

## outline

- ... introducing The Center for Vaccine Research
  - foundations
  - facilities
  - focus
  - faculty
- ... responding to SARS-CoV-2 emergence
  - in vitro studies
  - in vivo studies
- ... creativity drives a diversity of interventions
  - vaccines
  - antibodies and nanobodies
  - variants





## The Center for Vaccine Research



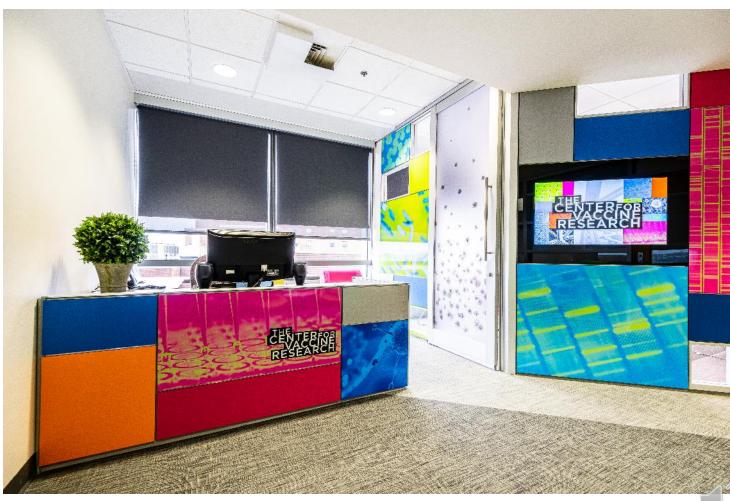






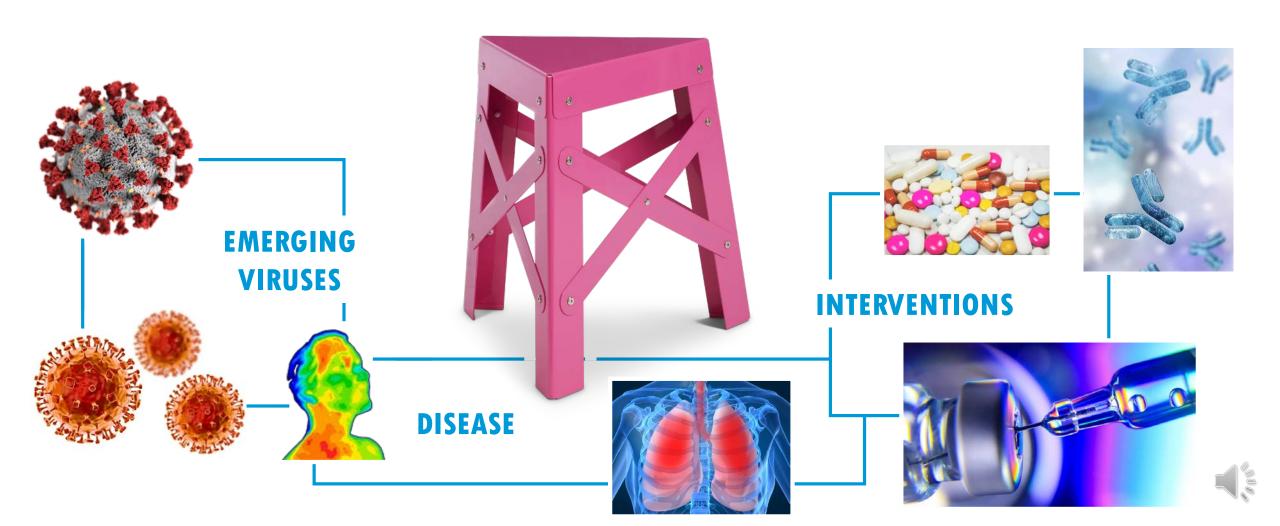
## The Center for Vaccine Research





## the foundations of CVR ...

creative approaches to mitigate infectious disease



#### Office of Biodefense Research Resources and Translational Research

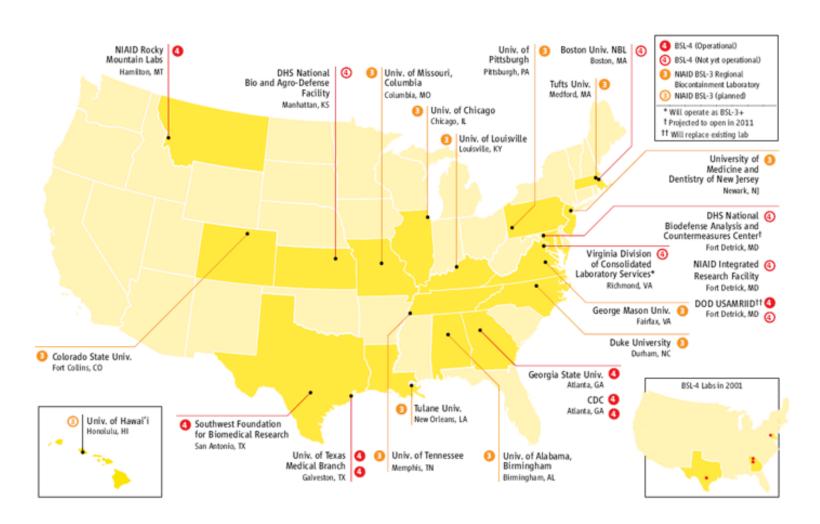
National Biocontainment Laboratories (NBL) and Regional Biocontainment Laboratories (RBL)







Department of Defense





## Regional Biocontainment Laboratory (RBL) at Pittsburgh

from cells ... to tissues ... to animal models of disease







## understanding respiratory infection and testing interventions

from cells ... to tissues ... to animal models of disease



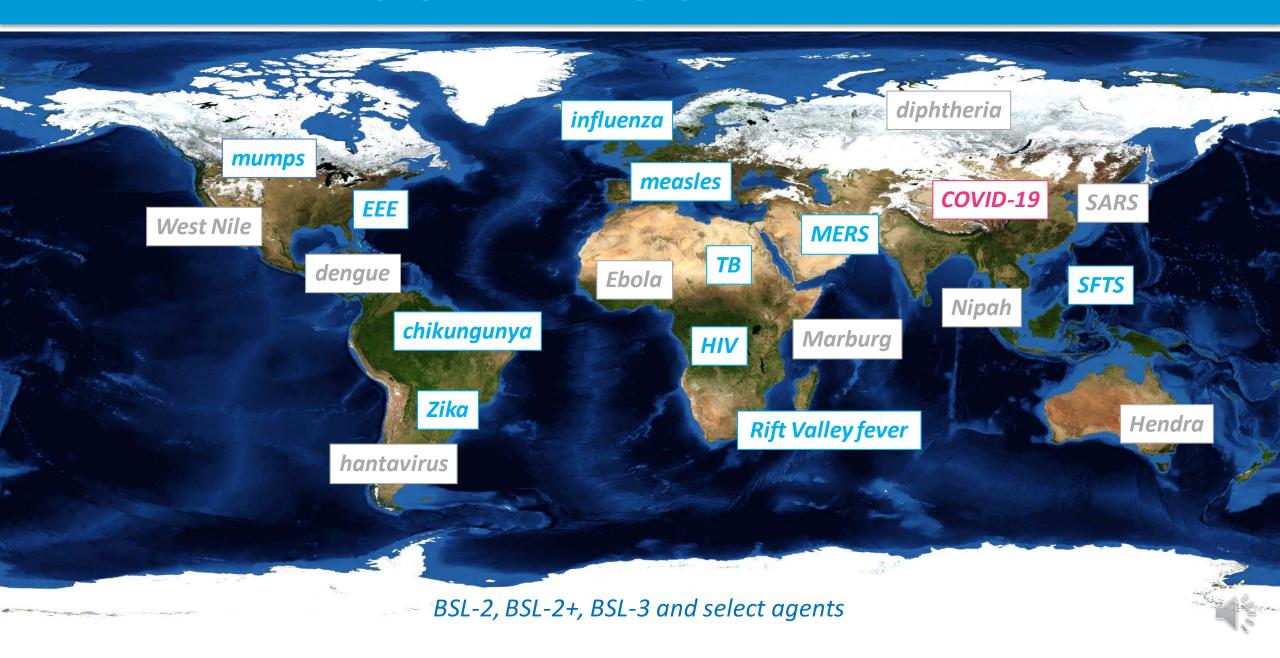








## emerging and re-emerging infectious diseases



## a hub for host-pathogen research and pre-clinical intervention development



## a hub for host-pathogen research and pre-clinical intervention development



## Center for Vaccine Research



#### People

Select Person Type...

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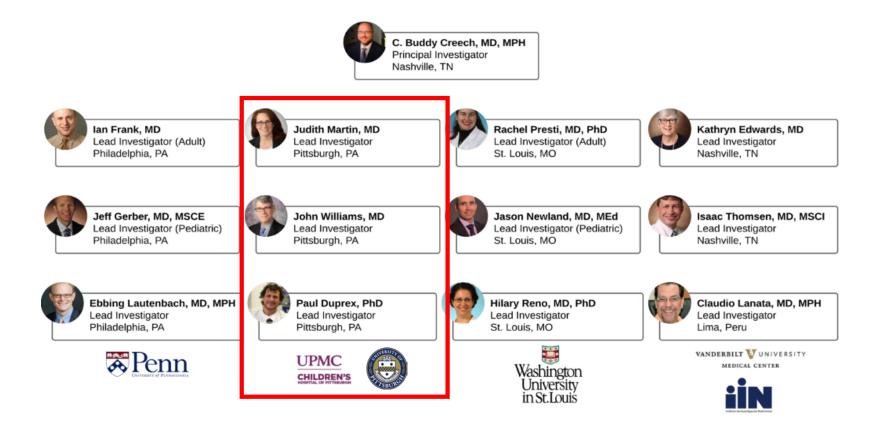


Richard Zimmerman, MD, MPH > zimmer@pitt.edu 412-383-2354



## NIAID vaccine and treatment evaluation units (VTEUs)

established in 1962 and conducted hundreds of clinical trials, many of which have contributed to vaccine licensure.



state-of-the-art capabilities for inhalation of pathogenic agents and modeling physiological response to disea

## Pittsburgh Vaccine Trials Unit













FROM NIH VACCINE TESTING AND EVALUATION UNIT TO ...

# PITTSBURGH VACCINE TRIALS UNIT





**University of Pittsburgh** 













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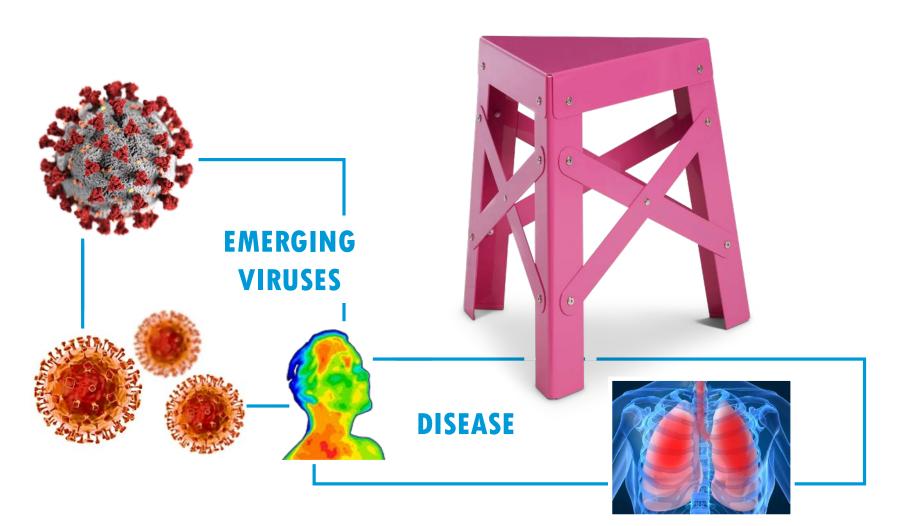
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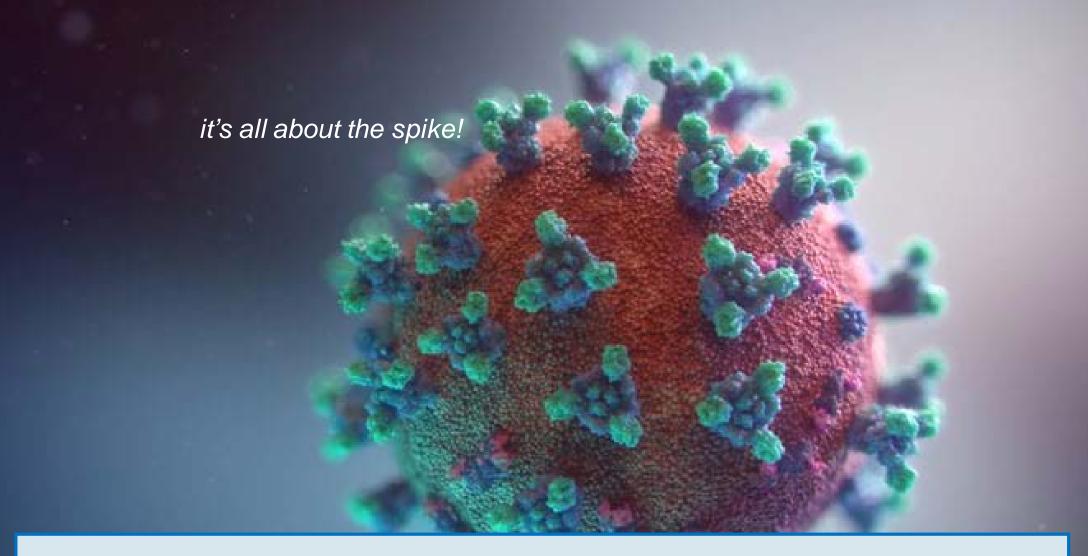


## outline

creative approaches to mitigate infectious disease







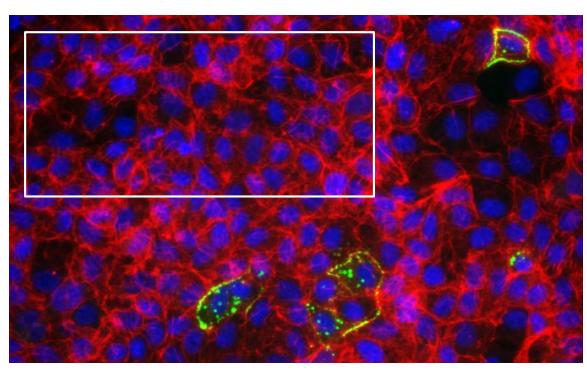
the genome of SARS-CoV-2





## SARS-CoV-2

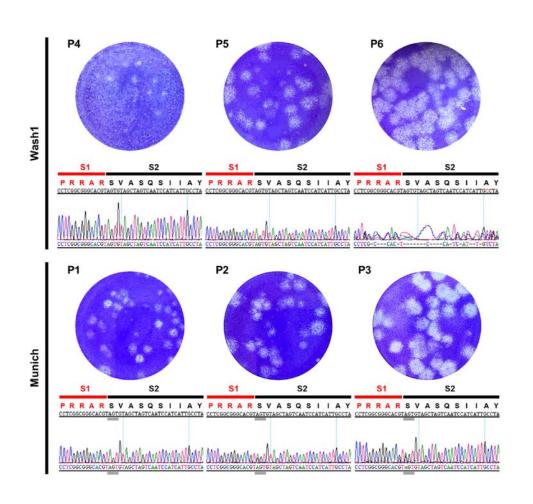
culturing coronavirus ... from cells ... to tissues ... to animal models of disease

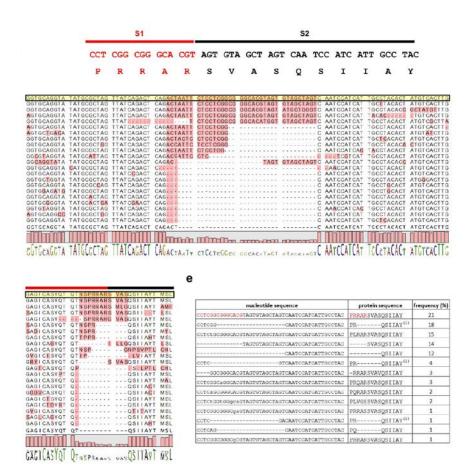




#### SARS-CoV-2

#### an evolving pathogen: the furin cleavage site



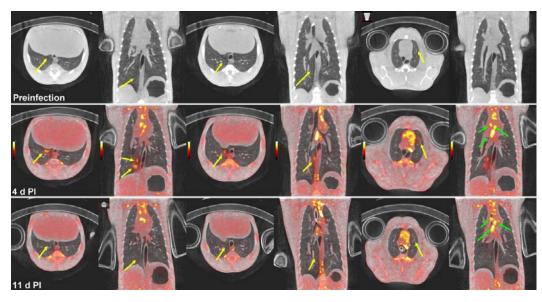


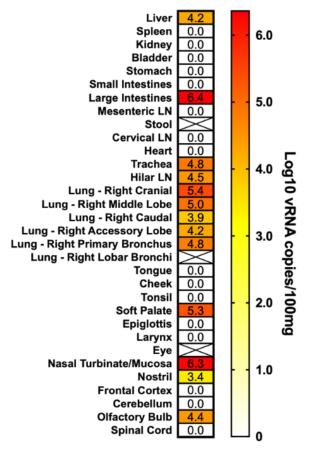
## pre-clinical capabilities in CVR



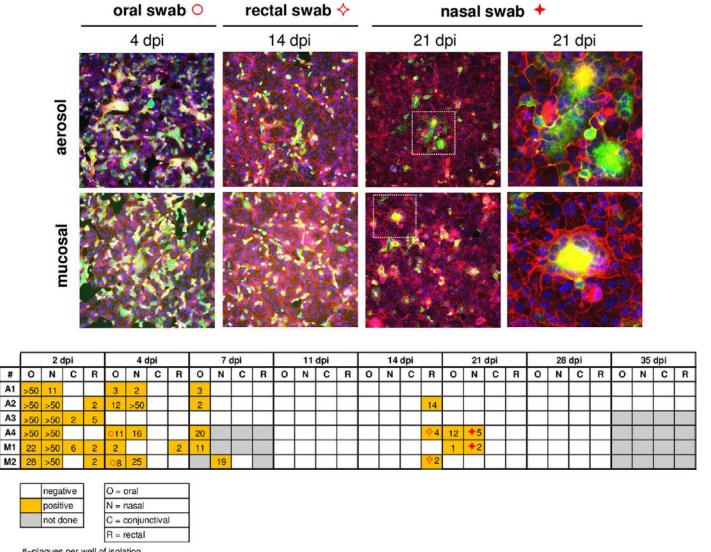






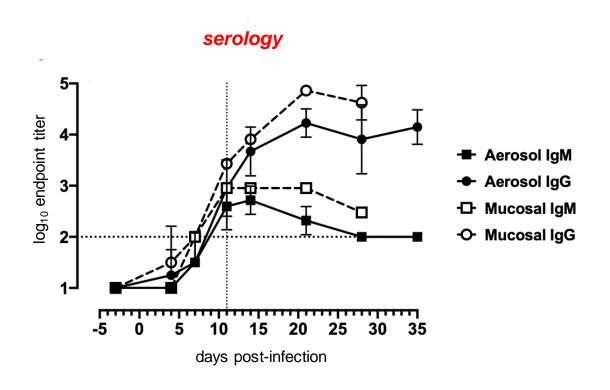


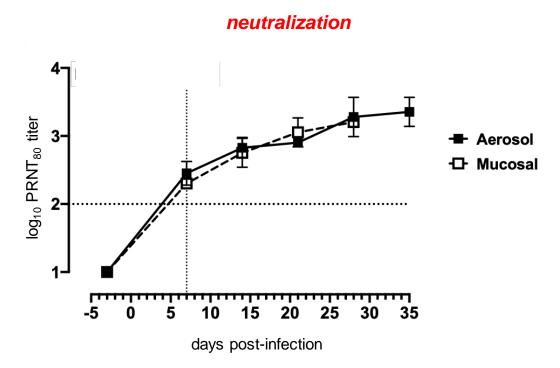
## virus isolation from swabs



## immunological analyses

#### simultaneous seroconversion for IgM and IgG





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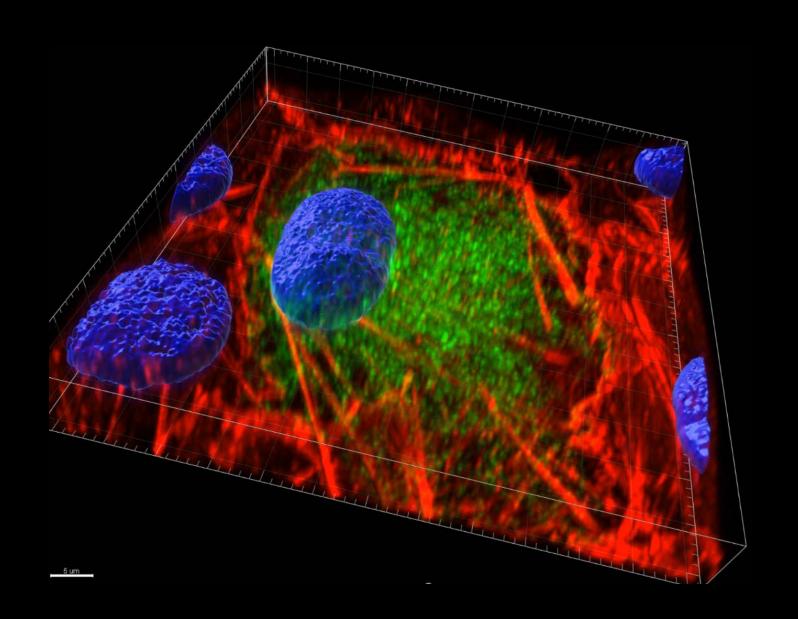
## outline

creative approaches to mitigate infectious disease





## measles vaccine on the inside ... spike on the outside outside ...









## transchromosomic cow antibodies

capitalizes on CVR GLP-like Quality Systems (QS) readiness



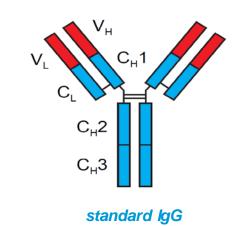


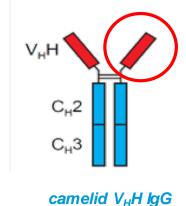


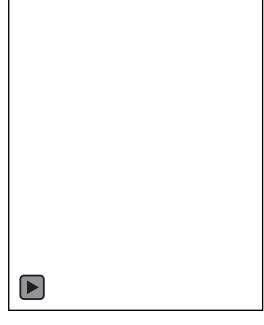
## V<sub>H</sub>H heavy-chain only antibodies

#### nanobodies

- minimal V<sub>H</sub>H domain for antigen binding
- highly soluble and thermostable
- high sequence similarity with human IgG
- better tissue penetration
- inhalable delivery
- robust and affordable manufacturing







nanobody ~15 kDa



## V<sub>H</sub>H heavy-chain only antibodies

Science

REPORTS

Cite as: Y. Xiang *et al.*, *Science* 10.1126/science.abe4747 (2020).

## Versatile and multivalent nanobodies efficiently neutralize SARS-CoV-2

Yufei Xiang<sup>1</sup>, Sham Nambulli<sup>2,3\*</sup>, Zhengyun Xiao<sup>1\*</sup>, Heng Liu<sup>4\*</sup>, Zhe Sang<sup>1,5</sup>, W. Paul Duprex<sup>2,3</sup>, Dina Schneidman-Duhovny<sup>6</sup>†, Cheng Zhang<sup>4</sup>†, Yi Shi<sup>1,5</sup>†

<sup>1</sup>Department of Cell Biology, University of Pittsburgh, Pittsburgh, PA, USA. <sup>2</sup>Center for Vaccine Research, University of Pittsburgh, PA, USA. <sup>3</sup>Department of Microbiology and Molecular Genetics, University of Pittsburgh, PH, USA. <sup>4</sup>Department of Pharmacology and Chemical Biology, University of Pittsburgh, Pittsburgh, PA, USA. <sup>5</sup>Pitt/CMU Program for Computational Biology, Pittsburgh, PA, USA. <sup>6</sup>School of Computer Science and Engineering, Institute of Life Sciences, The Hebrew University of Jerusalem, Israel.

\*These authors contributed equally to this work.

Cost-effective, efficacious therapeutics are urgently needed against the COVID-19 pandemic. Here, we used camelid immunization and proteomics to identify a large repertoire of highly potent neutralizing nanobodies (Nbs) to the SARS-CoV-2 spike (S) protein receptor-binding domain (RBD). We discovered Nbs with picomolar to femtomolar affinities that inhibit viral infection at sub-ng/ml concentration and determined a structure of one of the most potent in complex with RBD. Structural proteomics and integrative modeling revealed multiple distinct and non-overlapping epitopes and indicated an array of potential neutralization mechanisms. We constructed multivalent Nb constructs that achieved ultrahigh neutralization potency (IC50s as low as 0.058 ng/ml) and may prevent mutational escape. These thermostable Nbs can be rapidly produced in bulk from microbes and resist lyophilization, and aerosolization.

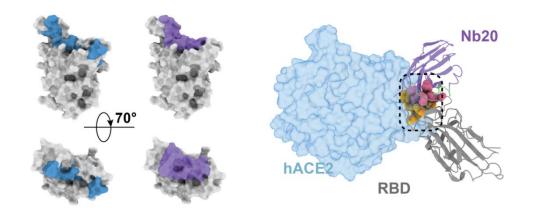


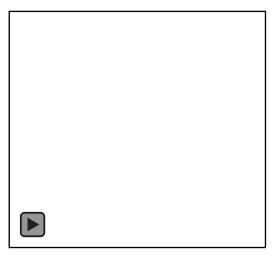




## discovery of thousands of highly potent, multi-epitope neutralizing nanobodies

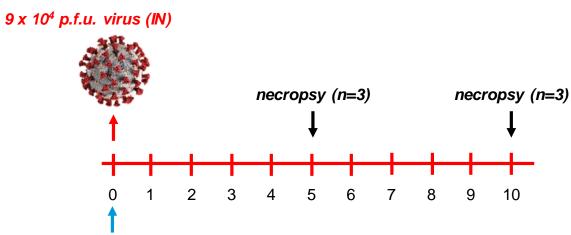
number of identifications	unique nanobody clones	CDR3 family "clonotypes"
total	16,555	617
high-affinity	8,208	346

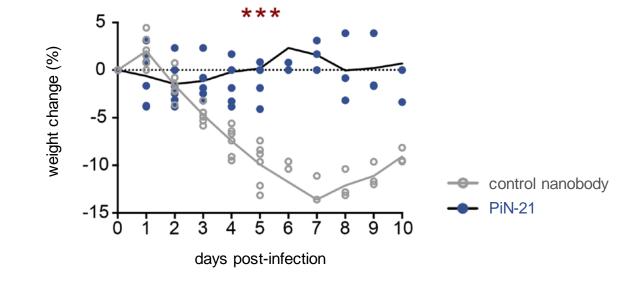




#### Syrian hamster model: intranasal co-administration

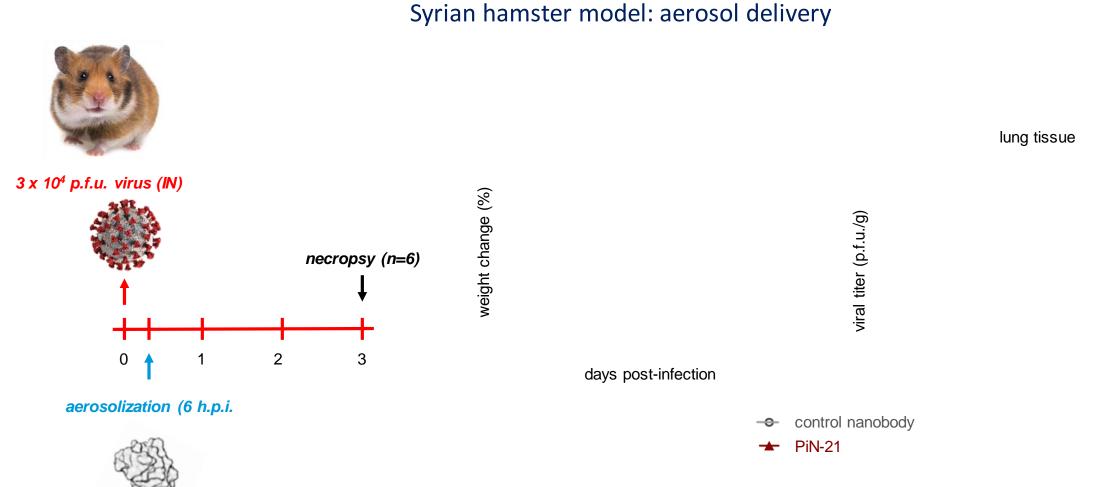






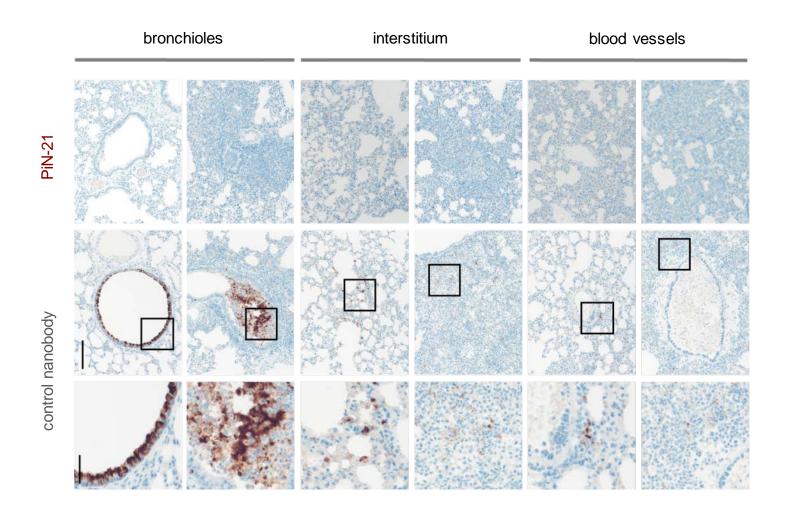


100 µg nanobody (IN)

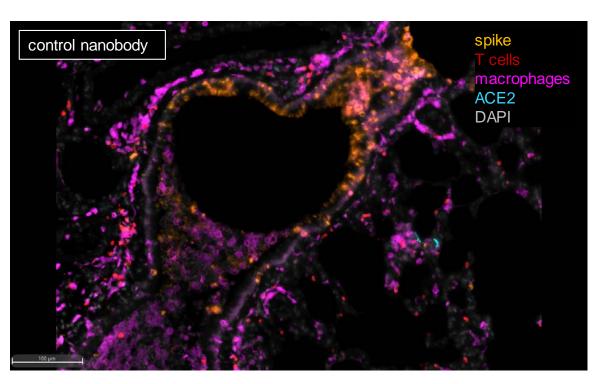


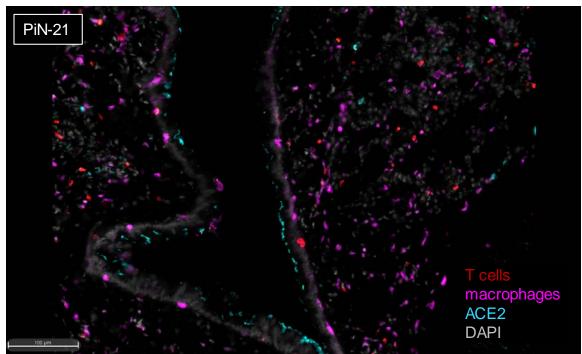


#### pathological assessment (3 d.p.i.)



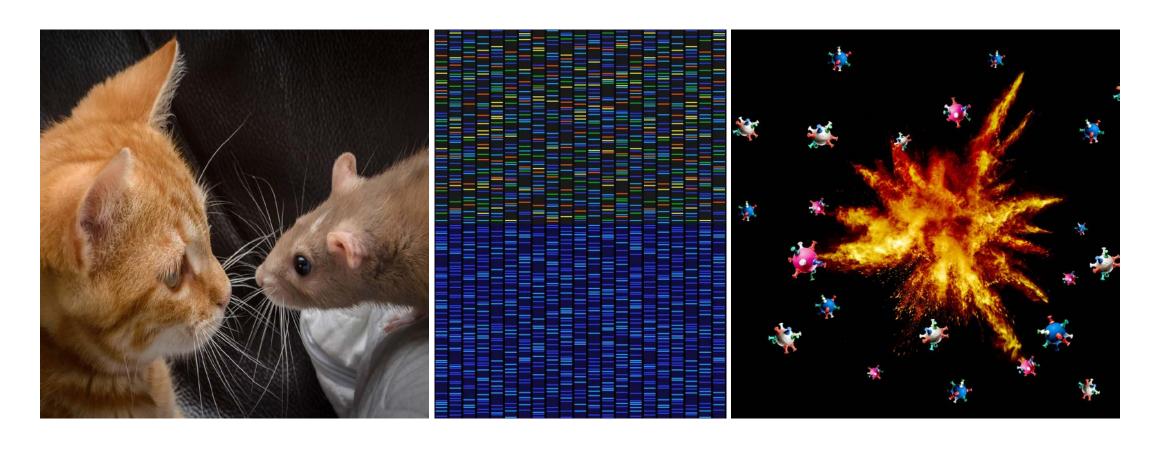
#### bronchointerstitial compartment





## however ... the virus is a constantly moving target

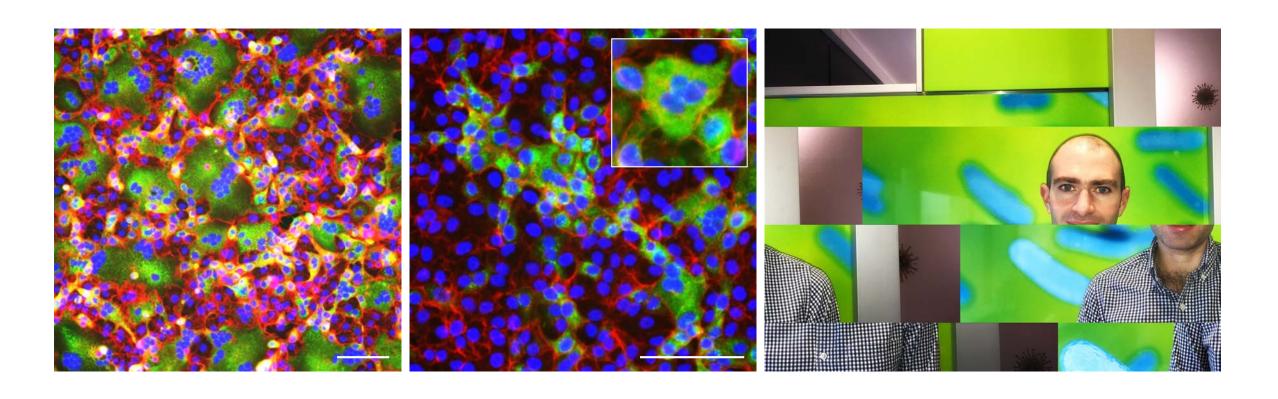
SARS-CoV-2 variants of interest and concern: a game of cat and mouse





## it all starts with the virus

long term chronic SARS-CoV-2 infection in an immunosuppressed patient



## SARS-CoV-2 variants arise during persistent infection of immunosuppressed

#### recurrent deletion regions (RDRs) in the spike protein

Science

Cite as: K. R. McCarthy *et al.*, *Science* 10.1126/science.abf6950 (2021).

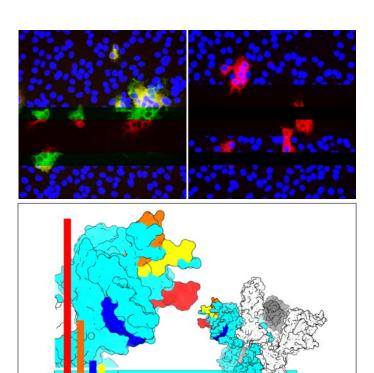
# Recurrent deletions in the SARS-CoV-2 spike glycoprotein drive antibody escape

Kevin R. McCarthy<sup>1,2,3\*</sup>, Linda J. Rennick<sup>1,2</sup>, Sham Nambulli<sup>1,2</sup>, Lindsey R. Robinson-McCarthy<sup>4</sup>, William G. Bain<sup>5,6,7</sup>, Ghady Haidar<sup>8,9</sup>, W. Paul Duprex<sup>1,2\*</sup>

<sup>1</sup>Center for Vaccine Research, University of Pittsburgh School of Medicine, Pittsburgh, PA, USA. <sup>2</sup>Department of Microbiology and Molecular Genetics, University of Pittsburgh School of Medicine, Pittsburgh, PA, USA. <sup>3</sup>Laboratory of Molecular Medicine, Boston Children's Hospital, Harvard Medical School, Boston, MA, USA. <sup>4</sup>Department of Genetics, Harvard Medical School, Boston, MA, USA. <sup>5</sup>Division of Pulmonary, Allergy, and Critical Care Medicine, Department of Internal Medicine, UPMC, Pittsburgh, PA, USA. <sup>6</sup>Division of Pulmonary, Allergy, and Critical Care Medicine, Department of Medicine, University of Pittsburgh School of Medicine, Pittsburgh, PA, USA. <sup>8</sup>Division of Infectious Disease, Department of Medicine, University of Pittsburgh School of Medicine, Pittsburgh, PA, USA. <sup>9</sup>Division of Infectious Disease, Department of Internal Medicine, UPMC, Pittsburgh, PA, USA.

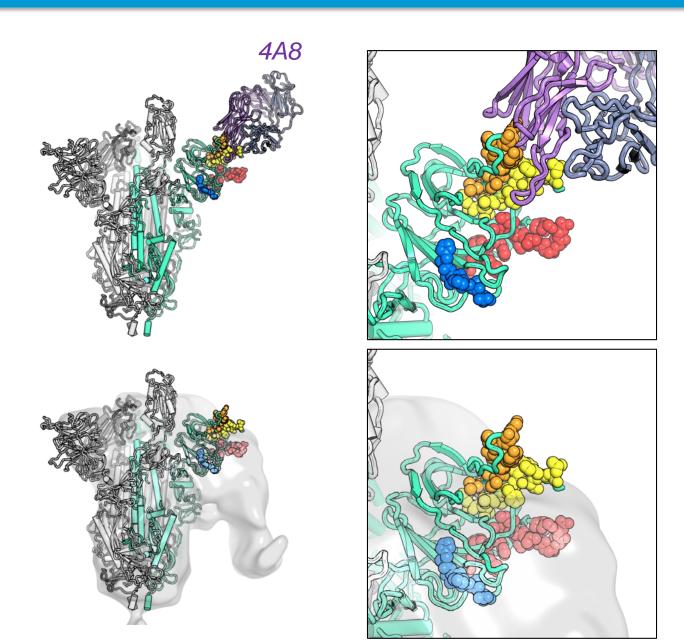
\*Corresponding author. Email: krm@pitt.edu (K.R.M.); pduprex@pitt.edu (W.P.D.)

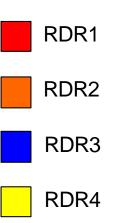
Zoonotic pandemics, like that caused by SARS-CoV-2, can follow the spillover of animal viruses into highly susceptible human populations. Their descendants have adapted to the human host and evolved to evade immune pressure. Coronaviruses acquire substitutions more slowly than other RNA viruses, due to a proofreading polymerase. In the spike glycoprotein, we find recurrent deletions overcome this slow substitution rate. Deletion variants arise in diverse genetic and geographic backgrounds, transmit efficiently, and are present in novel lineages, including those of current global concern. They frequently occupy recurrent deletion regions (RDRs), which map to defined antibody epitopes. Deletions in RDRs confer resistance to neutralizing antibodies. By altering stretches of amino acids, deletions appear to accelerate SARS-CoV-2 antigenic evolution and may, more generally, drive adaptive evolution.





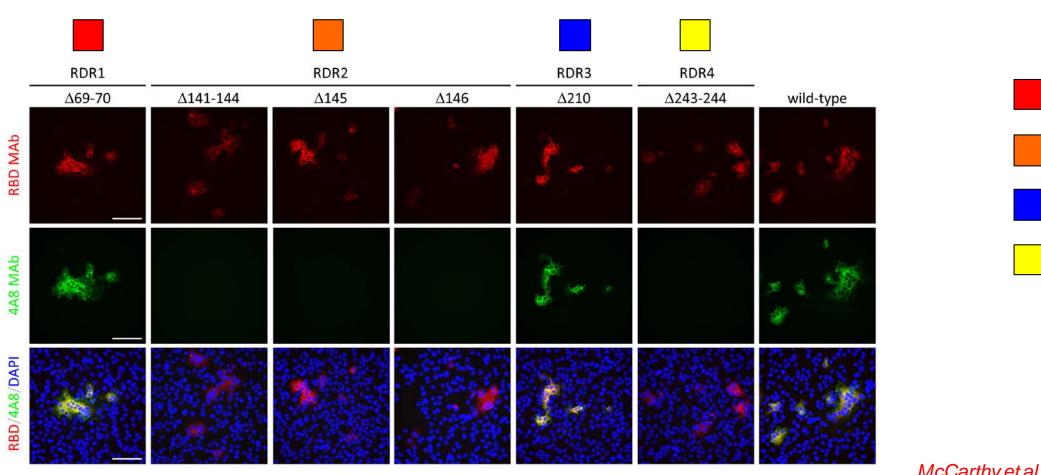
## RDRs map to discrete surfaces within antibody epitopes





## deletions in RDR1 and 4 disrupt 4A8 binding

#### indirect immunofluorescence



RDR1

RDR2

RDR3

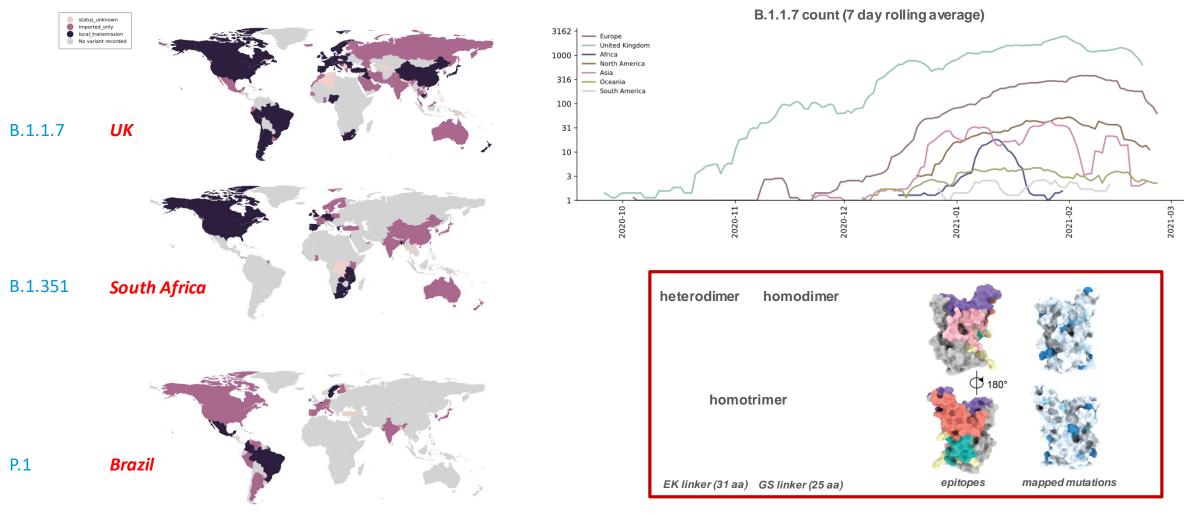
RDR4

## deletions in RDR1 and 4 completely abolish 4A8 neutralization activity

plaque reduction neutralization test 80 percent (PRNT<sub>80</sub>)

antibody	virus	antibody concentration (μg/ml)									
		25	12.5	6.25	3.125	1.56	0.78	0.39	0.2	0.1	0.05
4A8 (α-S)	PLTI1	-	-	-	-	-	-	-	-	-	-
	Munich: P3	+	+	+	+	+	+				-
2214 (α-ΗΑ)	PLTI1	-	-	-	-	-	-	ND	ND	ND	ND
	Munich: P3	-	-	-	-	-	-	ND	ND	ND	ND
	virus	serum dilution									
		1:100	1:200	1:400	1:800	1:1600	1:3200				
human convalescent serum	PLTI1	+	+	+	+	+	-				
	Munich: P3	+	+	+	+	+	-				

## multi-epitope, multivalent constructs to suppress virus mutational escape

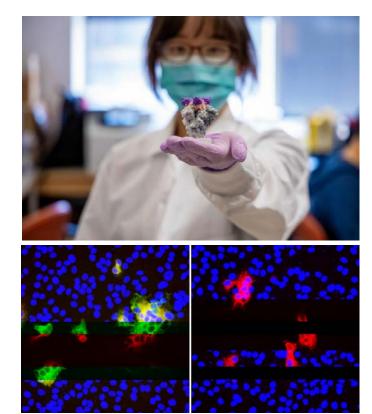




#### summary

#### the utility of nanobodies as a COVID-19 intervention

- exquisite potency in vitro (up to 0.058 ng/ml) and in vivo (< 0.6 mg/kg)</li>
- highly solubility and stability for drug storage and administration
- albumin fusion to nanobody extends *in vivo* half-life
- inhaled or intranasal delivery significantly impacts disease
- low cost of goods
- bind to five separate neutralization epitopes permitting heterodimeric constructs to be generated to address escape due to viral variants





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## acknowledgements



Linda Rennick Sham Nambulli Natasha Tilston-Lunel

JoAnne Flynn
Amy Hartman
William Klimstra
Kevin McCarthy
Anita McElroy
Doug Reed
Chuck Scanga



Yi Shi

Yufei Xiang Zhengyun Xiao Zhe Sang

Cheng Zhang
Heng Liu

Ghady Haidar William Bain Lindsey Robinson-McCarthy



Nicholas Crossland



Dina Schneidman-Duhovny





