi,^{1,2,*} and Josef M. Penninger,^{11,12,*} Karolinska Institute and Karolinska University Hospital, Department of Laboratory Medicine, Unit of Clinical Microbiology, 17177 Stockholm, Sweden

¹National Veterinary Institute, 751 89 Uppsala, Sweden

²National Institute for Organ Regeneration, Institute for Bioengineering of Catalonia (IBEC), The Barcelona Institute of Technology (BIST), 08028

³Institute of Molecular Biotechnology of the Austrian Academy of Sciences, Dr. Bohr-Gasse 3, 1030 Vienna, Austria

⁴Cell Therapy Program, Center for Applied Medical Research (CIMA), University of Navarra, 31008 Pamplona, Spain

⁵Aperion Biologics, Campus Vienna Biocenter 5, 1030 Vienna, Austria

⁶Catalan Research Centre for Biomedical Science at Li Ka Shing Knowledge Institute of St. Michael Hospital, University of Toronto, Toronto, ON M5B 1W8, Canada

⁷Catalan Institution for Research and Advanced Studies (ICREA), 08010 Barcelona, Spain

⁸Keenan Research Centre in Biomedical Engineering, University of British Columbia, Biomaterials and Nanomedicine, 28029 Madrid, Spain

⁹Catalan Institution for Research and Advanced Studies (ICREA), 08010 Barcelona, Spain

¹⁰Department of Medical Genetics, Life Science Institute, University of British Columbia, Vancouver, BC V6T 1Z3, Canada

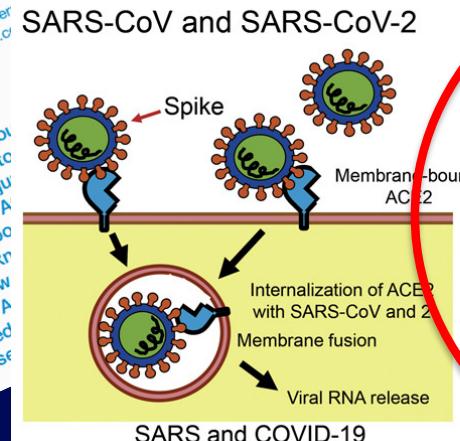
¹¹Lead Contact

¹²Correspondence: nmontser@ibec.cat (N.M.), ali.mirazimi@sva.se (A.M.), josef.penninger@ubc.ca (J.M.P.)

<https://doi.org/10.1016/j.cell.2020.05.016>

SUMMARY

We have previously reported that critical receptor internalization from injury and infection is required for SARS-CoV-2 infection. A recent study has proposed that ACE2 is the primary receptor for SARS-CoV-2. We now show that soluble human ACE2 (hrsACE2) binds to the SARS-CoV-2 spike protein and reduces internalization of ACE2 at the membrane, leading to reduced viral load. These findings provide a rationale for the use of hrsACE2 as a therapeutic agent for SARS-CoV-2 infection.



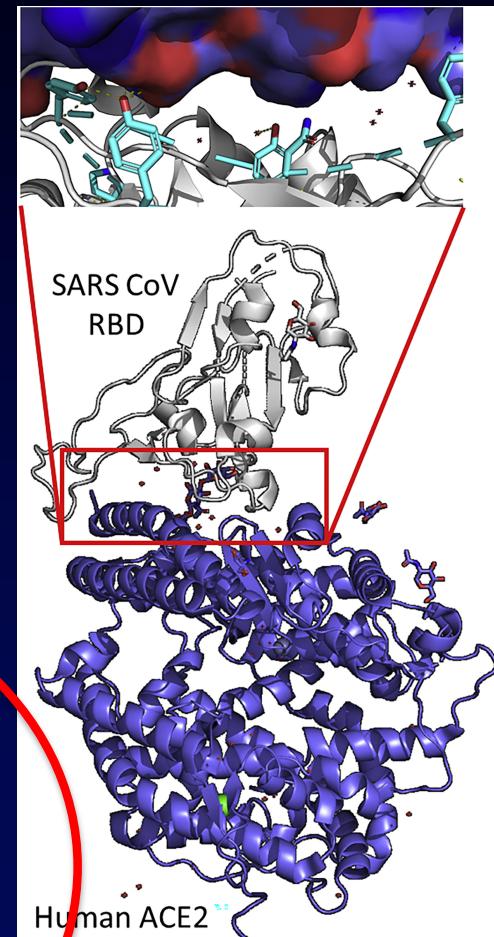
hrsACE2 binds to Spike and reduces binding to ACE2 at the membrane

Soluble ACE2

Membrane-bound ACE2

Less SARS-CoV-2 internalization

Reduced viral load

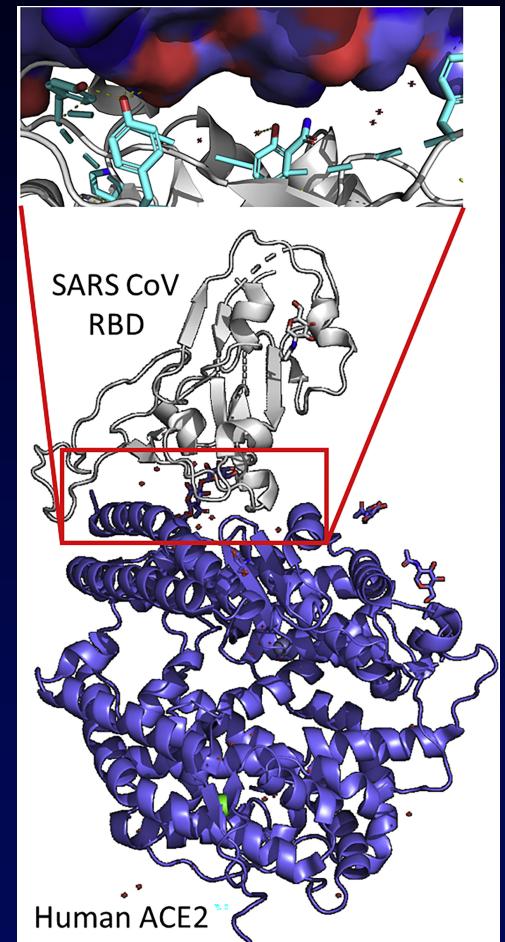
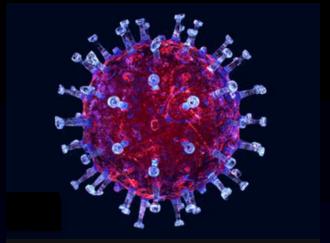


2020.5.14.



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- The ACE2 enzyme's gene is located on the X-chromosome.



- The ACE2 enzyme's gene is located on the X-chromosome.

The New York Times

Opinion

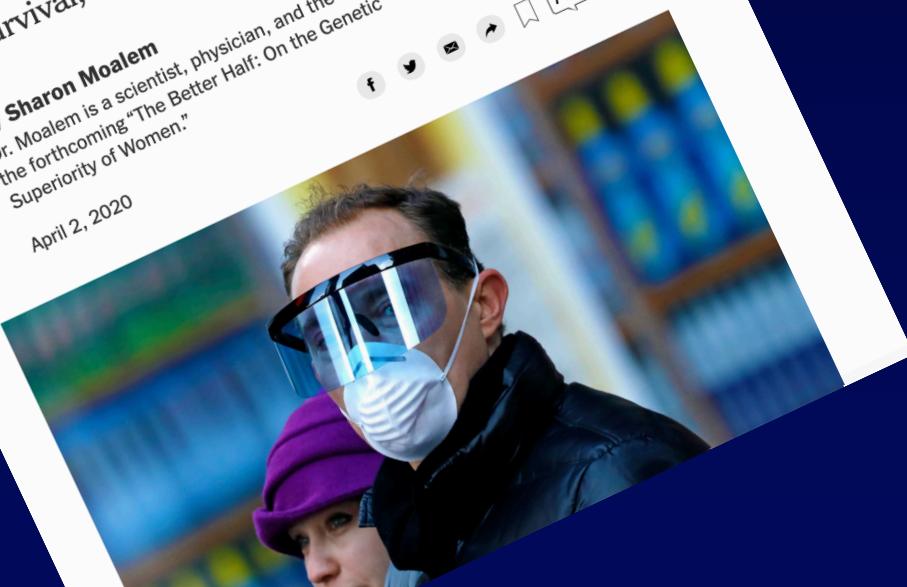
Why Are So Many More Men Dying from Coronavirus?

The disproportionate toll this virus is taking on males isn't an anomaly. When it comes to survival, men are the weaker sex.

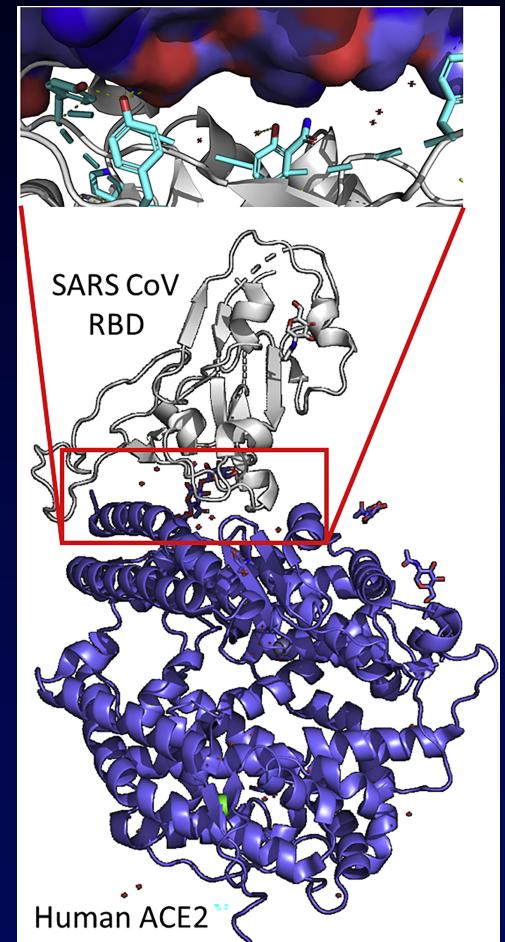
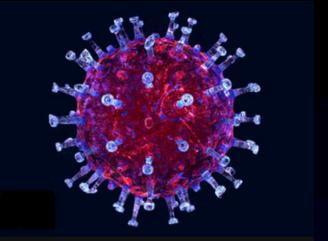
By **Sharon Moalem**
Dr. Moalem is a scientist, physician, and the author of the forthcoming "The Better Half: On the Genetic Superiority of Women."

April 2, 2020

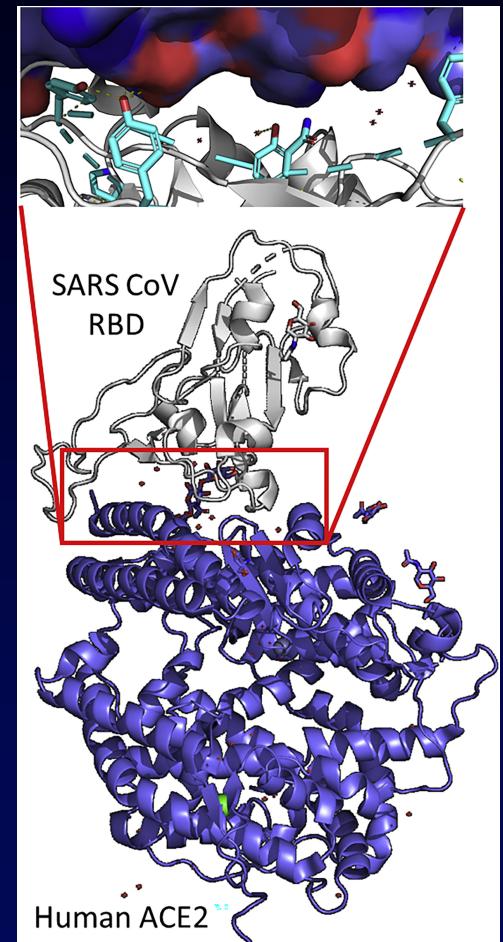
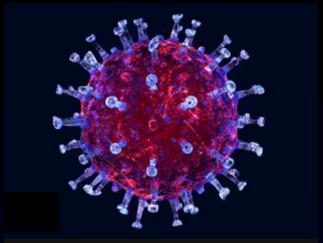
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2020.4.2.



- Another strategy:
Hinder the contact surface between
the S-protein and
the patient's ACE2.



- Another strategy:
Hinder the contact
surface between the
S-protein and the
patient's ACE2.

<https://doi.org/10.1038/s41586-020-2381-y>

nature
Accelerated Article Preview

A human neutralizing antibody targets the receptor binding site of SARS-CoV-2

Rui Shi, Chao Shan, Xiaomin Duan, Zhihai Chen, Peipei Liu, Jinwen Song, Tao Song, Xiaoshan Bi, Chao Han, Lianao Wu, Ge Gao, Xue Hu, Yanan Zhang, Zhou Tong, Weijin Huang, William Jun Liu, Lan Wang, Jianxun Qi, Hui Feng, Fu-sheng Wang, Qihui Wang, G

Received: 2 April 2020
Accepted: 19 May 2020

Published
online 26 May 2020
Accelerated Article Preview

Cite this article as: Shi, R. et al. A human
neutralizing antibody targets the receptor
binding site of SARS-CoV-2. *Nature*
<https://doi.org/10.1038/s41586-020-2381-y>
(2020).

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2020.5.26.

- Using monoclonal antibodies

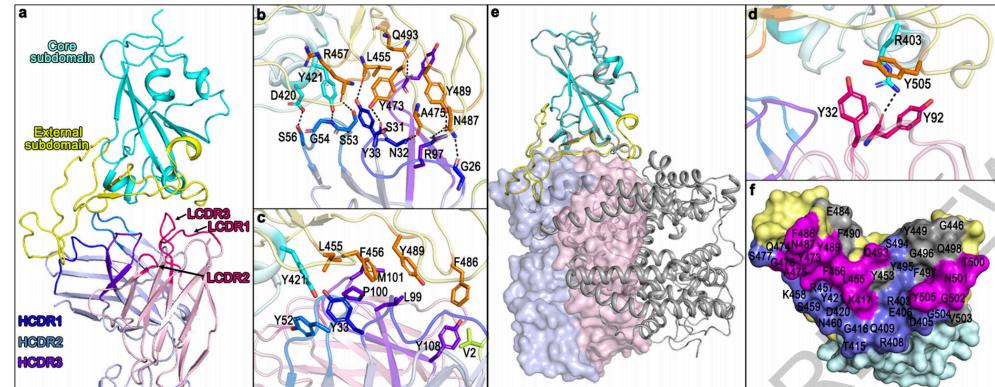
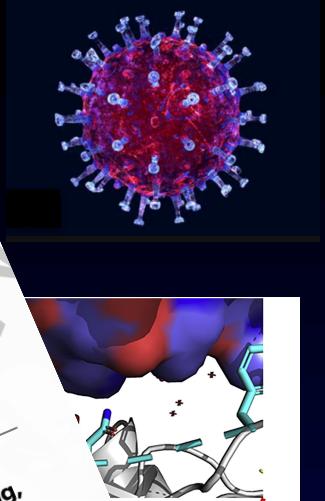


Fig. 4 | The crystal structure of CB6 and SARS-CoV-2-RBD complex and the competitive binding of CB6 and hACE2 with SARS-CoV-2-RBD. **a**, The complex structure of CB6 bound to SARS-CoV-2-RBD. The SARS-CoV-2-RBD is colored in cyan (core subdomain) and yellow (external subdomain). The variable fragment of CB6 is shown with HCDR1, HCDR2, and HCDR3 loops from the V_{λ} domain (purple) colored in blue, marine and purple, while the LCDR1, LCDR2 and LCDR3 loop from the V_{κ} domain (pink) are colored in hot-pink, respectively. **b–c**, Both hydrophilic interactions (b) and hydrophobic interactions (c) between CB6 heavy chain and SARS-CoV-2-RBD are displayed. **d**, The binding details between CB6 light chain and SARS-CoV-2-RBD are also presented. The hydrogen bonds are shown as dashed black lines.

e, Superimposition of CB6/SARS-CoV-2-RBD complex and hACE2/SARS-CoV-2-RBD (PDB code: 6LZG) revealed the steric competition between CB6 and hACE2 for RBD binding. CB6/SARS-CoV-2-RBD structure was superimposed on hACE2/SARS-CoV-2-RBD to demonstrate steric hindrance. hACE2 is shown as cartoon (gray). **f**, Competitive binding surfaces of CB6 with hACE2 on SARS-CoV-2-RBD. The SARS-CoV-2-RBD binding surface to ACE2 and CB6 is shown. The residues bound by both CB6 and hACE2 are colored in magenta. The residues in contact with CB6 alone are colored in blue. The amino acids on SARS-CoV-2-RBD interface contacting CB6 or ACE2 are labeled.



Current Status of Vaccine Development

Cell Host & Microbe

Forum

The Challenges of Vaccine Development against a New Virus during a Pandemic

Michael S. Diamond^{1,2,3,4,*} and Theodore C. Pierson^{5,*}

¹Department of Medicine, Washington University School of Medicine, St. Louis, MO 63110, USA
²Department of Molecular Microbiology, Washington University School of Medicine, St. Louis, MO 63110, USA
³Department of Pathology & Immunology, Washington University School of Medicine, St. Louis, MO 63110, USA
⁴Center for Human Immunology and Immunotherapy Programs, Washington University School of Medicine, St. Louis, MO 63110, USA
⁵Laboratory of Viral Diseases, National Institute of Allergy and Infectious Diseases, Bethesda, MD 20892, USA

*Correspondence: diamond@wustl.edu (M.S.D.), piersontc@mail.nih.gov (T.C.P.)
<https://doi.org/10.1016/j.chom.2020.04.021>

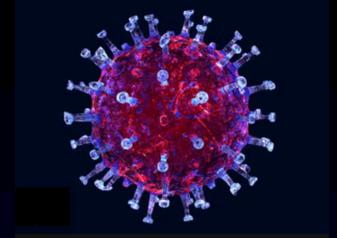
Historically, human coronaviruses have received limited attention from the research and medical communities. Although infections by human coronaviruses (e.g., HCoV-229E and HCoV-OC43) frequently cause common cold symptoms in healthy individuals, severe clinical illness is relatively rare even in immunocompromised individuals, infants, and the elderly. Considerably

zations, limited transmission and human disease. Ten years later, a second coronavirus, the Middle East respiratory syndrome coronavirus (MERS-CoV), was isolated from an individual suffering from severe respiratory disease and renal failure. As observed with SARS-CoV, MERS-CoV spread via travel and contact with infected individuals, resulting in transmission and mortality within and beyond

ment basic and translational studies that customarily guide vaccine development and evaluation under non-pandemic circumstances. Accordingly, we discuss the challenges of rapid vaccine development during a pandemic response.

The SARS-CoV-2 Pandemic
SARS-CoV-2 is a positive-sense single-stranded RNA virus first isolated in Wu-

CelPress



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The University of Dublin

Current Status of Vaccine Development

Cell Host & Microbe

Forum The Challenges of Vaccine Development against a New Virus during a Pandemic

CelPress

Madore C. Pierson^{5,*}
1. Washington University School of Medicine, St. Louis, MO 63110, USA
2. University School of Medicine, St. Louis, MO 63110, USA
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4. Washington University School of Medicine, St. Louis, MO 63110, USA
5. National Institutes of Health, Bethesda, MD 20892, USA
*T.C.P.

This virus has resulted in a global
clarion call for the im-
plementing a vaccine

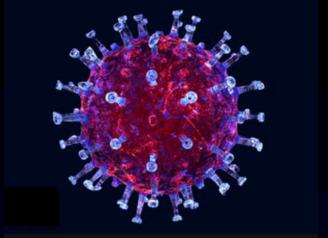


Table 1. Vaccine Candidates in Development against SARS-CoV-2

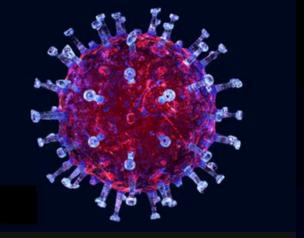
Vaccine Type	Platform	Protein Target	Clinical Trial Stage	Company or Institution	Vaccine Name	Status	
mRNA	Lipid-encapsulated mRNA	S	Phase 1	NCT04283461 (45 subjects)	Moderna	mRNA-1273	Recruiting
DNA	DNA plasmid	S	Phase 1	NCT04336410 (40 subjects)	Inovio Pharmaceuticals	INO-4800	Recruiting
Human adenovirus (Ad5)	Viral-vectored	S	Phase 1	NCT04313127 (108 subjects)	CanSino Biologics	Ad5-nCoV	Active
Chimpanzee adenovirus	Viral-vectored	S	Phase 1/2	NCT04324606 (510 subjects)	University of Oxford	ChAdOx1 nCoV-19 (4/20)	Planned
Spike protein	Bacterially produced soluble protein (oral)	S	Phase 1	NCT04334980 (84 subjects)	Symvivo Corporation	bacTRL-Spike (4/30)	Planned
BCG vaccine	Immune stimulatory	None	Phase 3	NCT04327206 (4170 subjects) NCT04328441 (1000 subjects)	Murdoch Childrens Research Institute University Medical Center, Netherlands	BCG vaccine	Recruiting

Information adapted from <https://ClinicalTrials.gov>.

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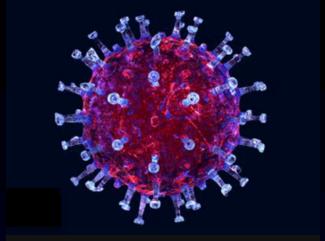
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Information adapted from <https://ClinicalTrials.gov>.

- The BCG Vaccine for Tb Prevention



Perspective
Trained Immunity: a Tool for Reducing Susceptibility to and the Severity of SARS-CoV-2 Infection

Mihai G. Netea,^{1,2,*} Evangelos J. Giamarellos-Bourboulis,³ Jorge Dominguez-Andrés,¹ Nigel Curtis,⁴ Reinout van Crevel,¹ Frank L. van de Veerdonk,¹ and Marc Bonten⁵
¹Department of Internal Medicine and ²Center for Inflammation Research, Radboud University Nijmegen Medical Center, Nijmegen, The Netherlands; ³Hellenic ⁴Academy of Medical Sciences, Athens, Greece; ⁵Department of Internal Medicine and ⁶Center for Inflammation Research, Radboud University Nijmegen Medical Center, Nijmegen, The Netherlands

COMMENT



BCG-induced trained immunity: can it offer protection against COVID-19?

Luke A. J. O'Neill^{1,2} and Mihai G. Netea^{1,2,3}

Bacillus Calmette-Guérin (BCG) vaccination has been reported to decrease susceptibility to respiratory tract infections, an effect proposed to be mediated by the general long-term boosting of innate immune mechanisms, also termed trained immunity. Here, we discuss the non-specific beneficial effects of BCG against viral infections and whether this vaccine may afford protection to COVID-19.

COVID-19 is a new form of respiratory tract infection that can be complicated by severe pneumonia and acute respiratory distress syndrome (ARDS). It is caused by a newly identified viral pathogen named on 11 February 2020 as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Most individuals infected with SARS-CoV-2 remain asymptomatic or develop a moderate disease that is mainly characterized by respiratory tract symptoms. However, a significant proportion of patients progress to severe pneumonia with even death, particularly in the elderly and those with co-morbidities such as obesity, cardiovascular, respiratory, and neurological diseases.

Introduction in Europe in the 1920s, epidemiological studies reported that BCG vaccination strongly reduced infant mortality, and this could not be explained by a reduction in tuberculosis alone (reviewed previously¹). Later on, similar studies in other locations, including randomized controlled trials, showed an up to 50% reduction of mortality induced by BCG in young infants². This reduction in childhood mortality by BCG appeared to be due to the protection against unrelated infectious agents and especially respiratory tract infections and neonatal sepsis. Although the authors did

not discuss the mechanism of protection, it is likely that this protection is mediated by trained immunity. In fact, the authors show that the elderly and those with co-morbidities (e.g., obesity, cardiovascular, respiratory, and neurological diseases) are most susceptible to COVID-19 and suffer from the most severe disease complications. In contrast, young children, including infants who are infected with other infections, have milder symptoms

Cause: (Not a virus but a bacteria)
***Mycobacterium tuberculosis* (MTB)**

- The BCG Vaccine for Tb Prevention

Perspective
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Mihai G. Netea,^{1,2,*} Evangelos J. Giannopoulos,³ Jorge Dominguez-Andrés,¹ Nigel Curtis,⁴ Reinout van Crevel,¹ Frank L. van de Veerdonk,¹ and Marc Bonten⁵
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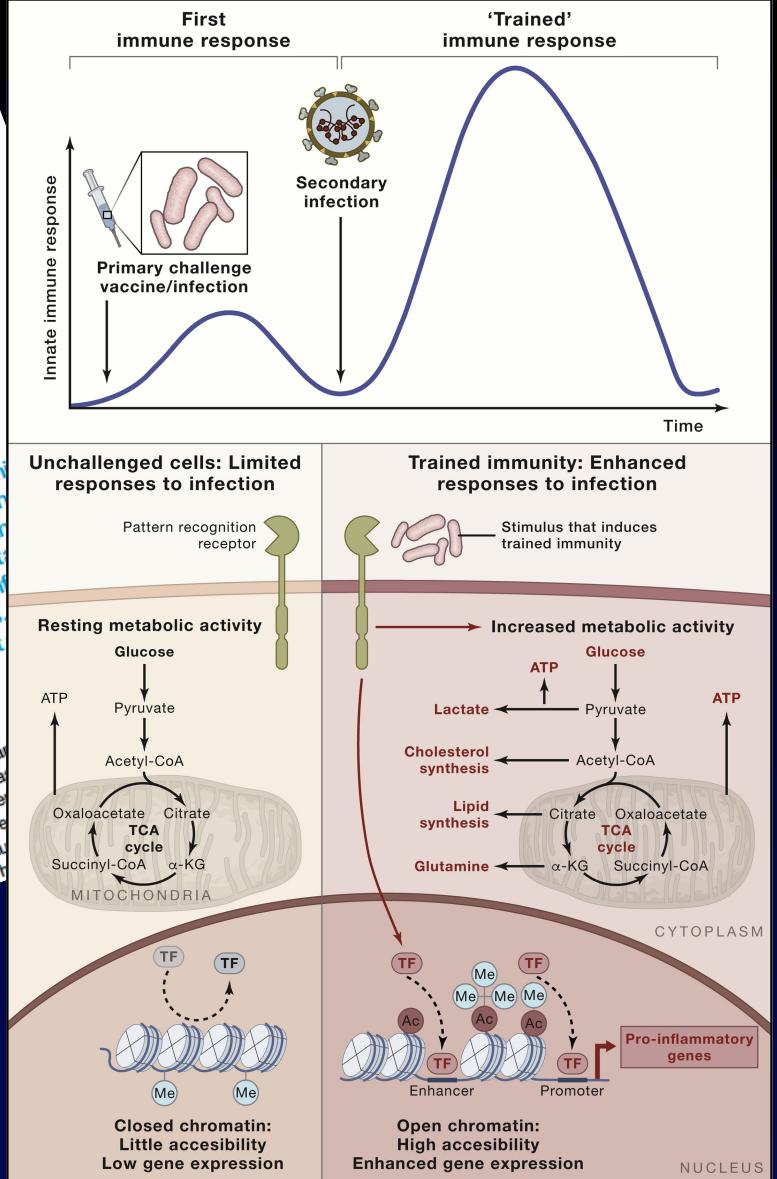
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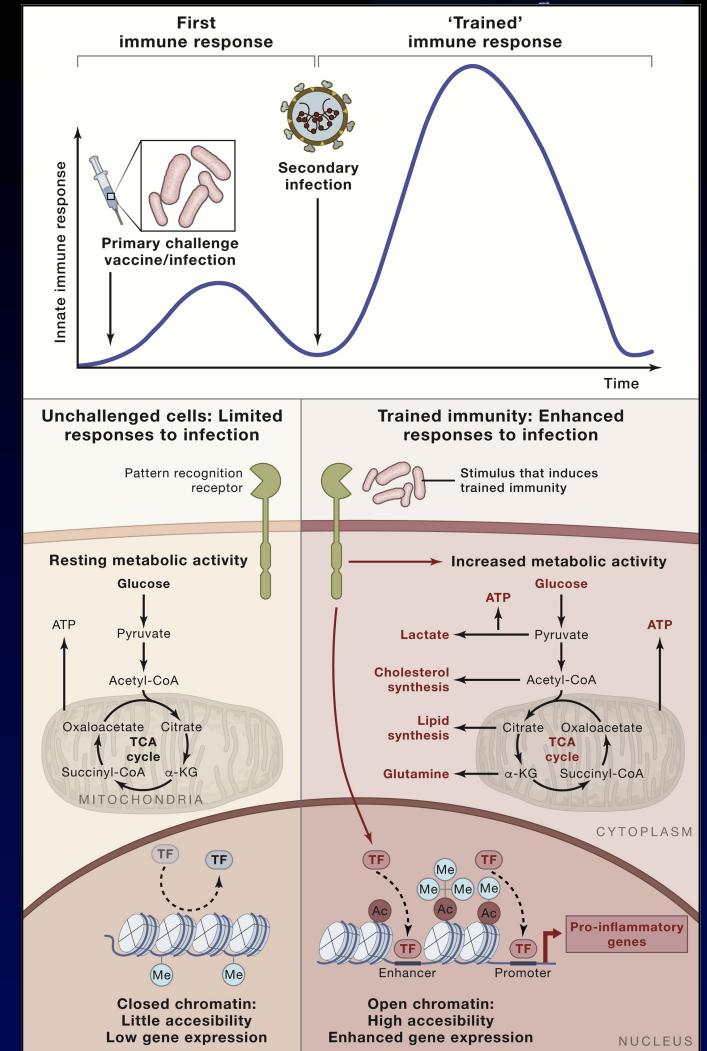
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- The BCG Vaccine for Tb Prevention



- The BCG
Vaccine for Tb
Prevention

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Significantly Improved COVID-19 Outcomes in Countries with
Higher BCG Vaccination Coverage: A Multivariable Analysis

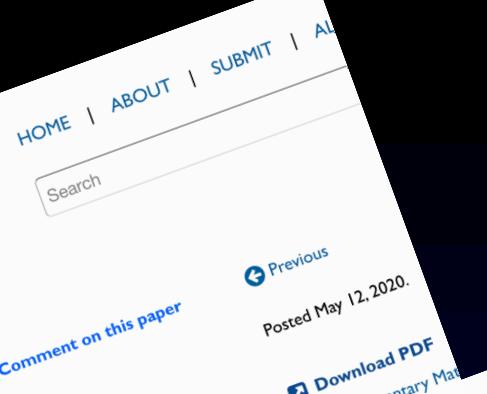
Danielle Klinger, Ido Blas, Nadav Rappoport, Michal Linial
doi: <https://doi.org/10.1101/2020.04.23.20077123>

This article is a preprint and has not been peer-reviewed
reports new medical research that has yet to be evaluated
to guide clinical practice.

Abstract Info/History Metrics

COVID-19 has spread to 210 countries within 3 months. The vaccination with BCG correlates with a better outcome. The analysis covers 55 countries, complying with preexisting size and deaths per million (DPM). We found a strong inverse correlation between BCG administration and DPM along time. The results from multivariable regression tests are demographic, and health-related quantitative properties. The dominant contribution of BCG administration years. Analyzing countries according to 32,200 group participants.

2020.5.12.



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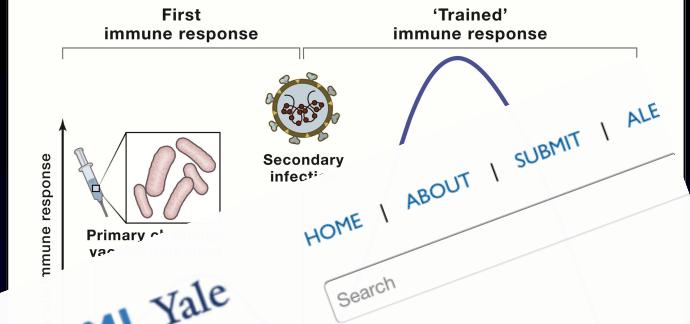
BCG vaccination and socioeconomic variables vs Covid-19
global features: clearing up a controversial issue

Luigi Ventura, Matteo Vitali, Vincenzo Romano Spica
doi: <https://doi.org/10.1101/2020.05.20.20107755>

This article is a preprint and has not been certified by peer review [what does this mean?]. It reports new medical research that has yet to be evaluated and so should not be used to guide clinical practice.

Abstract Info/History Metrics

2020.5.26.



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The University of Dublin



Hydroxychloroquine or chloroquine with or without a macrolide for treatment of COVID-19: a multinational registry analysis

Prof Mandeep R Mehra, MD • Sapan S Desai, MD • Prof Frank Ruschitzka, MD • Amit N Patel, MD
Published: May 22, 2020 • DOI: [https://doi.org/10.1016/S0140-6736\(20\)31180-6](https://doi.org/10.1016/S0140-6736(20)31180-6) • Check for updates

Summary

Summary
Introduction
Methods
Results
Discussion
Supplementary
Material
References

Background

Hydroxychloroquine or chloroquine, often in combination with a second-generation macrolide, are being widely used for treatment of COVID-19, despite no conclusive evidence of their benefit. Although generally safe when used for approved indications such as autoimmune disease or malaria, the safety and benefit of these treatment regimens are poorly evaluated in COVID-19.

Methods

We did a multinational registry analysis of the use of hydroxychloroquine or chloroquine with or without a macrolide for treatment of COVID-19. The registry comprised data from 671 hospitals in six continents. We included patients hospitalised between Dec 20,

- Administer

2020.5.22.



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Hydroxychloroquine / Choloroquine and its impact on the Immune System

THE LANCET

ARTICLES | ONLINE FIRST

Hydroxychloroquine or chloroquine with or without a macrolide for treatment of COVID-19: a multinational registry analysis

Prof Mandeep R Mehra, MD • Sapan S Desai, MD • Prof Frank Ruschitzka, MD • Amit N Patel, MD

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- Administer **X**

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Vitamin D and Inflammation

Open access

BMJ Nutrition,
Prevention & Health

Vitamin D and SARS-CoV-2 virus COVID-19 disease

Brief report

BMJNPB: first published as 10.1136/bmjnpb-2020-0

To cite: Lanham-New SA,
Webb AR, Cashman KD, et al.
Vitamin D and SARS-CoV-2
virus/COVID-19 disease.
BMJ Nutrition, Prevention &
Health 2020;0: doi:10.1136/
bmjnph-2020-000089
For numbered affiliations see
end of article.

Correspondence to
Professor Susan A Lanham-New,
Nutritional Sciences, University

BACKGROUND AND AIM
The spread of novel SARS-CoV-2 virus, and
the disease COVID-19 that is caused by
SARS-
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Vitamin D and Inflammation: Potential Implications for Severity of Covid-19

Irish
Medical
Journal
Established 1867

Issue: Ir Med J; Vol 113; No. 5; P81

1. The Irish Longitudinal Study on Ageing, School of Medicine, Trinity College Dublin, Ireland.
2. Institute of Translational Medicine, University of Liverpool.

2020.5.13.

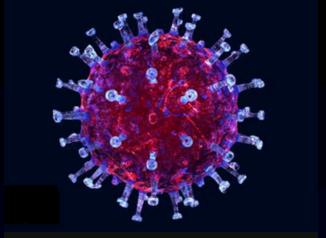
2020.5.

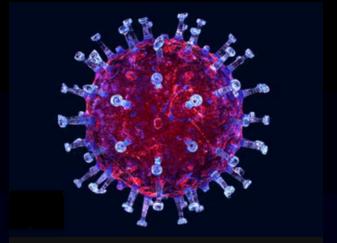
Abstract

Background

Recent research has indicated that vitamin D may have immune supporting properties through modulation of both adaptive and innate immune system through cytokines and regulation of cell signalling pathways. We hypothesize that vitamin D status may influence the severity of responses to Covid-19 and that the prevalence of vitamin D deficiency may be closely aligned to Covid-19 mortality.

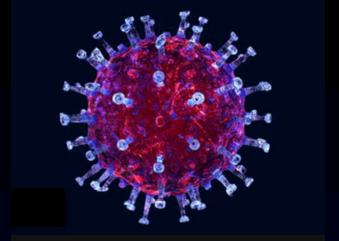
Language restriction) of vitamin D status (for older adults) in Ireland, Baile Átha Cliath





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The Proteomics & Metabolomics of Covid-19 Patients



2020.4.7.

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CSH Cold Spring Harbor Laboratory

BMJ Yale

Proteomic and Metabolomic Characterization of COVID-19 Patient Sera

Bo Shen, Xiao Yi, Yaoting Sun, Xiaojie Bi, Juping Du, Chao Zhang, Sheng Quan, Fangfei Zhang, Rui Sun, Liujia Qian, Weigang Ge, Wei Liu, Shuang Liang, Hao Chen, Ying Zhang, Jun Li, Jiaqin Xu, Zebao He, Baofu Chen, Jing Wang, Haixi Yan, Yufen Zheng, Donglian Wang, Jiansheng Zhu, Ziqing Kong, Zhouyang Kang, Xiao Liang, Xuan Ding, Tian Lu, Nan Xiang, Yi Judy Zhu, Huafen Liu, Haixiao Chen, Huanhuan Gao, Lu Li, Sainan Li, Qi Xiao, Xue Cai, Huanhuan Gao, Tiannan Guo

doi: <https://doi.org/10.1101/2020.04.07.20054585>

This article is a preprint and has not been peer-reviewed [what does this mean?]. It reports new medical research that has yet to be evaluated and so should not be used to guide clinical practice.

Abstract Info/History Metrics

Abstract

Severe COVID-19 patients account for most of the mortality of this disease. Early detection and effective treatment of severe patients remain major challenges. Here, we and proteomic and metabolomic profiling of sera from 46 COVID-19 and 53 We then trained a machine learning model using proteomic and from a training cohort of 18 non-severe and 13 severe severe patients with an accuracy of 93.5%, and patients, seven of which were correctly

Comment on this paper

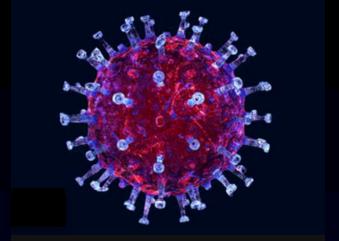
Preview PDF

- 21 Covid-19 Severe Cases
- 25 Covid-19 Minor Cases
- 25 non-Covid-19 patients
- 28 Healthy Controls



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- Biomarker Identification
- Elucidation of the Pathways
- Early Diagnosis of severe Covid-19 cases



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The Proteomics & Metabolomics of Covid-19 Patients

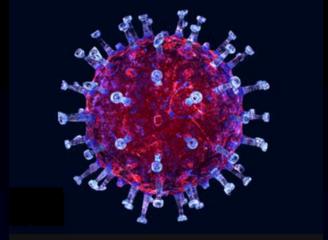
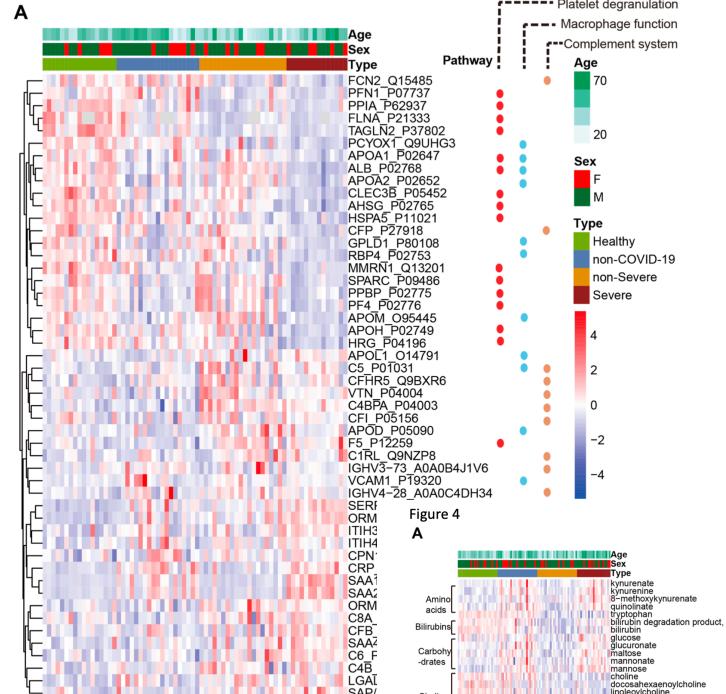
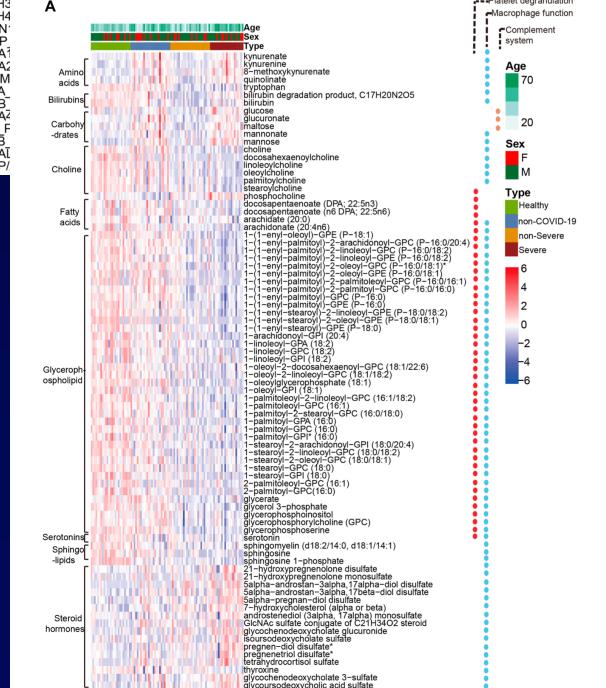


Figure 3



Fig



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The Proteomics & Metabolomics of Covid-19 Patients

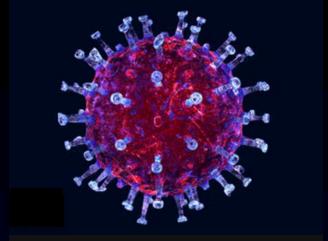


Figure 3

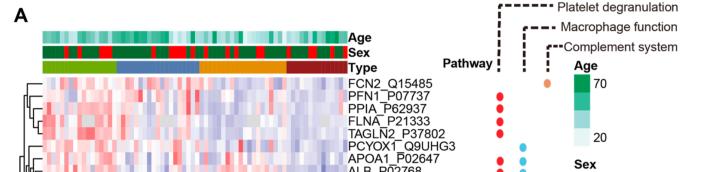


Figure S4

A

Proteins

non-COVID-19 / Healthy

non-Severe / Healthy

Severe / Healthy

B

Metabolites

non-Severe / Healthy

non-COVID-19 / Healthy

71 (3)

1

45

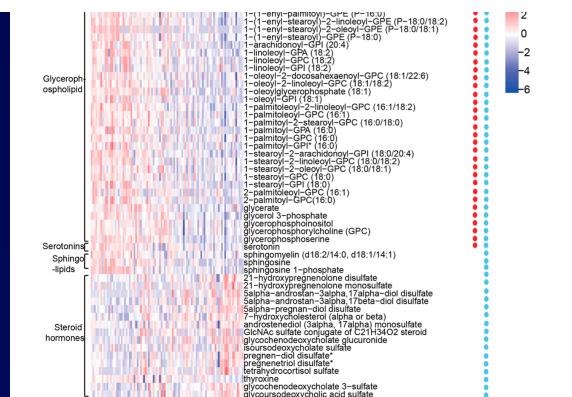
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The Proteomics & Metabolomics of Covid-19 Patients

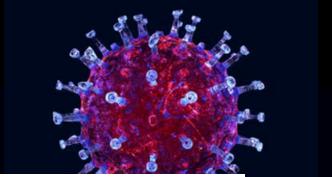


Figure 3

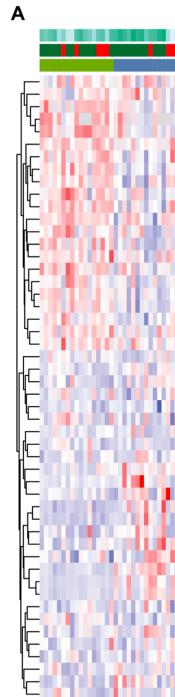
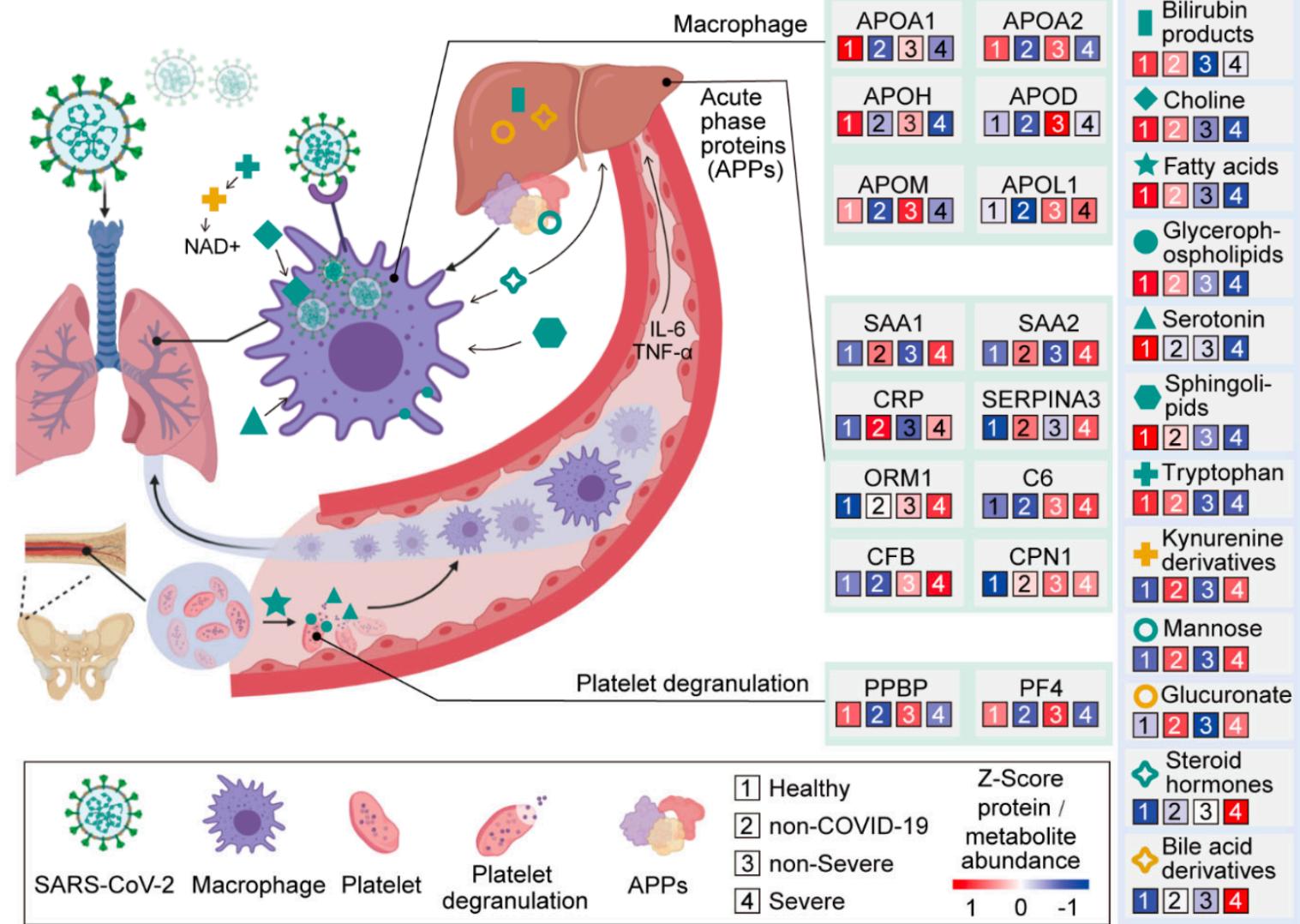


Figure 5



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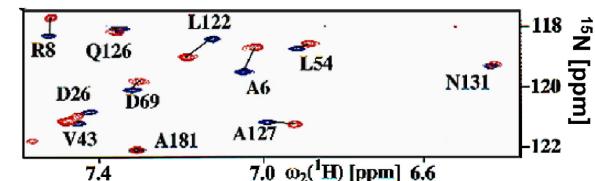
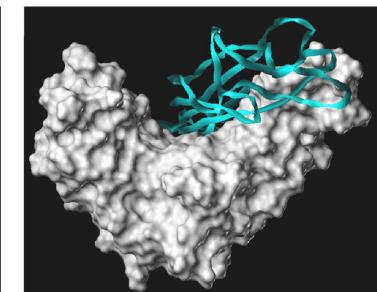
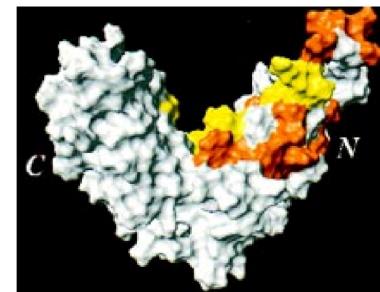
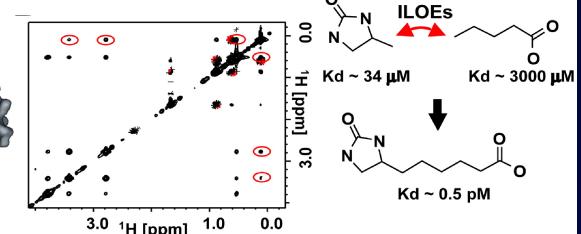
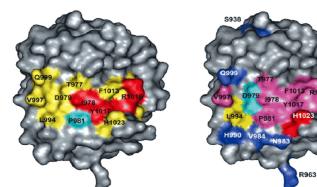
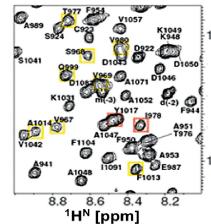
Mok group expertise: Technology and/or Instrumentation

The NMR Facility at TCD

What is NMR?

- High-resolution, atomic-level methodology for the determination of chemical and biochemical structures of molecules.
- Proteins, nucleic acids, sugars, lipids, drugs

The principle of NMR is identical to:

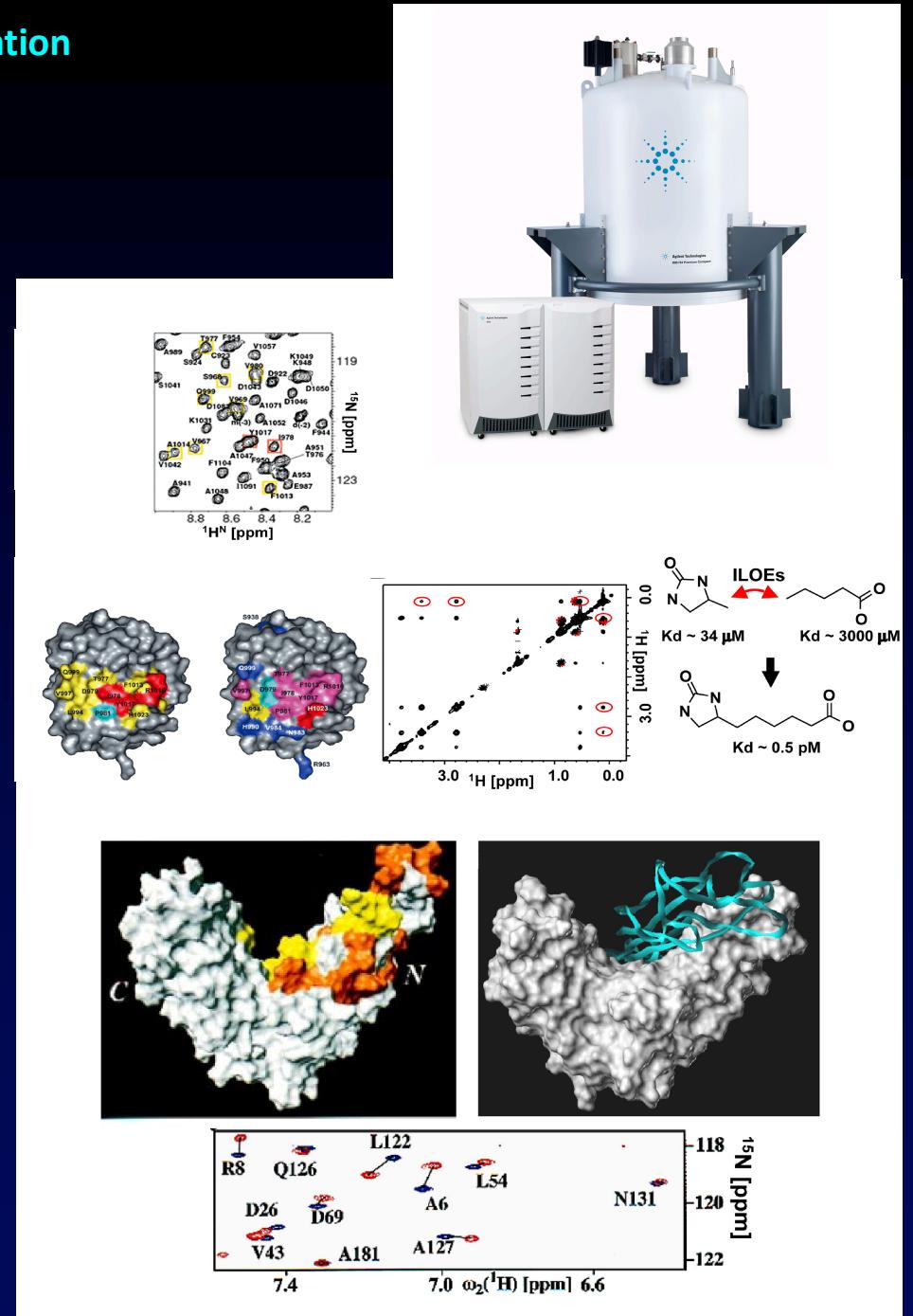


The NMR Facility at TCD

High-resolution NMR capacity realises:

- **Novel drug development** (“SAR-by-NMR”)
- **The validation of molecular identity** (biosimilars / protein aggregation)
- **Metabolomics of cells, serum, urine – Large-scale biobank profiling**
- **Atomic-level 3D biomolecular structure**
- **Structure elucidation of nano-scale / inorganic materials**

- Currently the highest magnetic field in all of Ireland and NI.
- Equipped with $^1\text{H}/^{15}\text{N}/^{13}\text{C}$ cold (cryo) probe, biomolecular solid state MAS probes, triple axial pulsed-field gradient probes, etc.
- With the cold probe, capabilities of detecting metabolites and *in vivo* sample concentrations of sub- μM olar range.



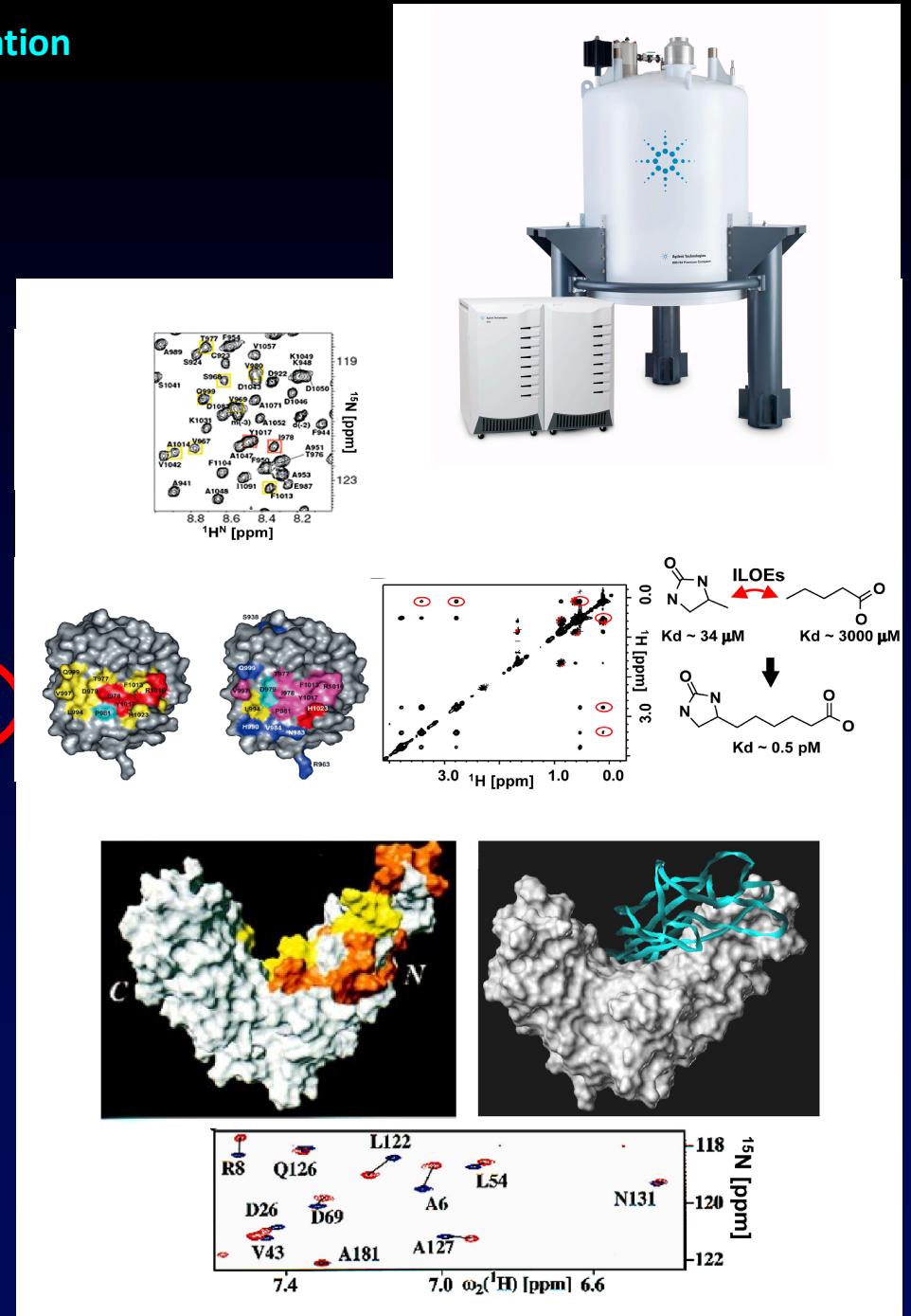
Mok group expertise: Technology and/or Instrumentation

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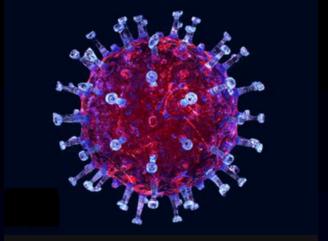
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Predicting potential drugs through the analysis of SARS-CoV-2 proteins



The Protein Journal
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The Proteins of Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2 or n-CoV19), the Cause of COVID-19

Francis K. Yoshimoto¹ 

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Abstract

The devastating effects of the recent global pandemic (termed COVID-19 for “coronavirus disease 2019”) caused by the severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) are paramount with new cases and deaths growing at an exponential rate. In order to provide a better understanding of SARS-CoV-2, this article will review the proteins found in the SARS-CoV-2 that caused this global pandemic.

Keywords Proteins · Virus · SARS-CoV-2

1 Introduction

Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) is the virus that caused the global pandemic that was first reported [1] on December 31, 2019 [2]. Taxonomically, SARS-CoV-2 belongs to the realm *Riboviria*, order *Nidovirales*, suborder *Cornidovirineae*, family *Coronaviridae*, subfamily *Orthocoronavirinae*, genus *Betacoronavirus* (lineage

these viruses enable a more rational approach to designing more effective antiviral drugs [9, 10]. The majority of proteins of SARS-CoV have been characterized in detail. The proteins of SARS-CoV consist of two large polyproteins: ORF1a and ORF1ab (that proteolytically cleave to form 16 nonstructural proteins), four structural proteins: spike (S), envelope (E), membrane (M), and nucleocapsid (N), and eight accessory proteins: ORF3a, ORF3b (NP_828853.1, not

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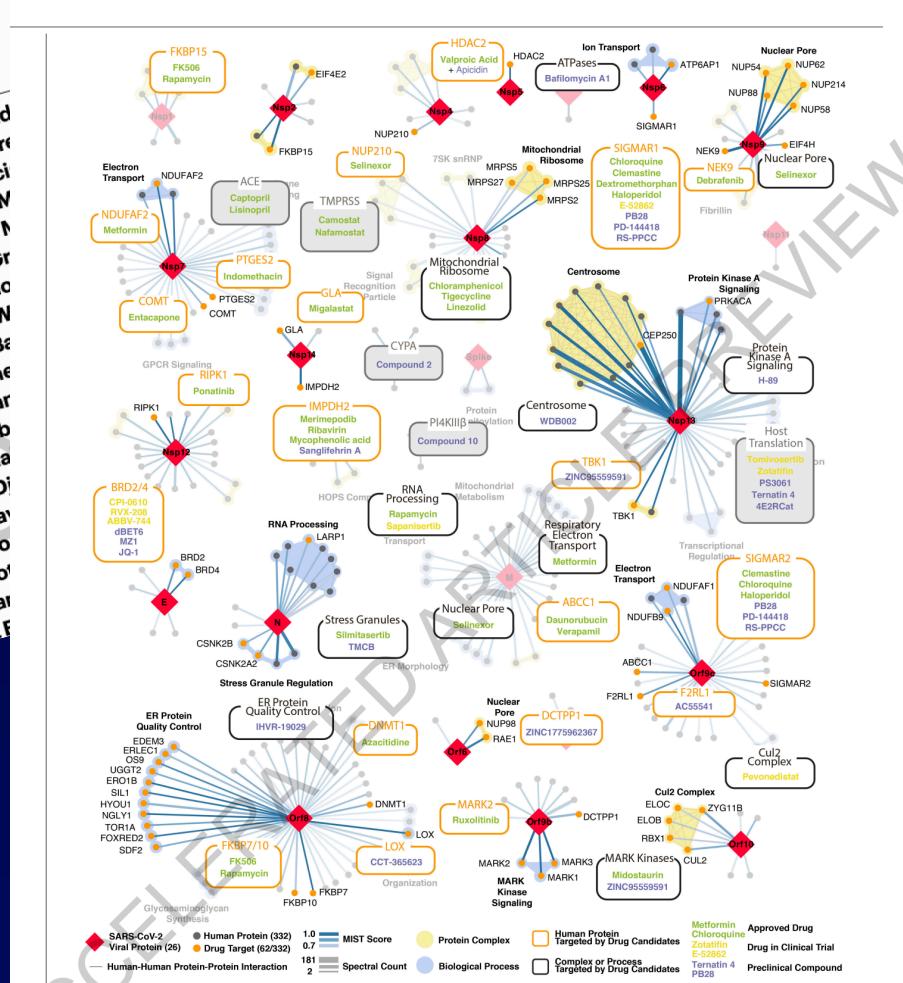
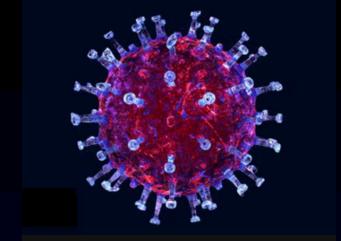


Fig. 5 | Drug-human target network. PPIs of SARS-CoV-2 baits with approved drugs (green), clinical candidates (yellow), and preclinical candidates (purple) with experimental activities against the host proteins (white background) or previously known host factors (grey background) are shown.

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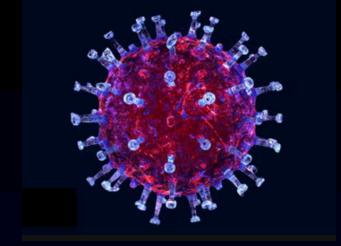
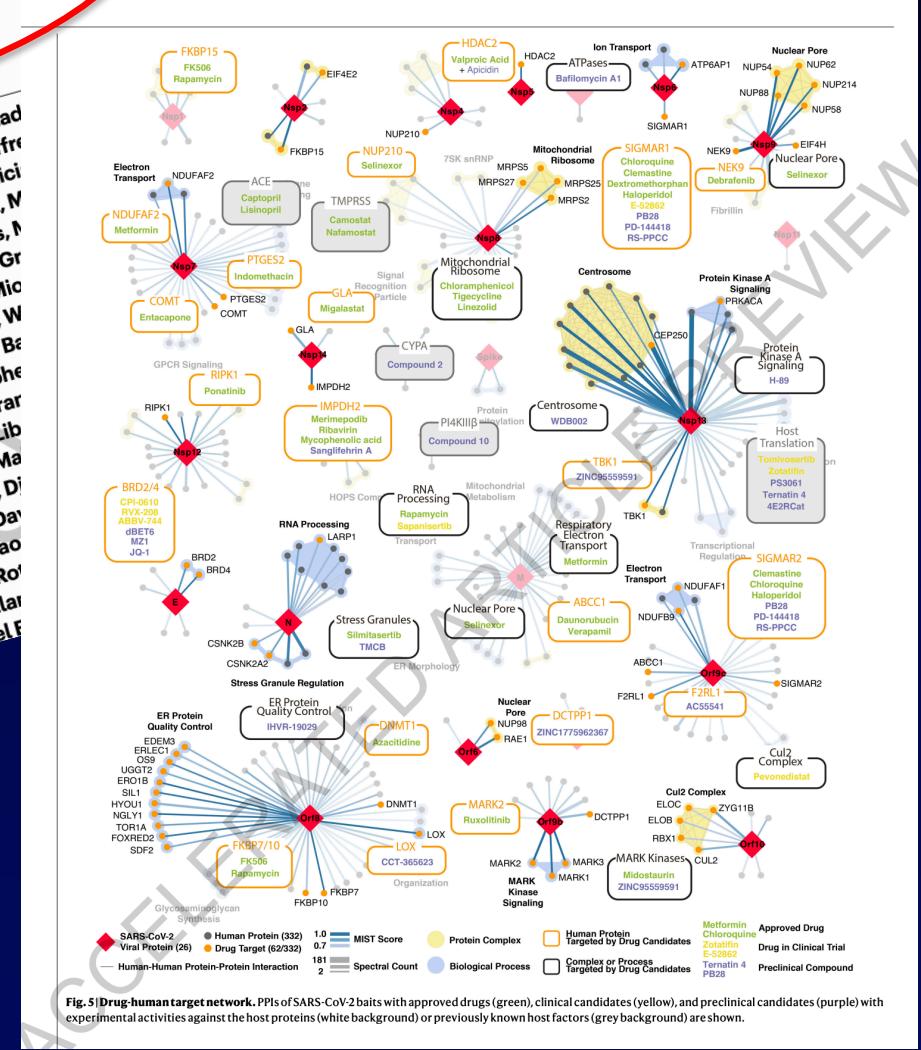
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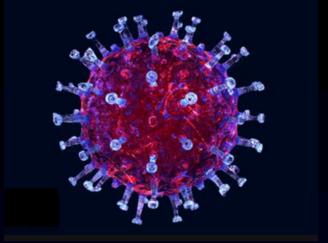
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Keywords Proteins · Virus · SARS CoV-2

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The Proteins of Severe (SARS CoV-2 or n-COV)

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Abstract

The devastating effects of severe acute respiratory syndrome are exponential. In order to combat SARS CoV-2 that causes COVID-19, we analyzed the SARS CoV-2 genome to predict the proteins that are encoded by the genome.

Keywords Proteins · Viruses · SARS-CoV-2

1 Introduction

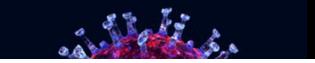
Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the virus that causes COVID-19. SARS-CoV-2 was first reported [1] in December 2019 in Wuhan, China. SARS-CoV-2 belongs to the genus *Coronavirinae*, suborder *Coronavirales*, and order *Coronavirales*.

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Table 6 Drugs that potentially target (modulate) proteins that interact with SARS CoV-2 proteins as described in reference [66]

Entry	Viral Protein-(Human Gene)	Compound Name(s)
1	E protein-(BRD2/4)	JQ1, ^a RVX-208 ^b
2	N protein-(CSNK2A2)	Silmitasertib (cancer), ^c TMCB ^a
3	NSP5-(HDAC2)	Apicidin, ^a Valproic acid (CNS disease, cancer) ^c
4	NSP6-(ATP6AP1)	Bafilomycin A1 ^a
5	NSP6-(SIGMAR1)	E-52862, ^b PD-144418, ^a RS-PPCC, ^a PB28, ^a Haloperidol (CNS disease) ^c
6	NSP6-(SLC6A15)	Loratadine (antihistamine) ³
7	ORF9C-(TMEM97)	PB28, ^a haloperidol (CNS disease) ^c
8	M protein-(ATP6V1A)	Bafilomycin A1 ^a
9	NSP7-(COMT)	Entacapone (Parkinson's disease) ^c
10	NSP7-(PTGES2)	Indomethacin (inflammation/pain) ^c
11	NSP7-(NDUFs)	Metformin (diabetes) ^c
12	ORF9C-(NDUFs)	Metformin ^c
13	NSP12-(RIPK1)	Ponatinib (cancer) ^c
14	NSP13-(PRKACA)	H-89 ^a
15	NSP14-(IMPDH2)	Merimepodib ^b
16	NSP14-(GLA)	Migalastat (Fabry disease) ^c
17	NSP14-(IMPDH2)	Mycophenolic acid (organ rejection), ³ ribavirin (virus) ^c
18	ORF8-(DNMT1)	Azacitidine ^c
19	ORF8-(LOX)	CCT 365623 ^a
20	ORF9b-(MARK2/3)	Midostaurin, ³ Ruxolitinib ^c
21	ORF9b-(DCTPP1)	ZINC1775962367, ^a ZINC4326719, ^a ZINC4511851 ^a
22	ORF9b/NSP13-(MARK3/TBK1)	ZINC95559591 ^a
23	ORF9C-(F2RL1)	AC-55541, ^a AZ8838 ^b
24	ORF9C-(ABCC1)	Daunorubicin ^c
25	ORF9C-(F2RL1)	GB 110 ^a
26	ORF9C-(ABCC1)	S-Verapamil (hypertension) ^c
27	ORF9C-(F2RL1)	AZ3451 ^a
28	M-Protein-(SLC1A3)	UCPH-101 ^a
29	E protein-(BRD2/4)	ABBV-744, ^b dBET6, ^a MZ1, ^a CPI-0610 ^b
30	N protein-(LARP1)	Sapanisertib, ^b Rapamycin (organ rejection) ^c
31	NSP2-(FKBP15)	Rapamycin ^c
32	ORF8-(FKBP7/10)	Rapamycin ^c
33	NSP2-(EIF4E2/H)	Zotarolimus ^b
34	ORF10-(VCP)	CB5083 ^b
35	NSP6-(SIGMAR1)	Chloroquine (malaria) ^c



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Keywords Proteins · Virology

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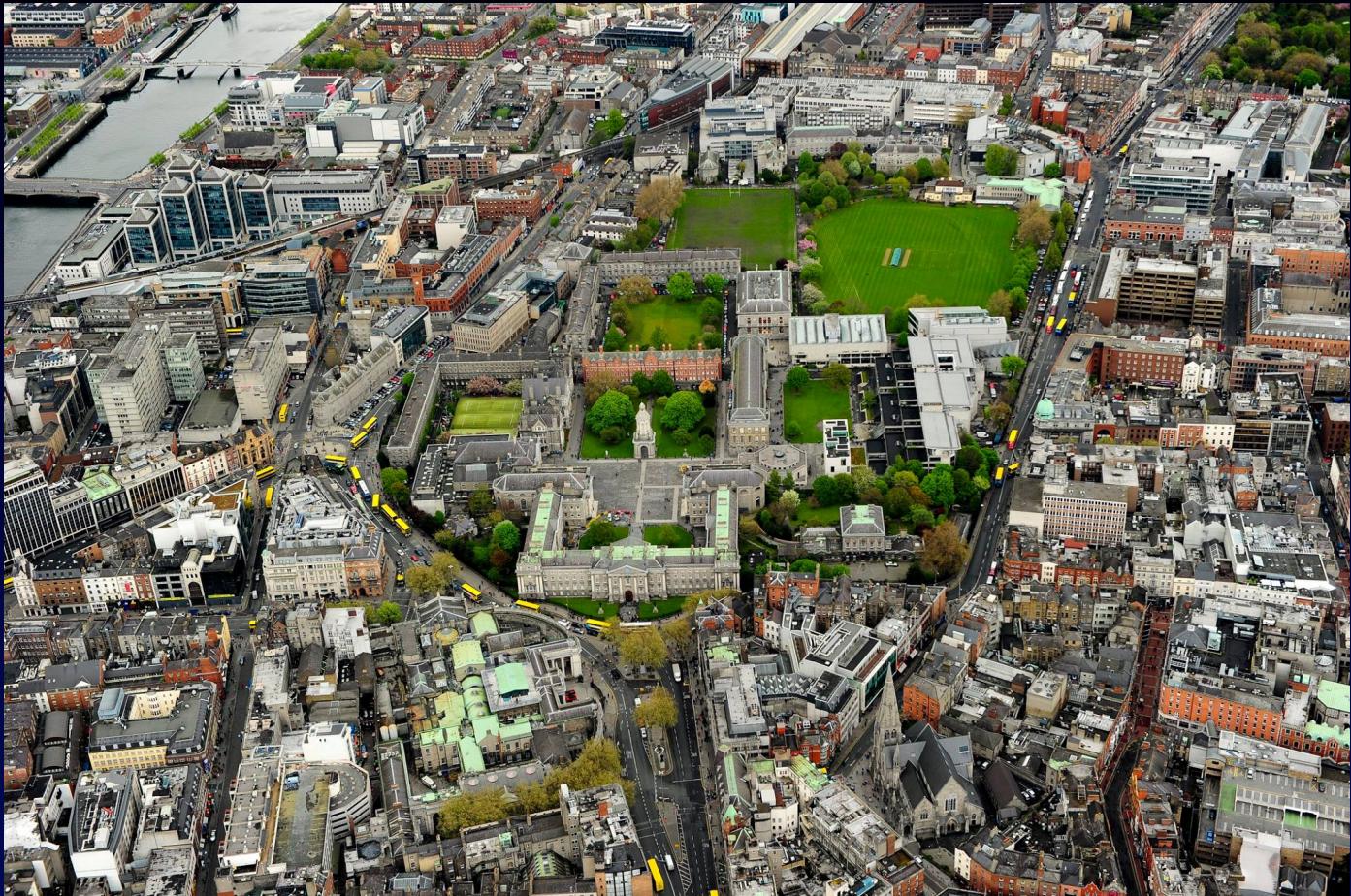


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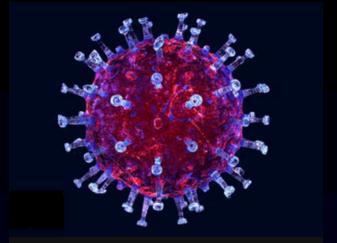
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