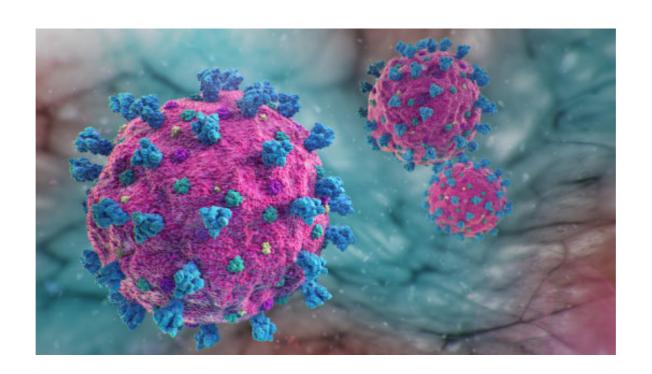
# Viral Entry

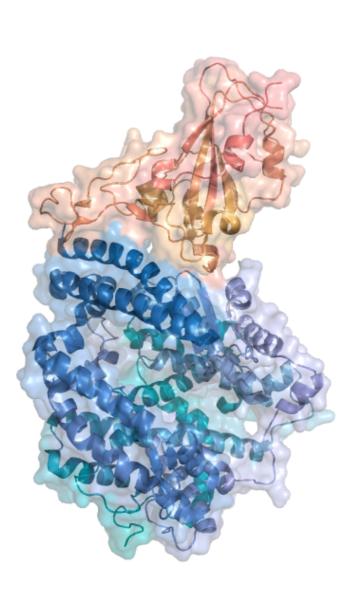


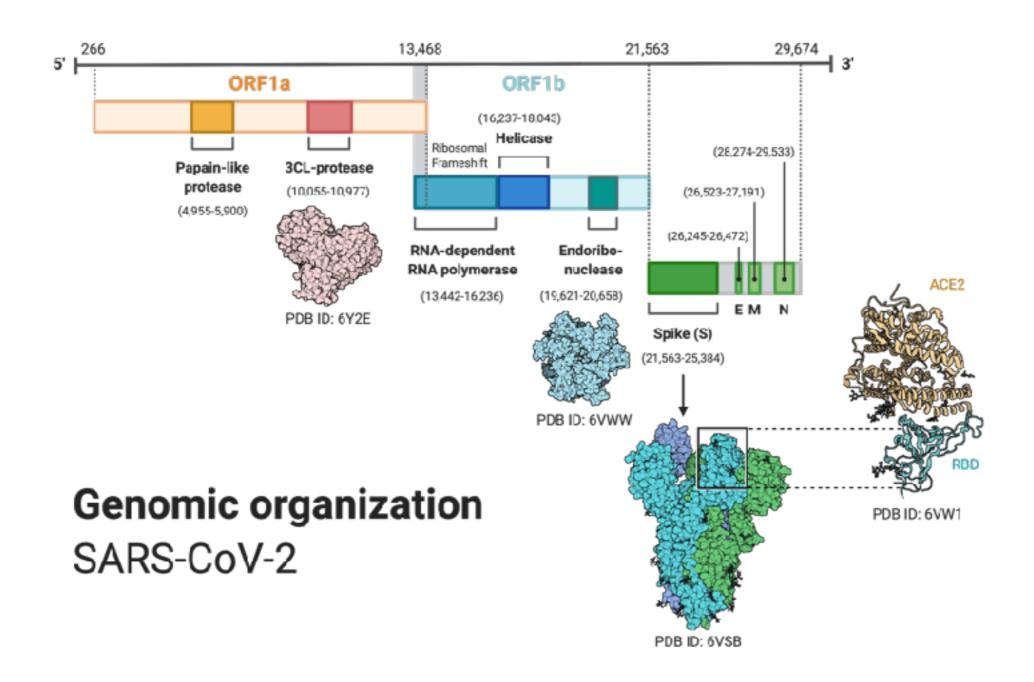
MacMillan Group Meeting May 04, 2020

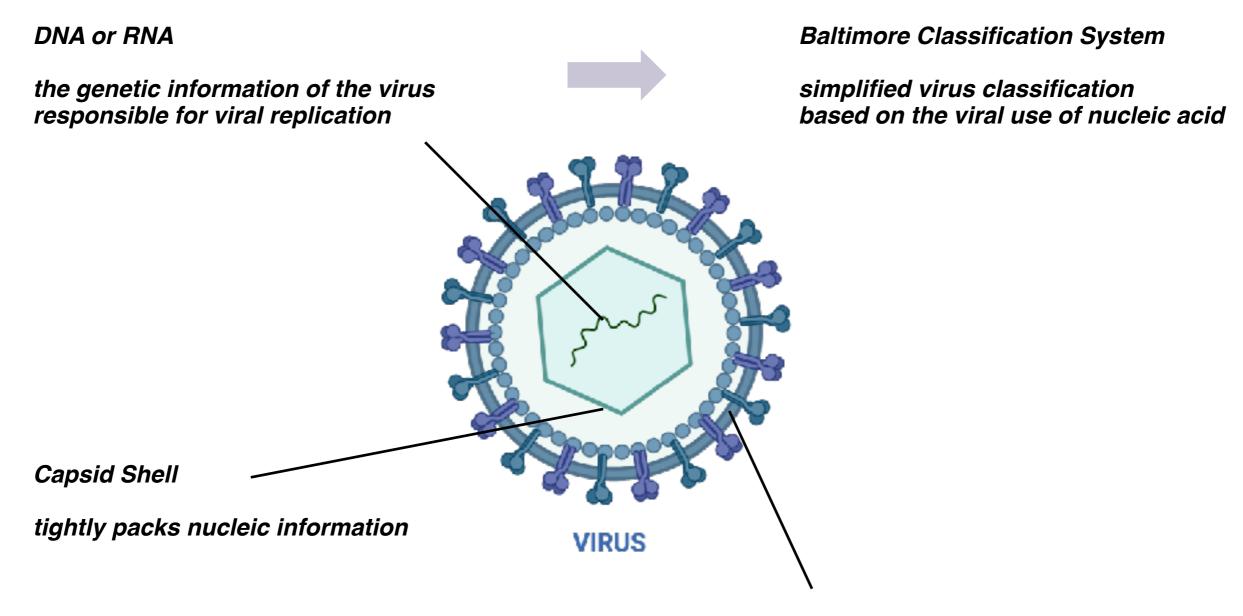
Daniel Kim

#### Outline

- Brief Overview of Viruses & Nomenclature
- General Mechanisms of Viral Entry
- Important Factors for Successful Viral Entry
  - ► Attachement
  - ► Signaling
  - ► Endocytosis
  - ► Penetration
  - ▶ Uncoating
- Details Associated Towards SARS-CoV-2 & Other Examples







Lipid Bilayer Membrane

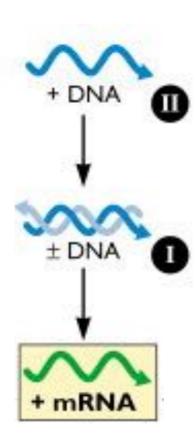
found only in envelope viruses & contains additional virally encoded proteins

Baltimore Classification System



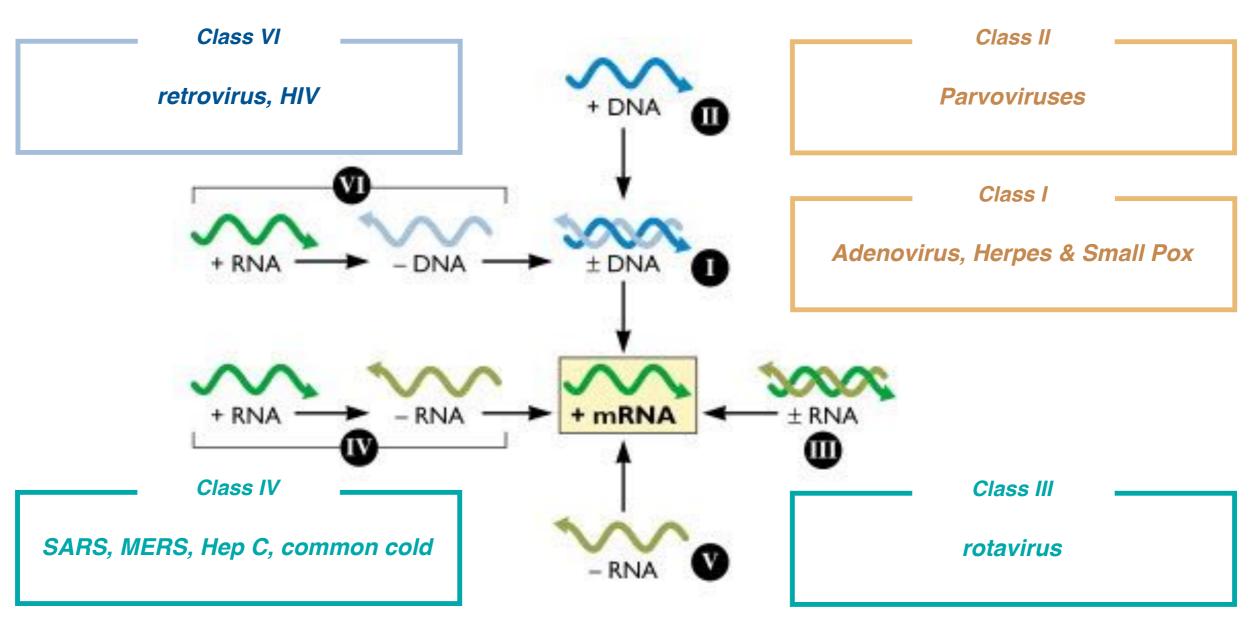
mRNA encodes for proteins

#### Baltimore Classification System



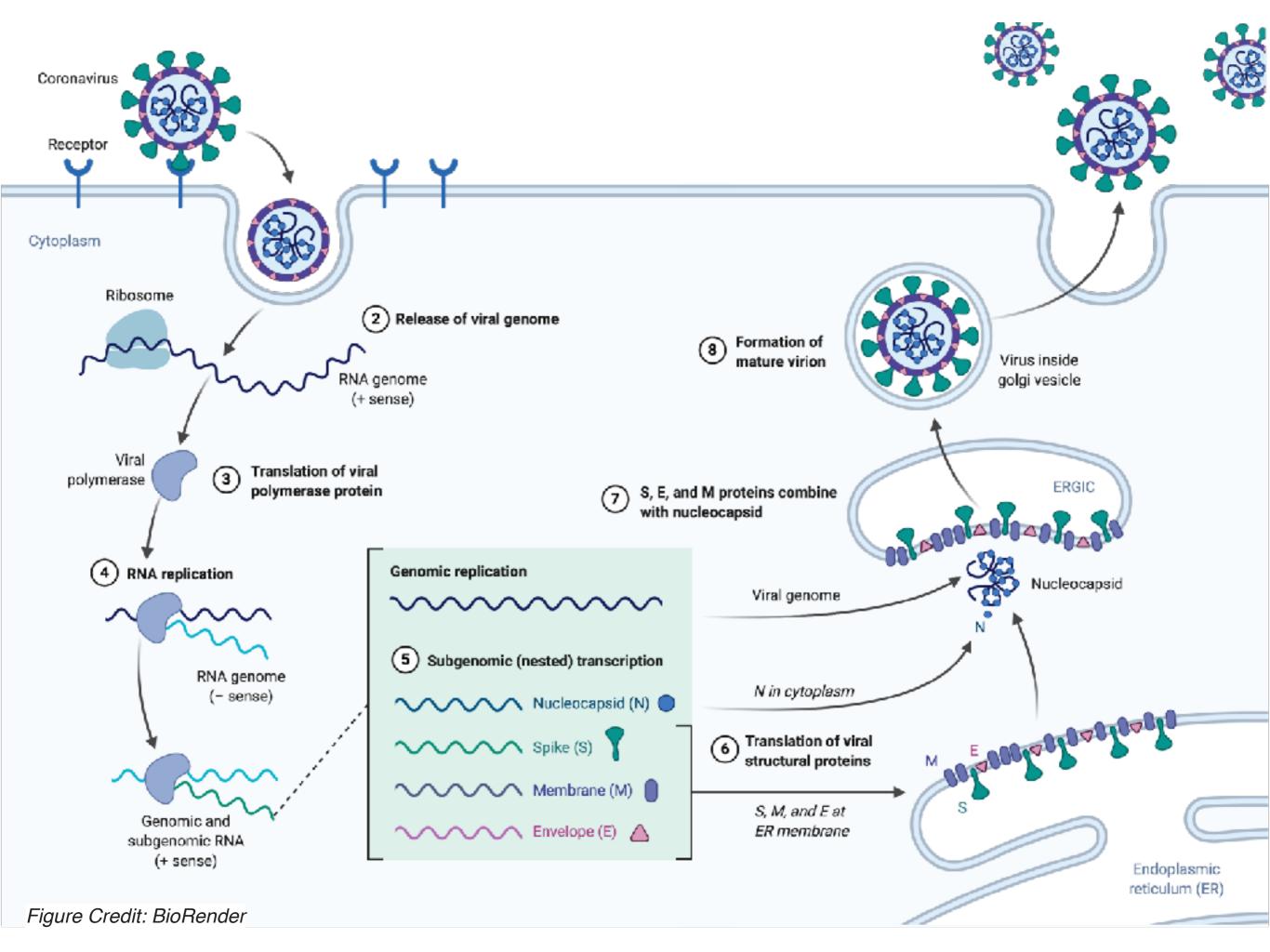
Transcription
RNA polymerase copies DNA sequence into RNA

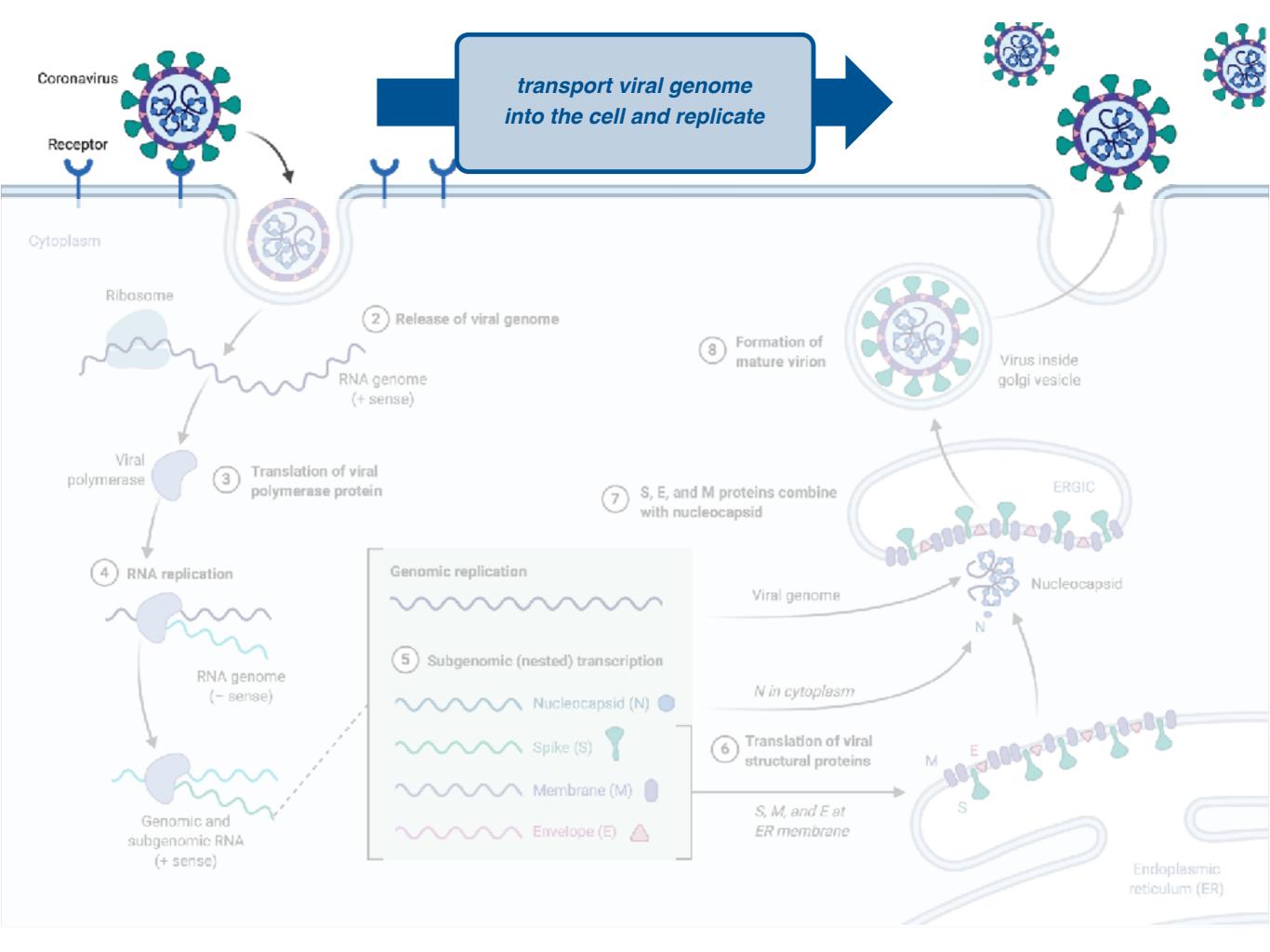
#### Baltimore Classification System



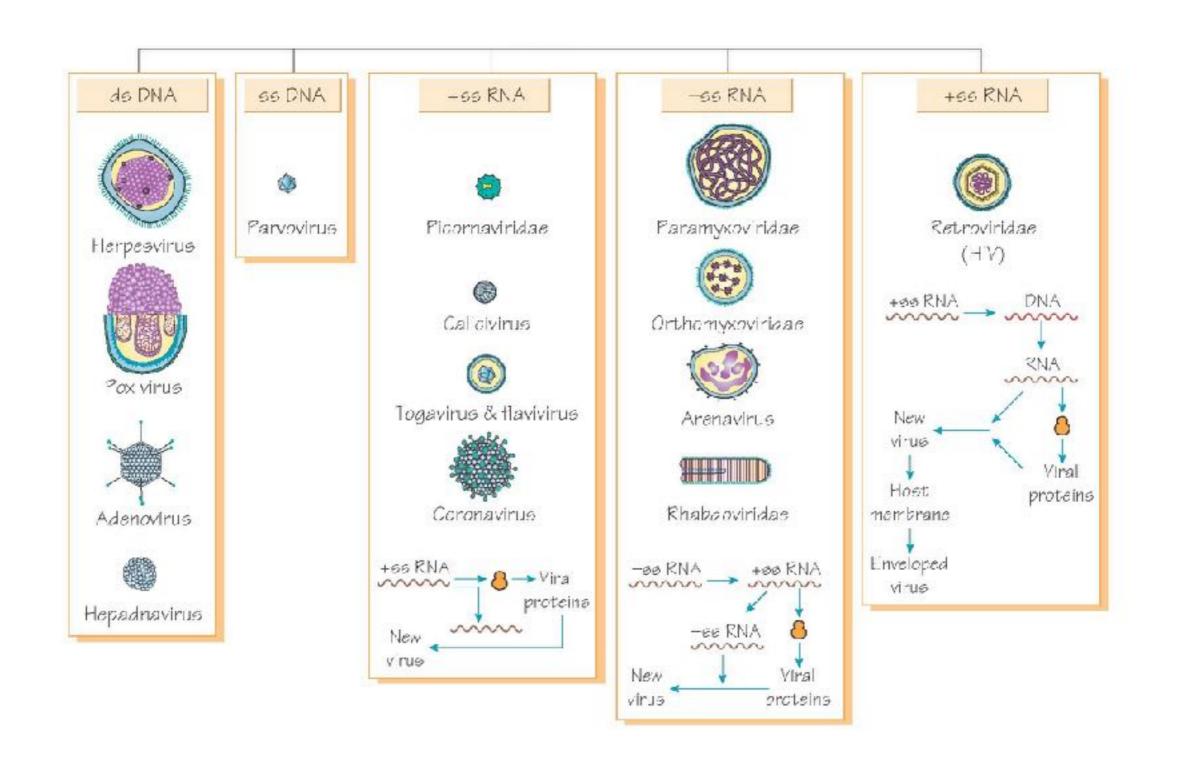
Class V

influenza, ebola, marburg

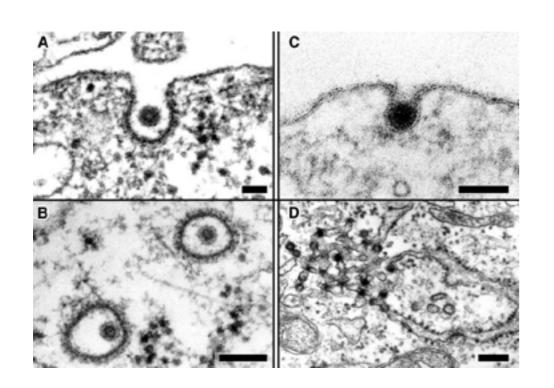




## Examples of Different Classes of Viruses



### Challenges of Understanding Viral Entry



**Understanding Size** 

× 1,000,000 size magnification

virus

animal cell

orange

circus tent

**Techniques** 

light & electron microscopy

in vitro modeling

perterbations via

chemical inhibitors mutant cells or viruses siRNA silencing Expertise

virology

cell & molecular biology

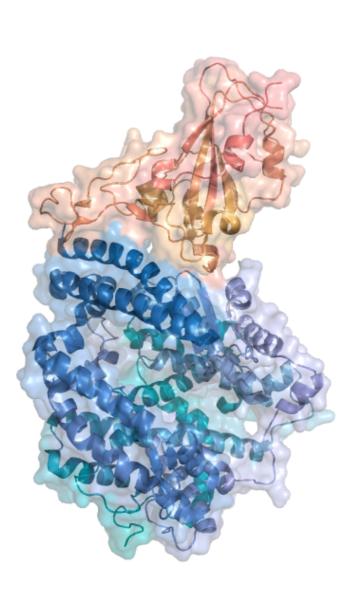
biochemistry & biophysics

systems biology

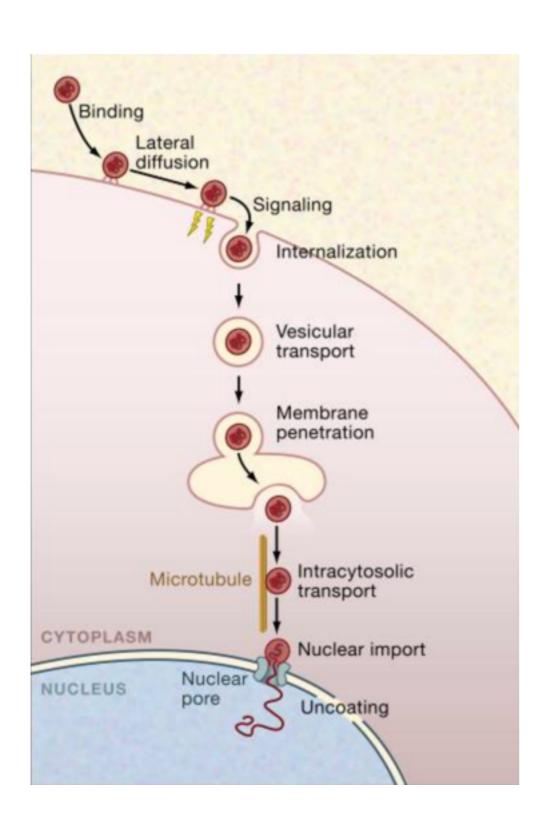
computer science

#### Outline

- Brief Overview of Viruses & Nomenclature
- General Mechanisms of Viral Entry
- Important Factors for Successful Viral Entry
  - ► Attachement
  - ► Signaling
  - ► Endocytosis
  - ► Penetration
  - ▶ Uncoating
- Details Associated Towards SARS-CoV-2 & Other Examples



## Viral Entry Overview



General Lessons Learned

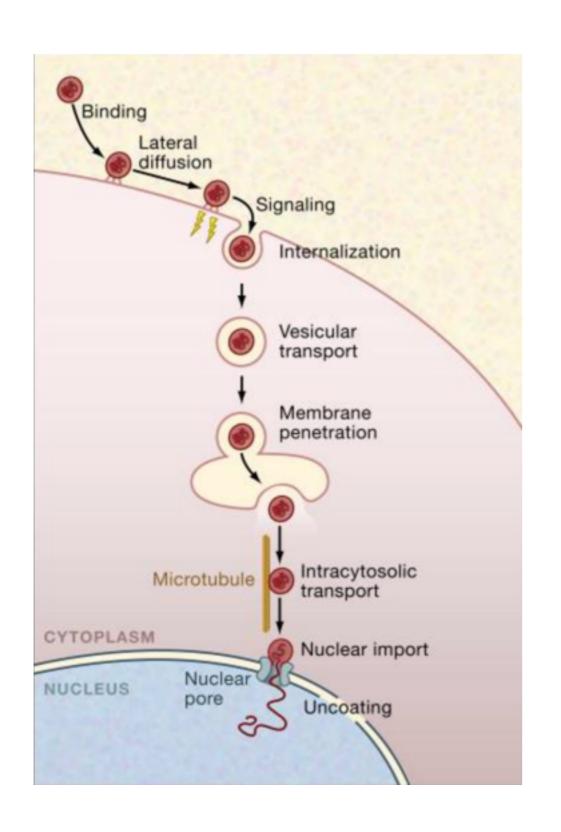
entry into the cell is a process of multiple steps not simple, very complex system

uncoating: built-in program (passive)

virus proteins are meta-stable

proteins respond to cellular cues

## Viral Entry Overview



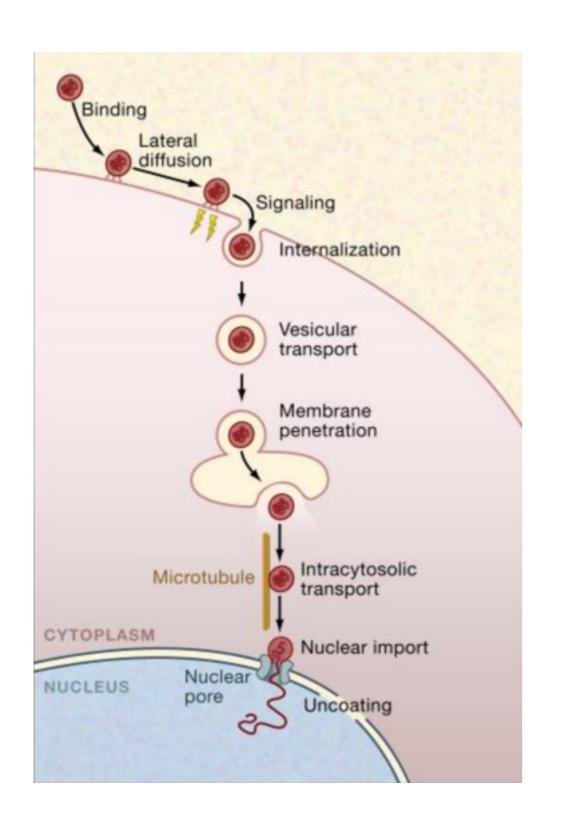
General Lessons Learned

cellular processes & cellular factors are critical components

viruses activate cellular signaling pathways

viruses 'speak' the language of the cell

## Cellular Cues for Viral Entry



what leads to stepwise mechanisms?

binding to cell surface receptors

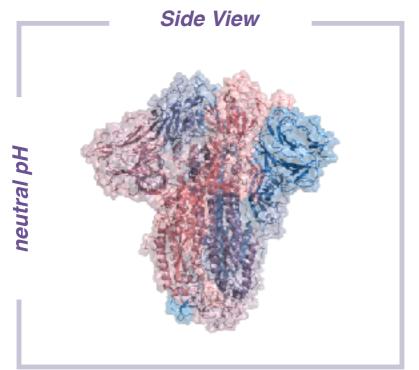
exposure to lower pH

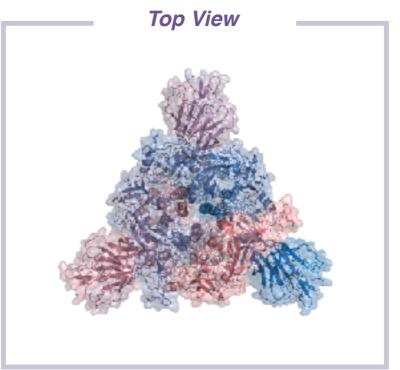
cleavage by cellular proteases

re-entry into a reducing environment

exposure to other enzymes (thiol-oxidoreductases)

## Example of pH Response in SARS-CoV-2 Spike Protein

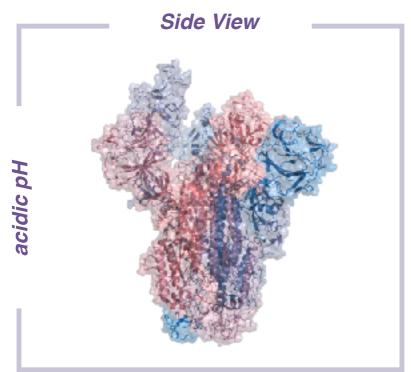


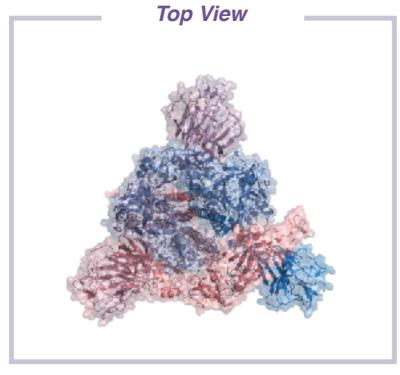


spike protein in novel 2019 SARS-CoV-2 virus

PDB: 6ACC & 6ACD

endocytosis changes viral surroundings to a more acidic (lower pH) environment



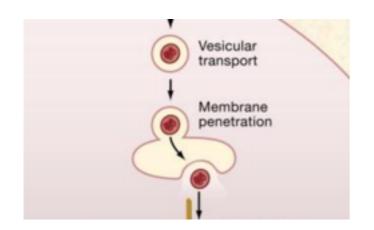


viral proteins exhibit meta-stable state

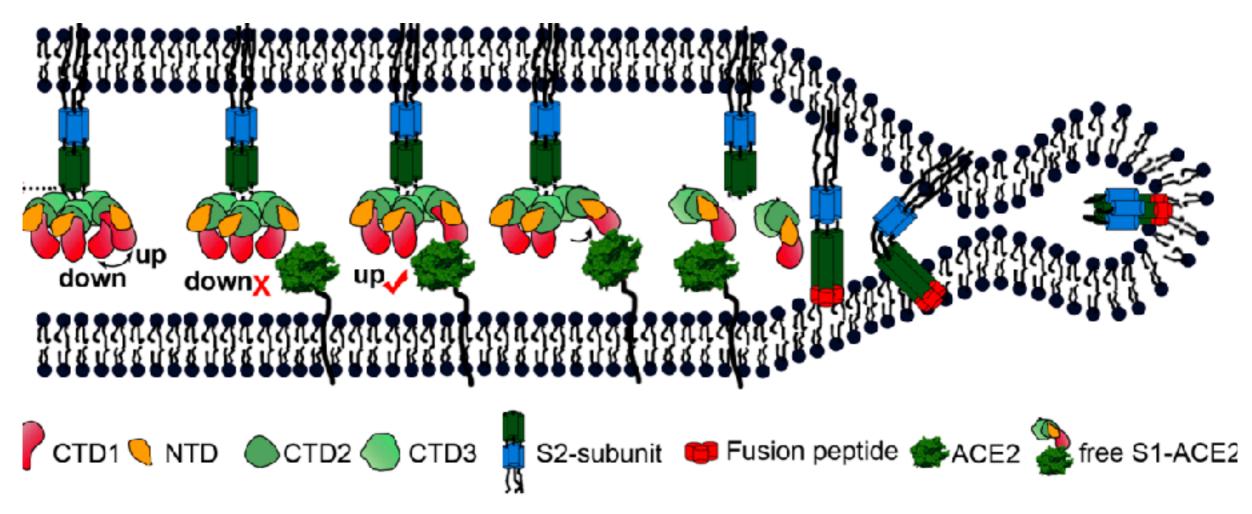


stepwise process for viral entry

#### Example of pH Response in SARS-CoV-2 Spike Protein

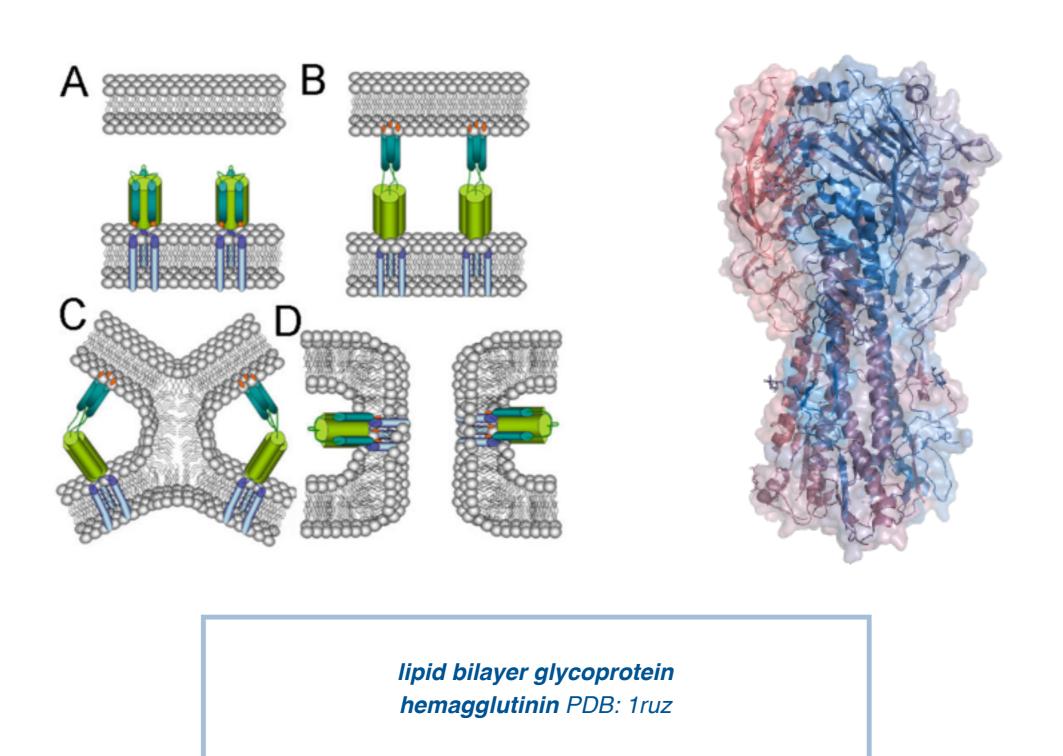


large conformational changes in response to pH facilitates endocytosis

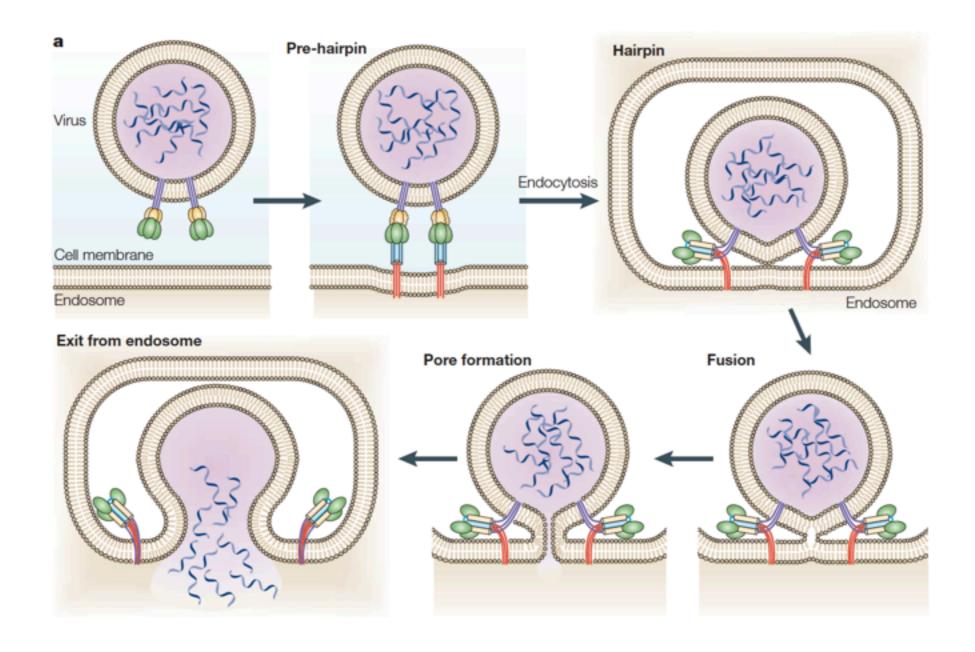


Song, W.; Gui, M.; Wang, X.; Xiang, Y. Cryo-EM structure of the SARS coronavirus spike glycoprotein in complex with its host cell receptor ACE2. DOI: 10.1371.journal.ppat.1007236.

## Example of pH Response in Influenza HA Protein

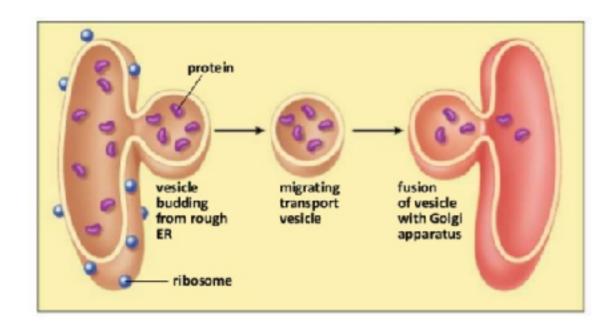


## Example of pH Response in Influenza HA Protein



# Enveloped vs Non-Enveloped Viruses

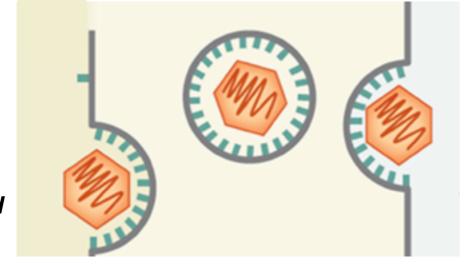
# Vesicle transport



enveloped viruses use lipid bilayer

similar mechanism as a vesicle

mechanism to transport from infected cell to uninfected cell



Infected Cell

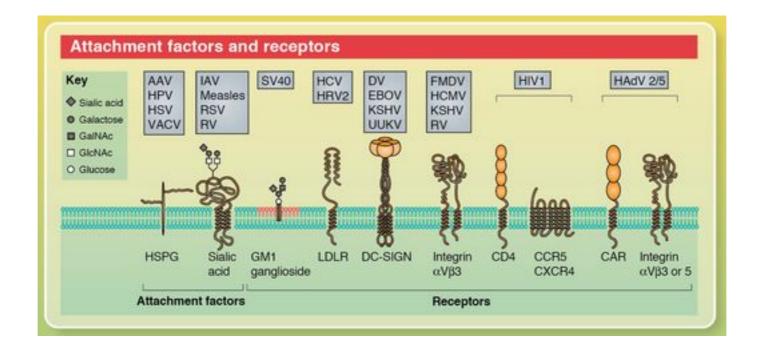
budding

fusion

Uninfected

Cell

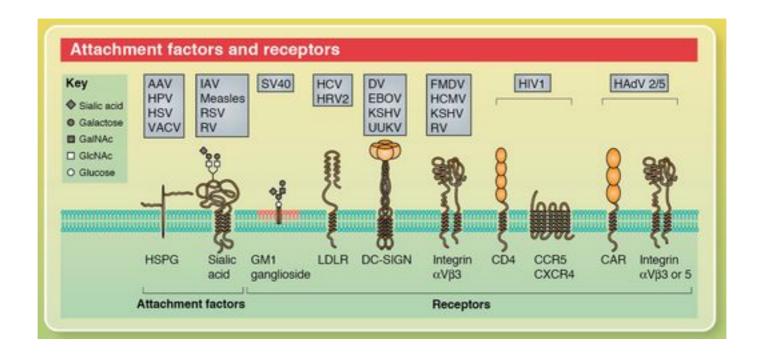
#### a virus cannot infect a cell it cannot bind to



attachement factors: simply bind the virus

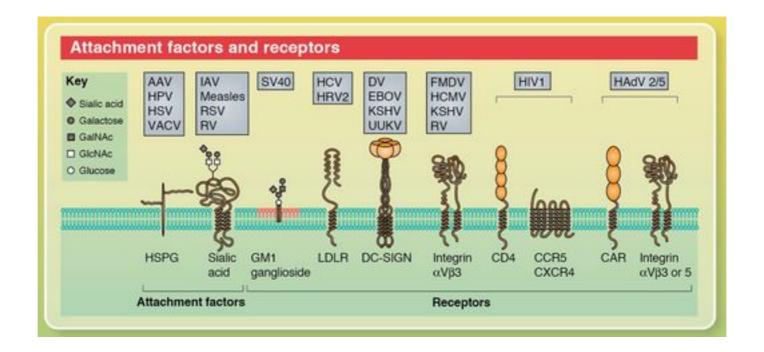
(to increase concentration of viral particles on cell surface)

a virus cannot infect a cell it cannot bind to



receptors: bind virus & provides additional signaling or viral conformational changes (mechanisms vary, but can also start the endocytosis process)

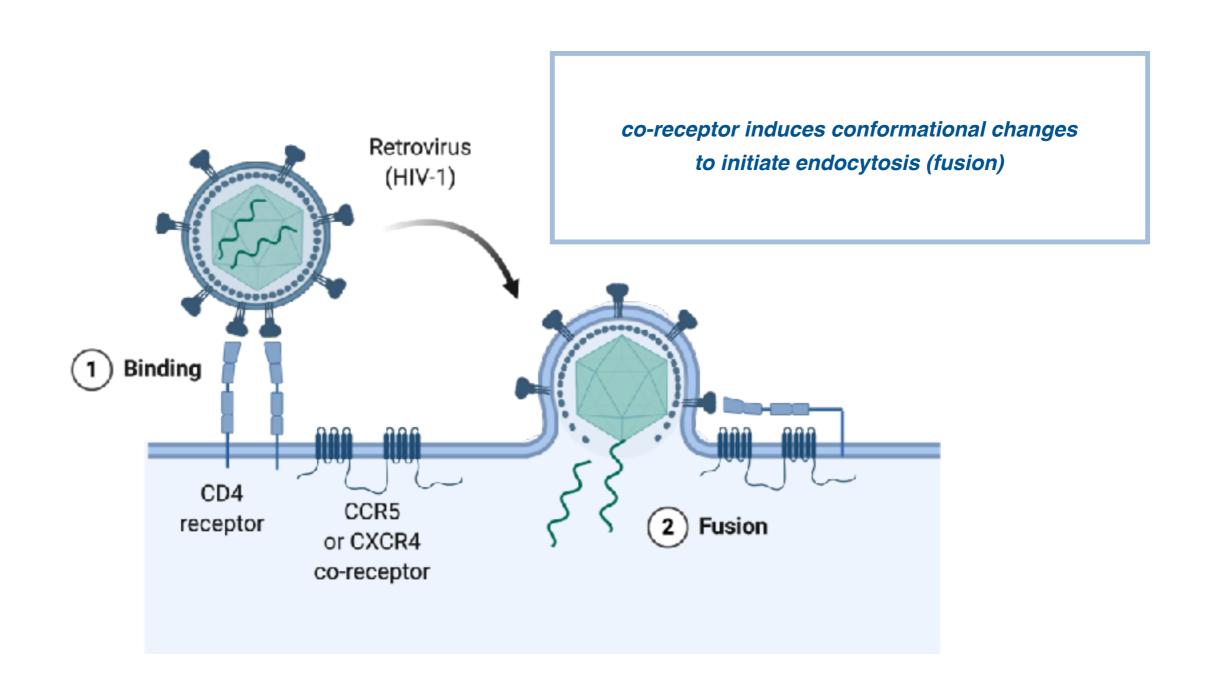
#### a virus cannot infect a cell it cannot bind to



important note: most viruses are known to have more than one type of receptor binding

they can also be **multivalent** (binding to multiple receptor or attachement factors at the same time)

## HIV-1 is Multivalent & Uses Multiple Receptors



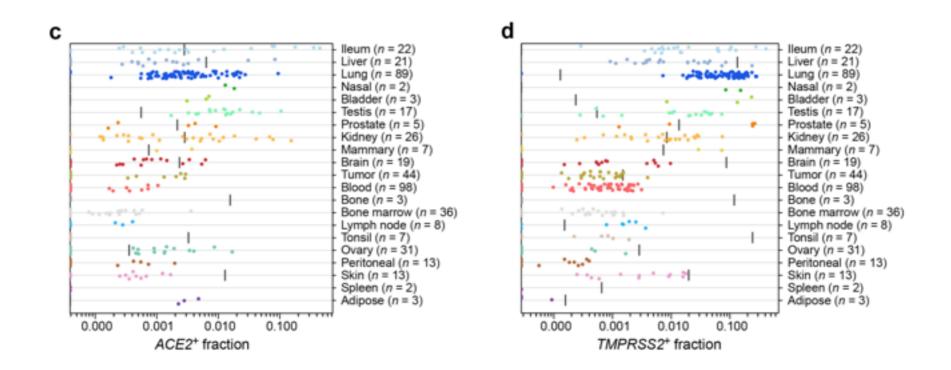
## Examples of Viruses & Their Target Receptors

Virus	Entry protein*	Receptor <sup>‡</sup>	Co-receptor	Alternative receptor §	Notes
Influenza A	Haemagglutinin	Sialic acid (mM)	Unknown	unknown	There are no indications that influenza needs co-receptor(s) for entry
HIV-1	gp160 (gp120)	CD4 (nM)	CCR5, CXCR4, other (nM–μM)	Galactosyl ceramide (μΜ)	Some HIV-1 isolates are CD4-independent and can use CCR5 or CXCR4 as receptors; affinities for coreceptors are higher in the presence of CD4; entry in the absence of CD4 is typically much less efficient.
SARS-CoV	S (S1)	ACE2 (nM)	Unknown	Unknown	
Herpes simplex virus 1 (HSV-1)	Glycoprotein D (gD)	HveA (μM)	Unknown	Unknown	Several other viral (gB, gC, and the heterodimer gH/gL) and cellular (heparin sulphate, nectin-1) receptors are implicated in the complex entry mechanism; a truncated form of gD exhibits 100-fold higher affinity for HveA
Poliovirus 1	Capsid shell (VP1, VP2, VP3)	CD155 (nM–μM)	Unknown	Unknown	CD155 is the receptor for all three serotypes; affinities forcell surface receptors significantly differ from those for soluble receptors and are also temperature-dependent.
Rhinovirus 3 (HRV3)	Capsid shell (VP1, VP2, VP3)	ICAM-1 (μM range)	Unknown	Unknown	Minor-group human rhinoviruses use VLDL-R as a receptor; there are structural similarities between ICAM-1 binding to capsid shell and CD4 binding to gp120.
Adenovirus 2	Fibre, penton base	CAR (nM)	αv integrins	Sialic acid and heparin sulphate proteoglycans	Adenovirus fibre attaches to the CAR and integrins interact with the penton base, leading to internalization.
Reovirus 1	σ1	JAM-1 (nM)	Unknown	Sialic acid	There are structural similarities between adenovirus fibre and $\sigma$ 1, and between CAR and JAM-1. All serotypes bind JAM-1.

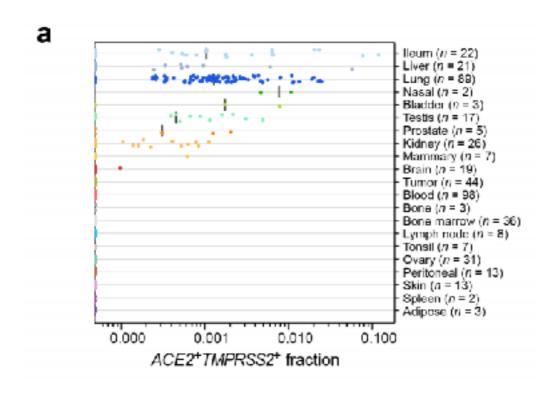
Dimitrov, D. Virus entry: molecular mechanisms and biomedical applications. Nat Rev Microbiol 2, 109–122 (2004).

Hoffmann, M. et. al. SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor. *Cell* 181, 271–280 (2020).

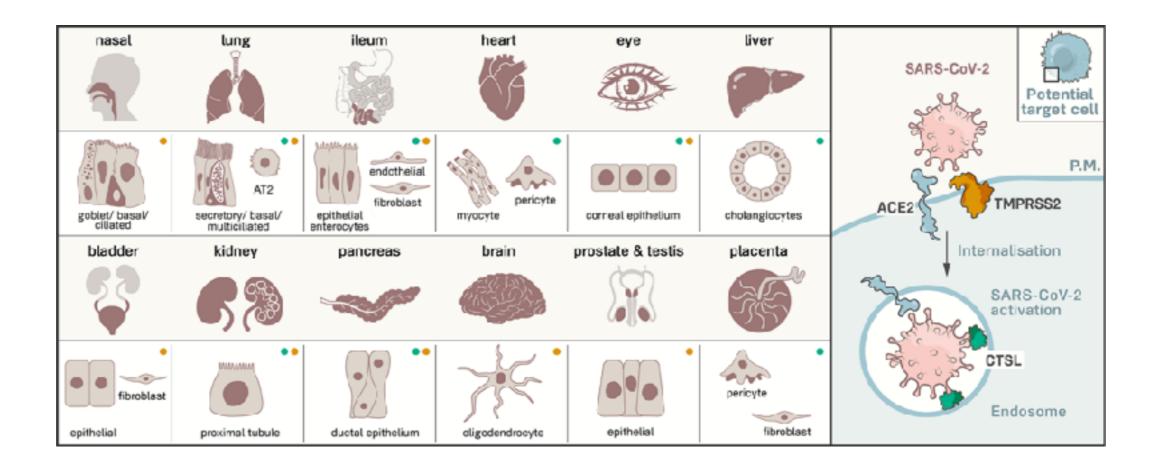
the choice of the cell surface receptor determines which **cell types** and which **species** the virus can infect



the choice of the cell surface receptor determines which **cell types** and which **species** the virus can infect



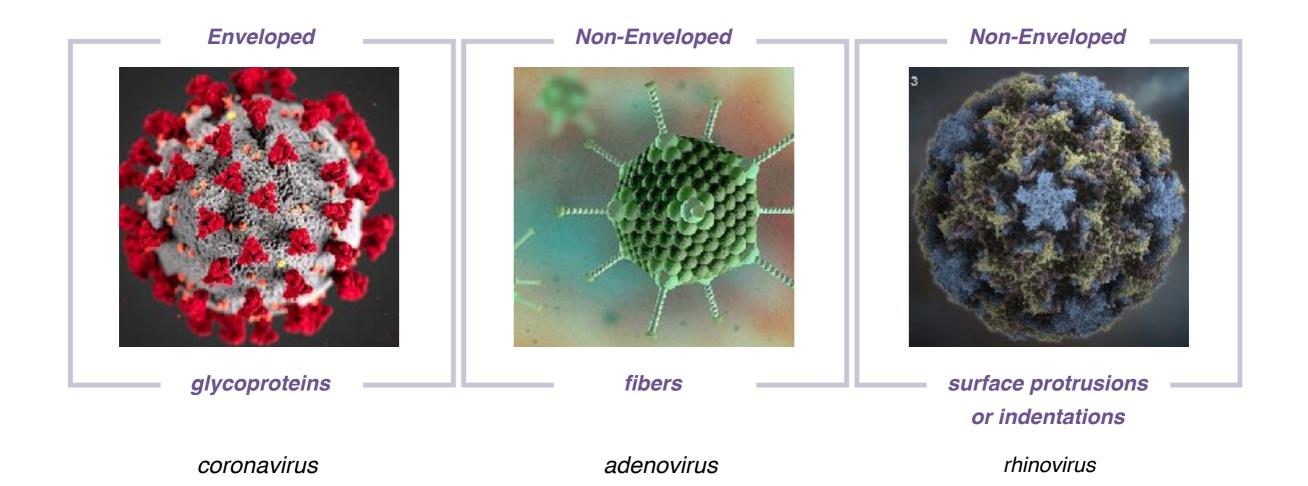
the choice of the cell surface receptor determines which **cell types** and which **species** the virus can infect



Muus, C. et. al. BioRxiv April 21, 2020. DOI: 10.1101/2020.04.19.049254.

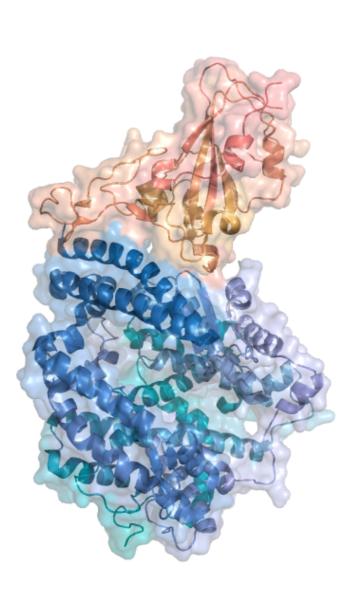
Figure from *The Scientist*. Receptors for SARS-CoV-2 Present in Wide Variety of Human Cells.

# What Binds to Receptors?



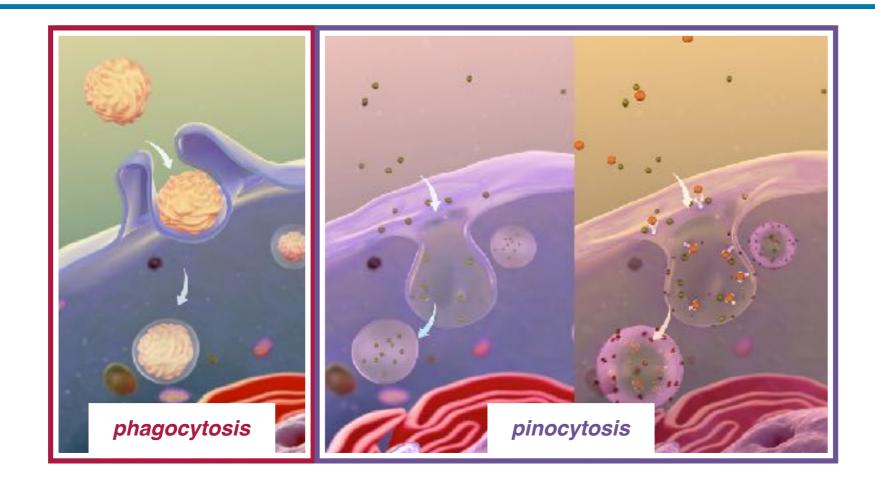
#### Outline

- Brief Overview of Viruses & Nomenclature
- General Mechanisms of Viral Entry
- Important Factors for Successful Viral Entry
  - ► Attachement
  - ► Signaling
  - ► Endocytosis
  - ► Penetration
  - ▶ Uncoating
- Details Associated Towards SARS-CoV-2 & Other Examples



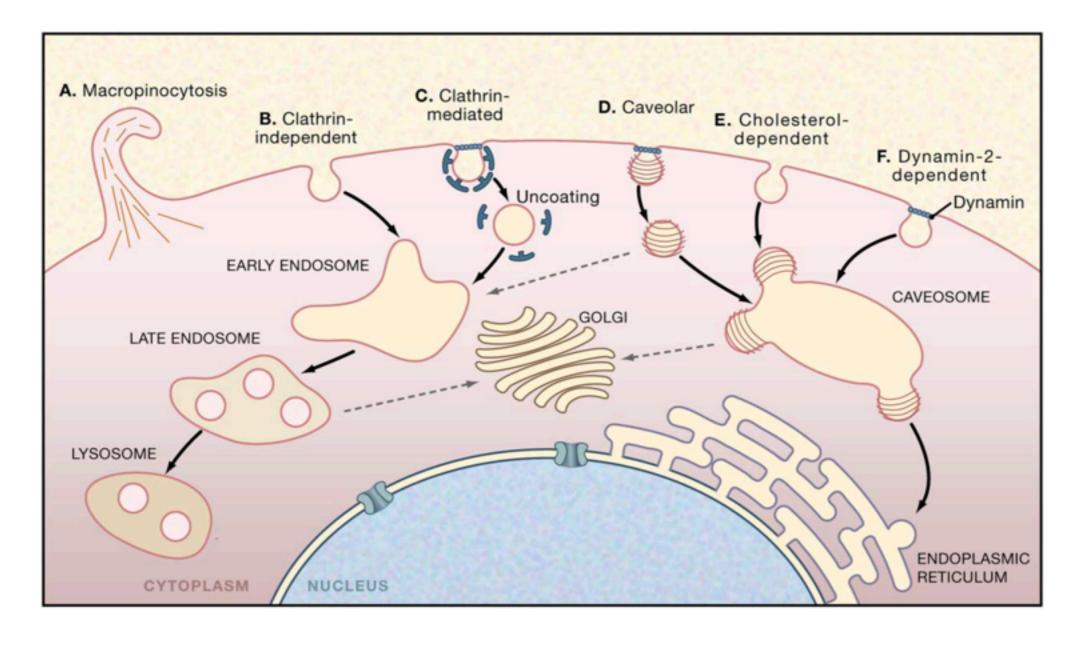
endocytosis is the uptake of fluids, solutes, membrane, and particles by invagination of the plasma membrane and formation of cytoplasmic vesicles

receptor-mediated endocytosis: uptake depends on its binding to a receptor



#### dynamin vs dynamin-independent processes

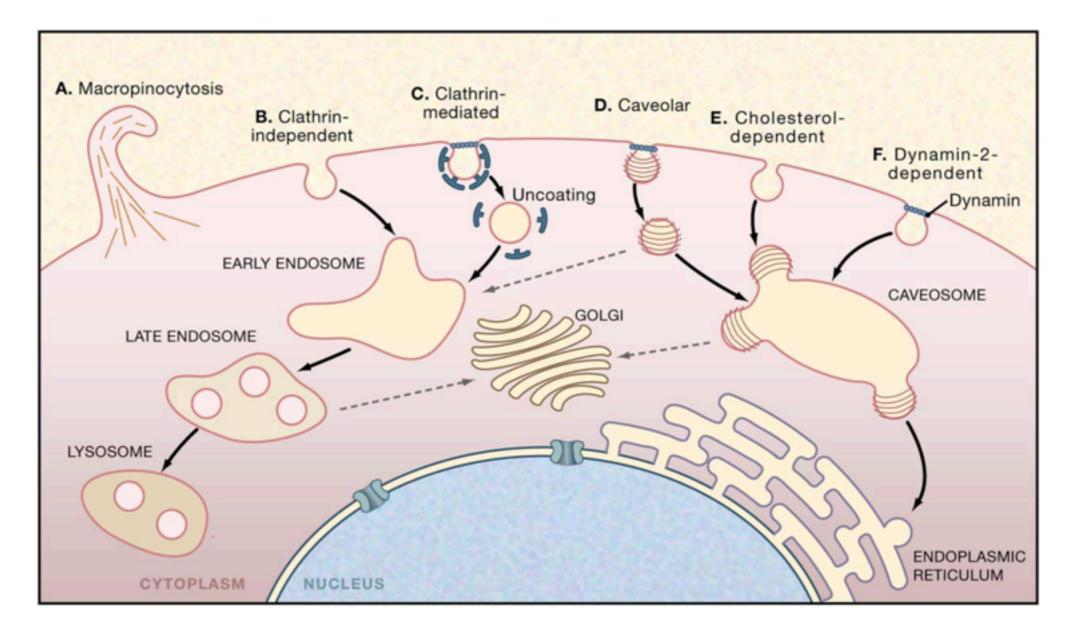
dynamin is a GTPase protein responsibile in the scission of newly formed vesicles



Marsh, M., Helenius, A. Virus Entry: Open Sesame. Cell 124, 729-740 (2006).

#### pH changes

◆ surface (7.0) ◆ early endosome (6.0–6.5) ◆ late endosome (5.0–5.5) ◆ lysosome (4.5–5)

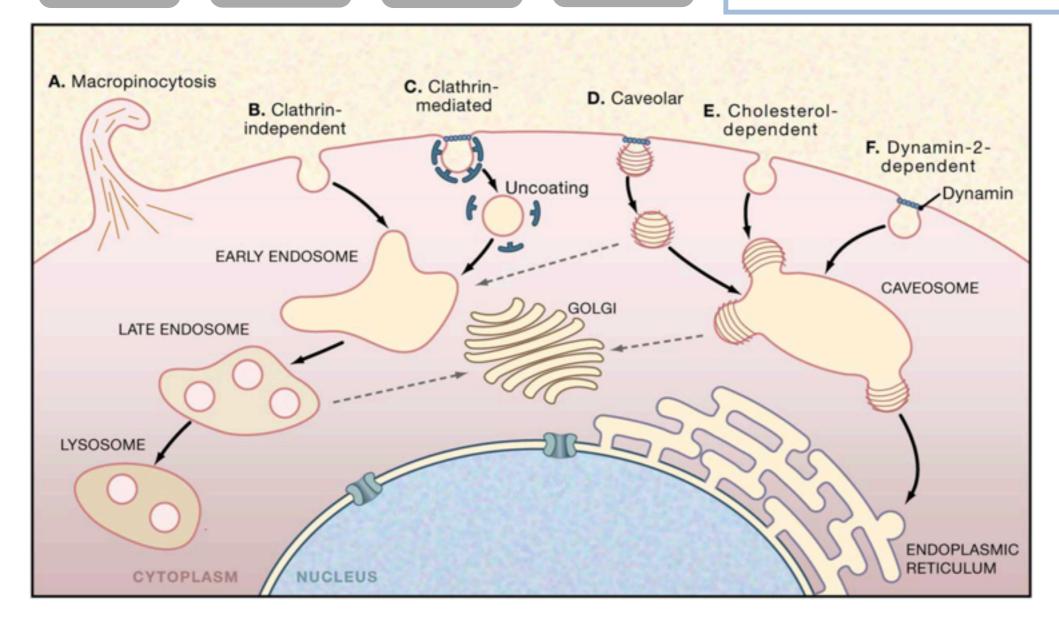


Marsh, M., Helenius, A. Virus Entry: Open Sesame. Cell 124, 729-740 (2006).

vaccinia adeno B HSV1 influenza HPV16 LCMV SFV VSV influenza flavi adeno 2/5

SV40 BK

viruses can have multiple endocytosis mechanisms

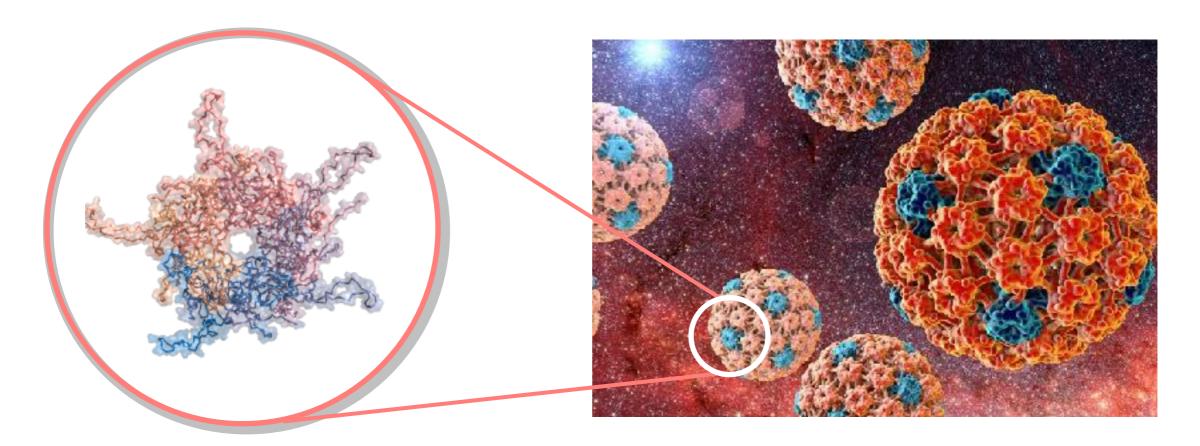


Marsh, M., Helenius, A. Virus Entry: Open Sesame. Cell 124, 729-740 (2006).

#### endocytosis mechanism defines what cellular machinery is being used

- ◆ clathrin, adapters, dynamin, caveolin
- ◆ cytoskeleton (actin, microtubule)
- ◆ signaling molecules (kinases)
- ◆ regulatory factors (Rho GTPases, Rabs, Arfs)
- ♦ ion channels (Na<sup>+</sup>/H<sup>+</sup> exchangers, Ca<sup>+2</sup> channels)
- ◆ acidification machinery (vATPases, CLICs)
- ◆ lipids (cholesterol, phosphatidylinosities)

## Developing a Picture of Viral Entry: Human Papillomavirus 16



endocytosis to late endosome noncoated pit (visually seen by microscopy)

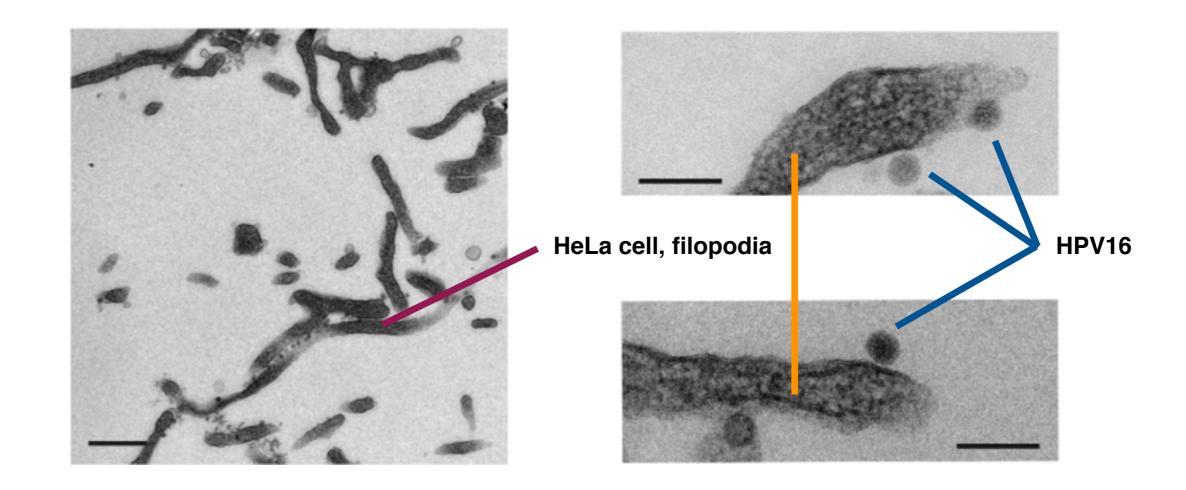
 $t_{1/2}$  endocytosis = 3 hours  $t_{1/2}$  acid-activation = 10 hours

#### not required

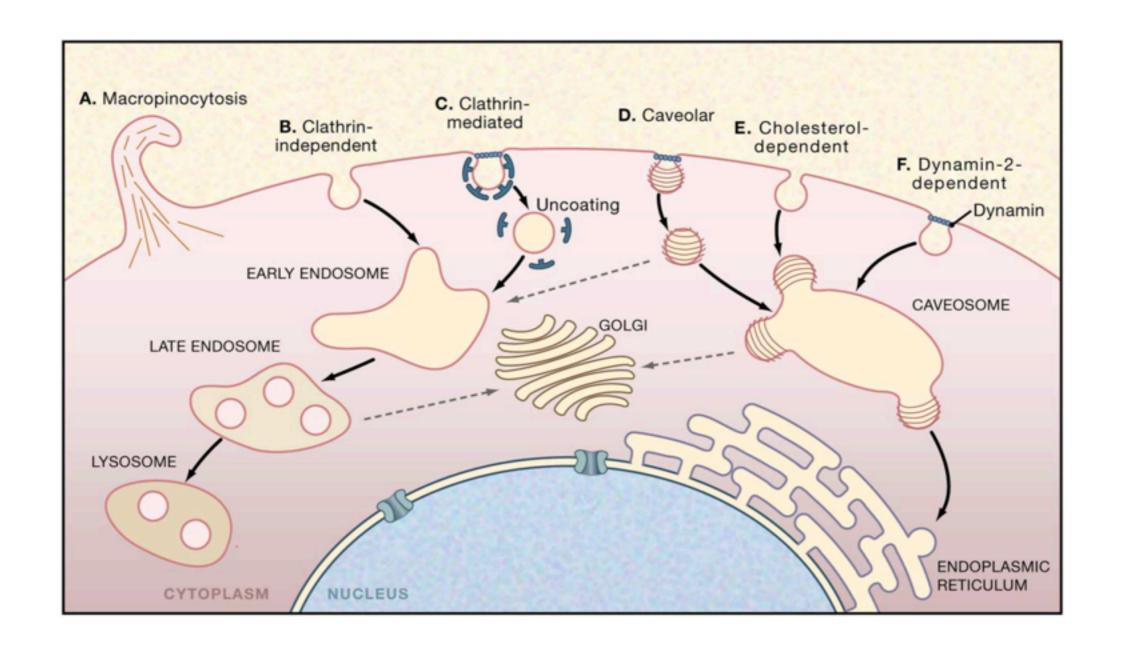
- ◆ clathrin
- **♦** *AP2*
- ♦ dynamin-2
- **♦** *Arf 6*
- ◆ cholesterols or lipid rafts
- ◆ caveolin, flotillin
- ◆ cdc42 or rac1

#### required

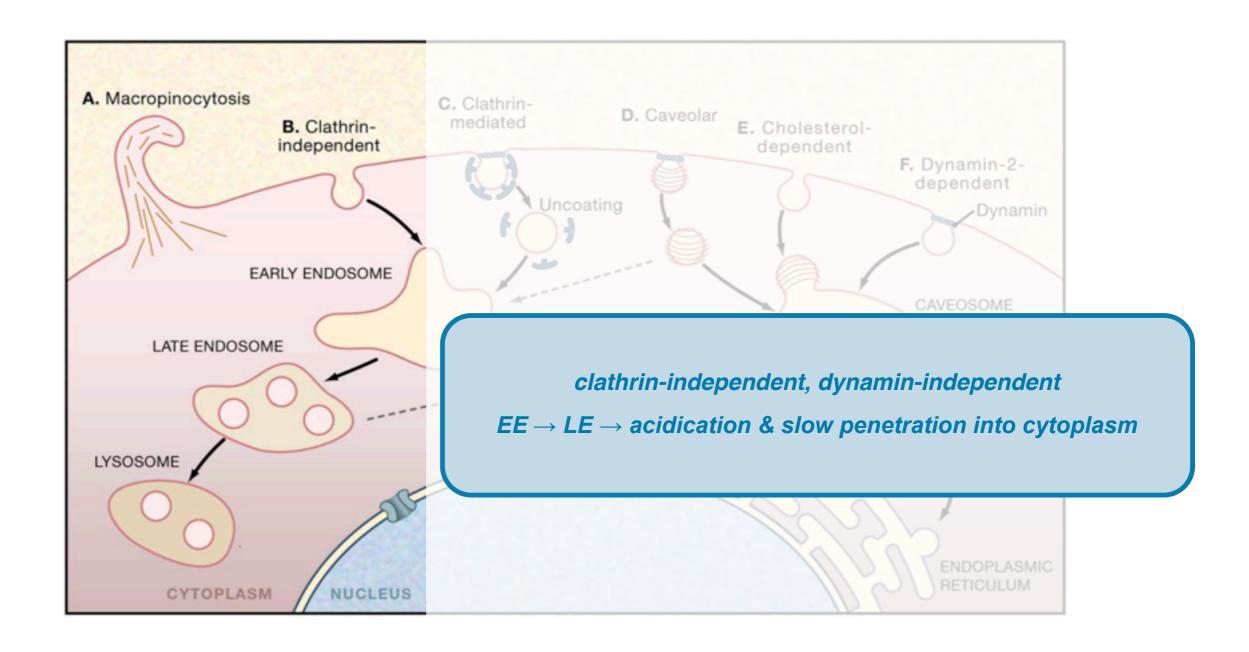
- ◆ acidification
- ◆ protein kinase C zeta
- ◆ Tyr-kinases & phosphatases
- ◆ PI(3)kinase
- ◆ N-WASP
- ◆ Na<sup>+</sup>/H<sup>+</sup> exchangers
- ◆ actin & microtubules
- ◆ Arf 1
- ♦ Rab5, Rab34



Schelhaas, M.; Ewers, H.; Rajamäki, M.-L.; Day, P. M.; Schiller, J. T.; Helenius, A. (2008) Human Papillomavirus Type 16 Entry: Retrograde Cell Surface Transport along Actin-Rich Protrusions. PLoS Pathog 4(9): e1000148. DOI: 10.1371/journal.ppat.1000148

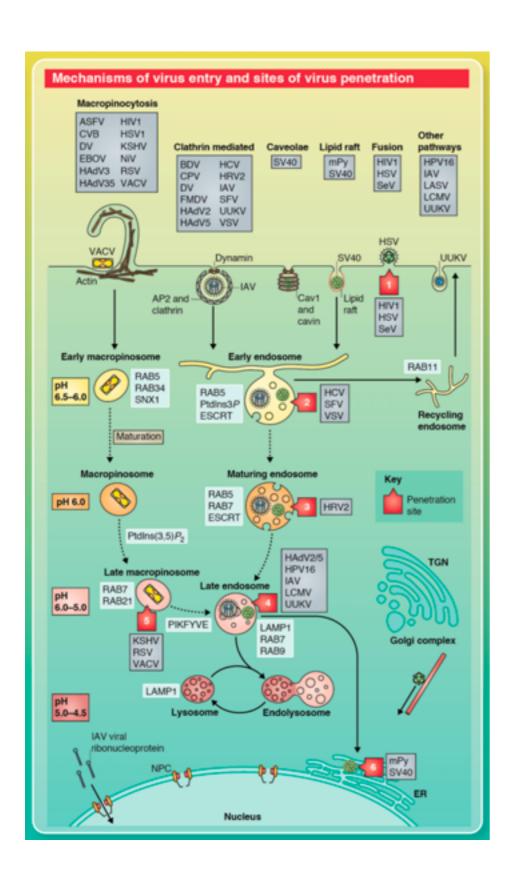


Schelhaas, M.; Ewers, H.; Rajamäki, M.-L.; Day, P. M.; Schiller, J. T.; Helenius, A. (2008) Human Papillomavirus Type 16 Entry: Retrograde Cell Surface Transport along Actin-Rich Protrusions. PLoS Pathog 4(9): e1000148. DOI: 10.1371/journal.ppat.1000148



Schelhaas, M.; Ewers, H.; Rajamäki, M.-L.; Day, P. M.; Schiller, J. T.; Helenius, A. (2008) Human Papillomavirus Type 16 Entry: Retrograde Cell Surface Transport along Actin-Rich Protrusions. PLoS Pathog 4(9): e1000148. DOI: 10.1371/journal.ppat.1000148

#### Cell Penetration



penetration: the event that allows the viral genome to move into the cytosol

during viral entry, virus is mostly passive

mostly responding to cellular cues & machinery

penetration requires the viral participation

penetration can occur anywhere along the endocytic route cell membrane, EE, LE, Lysosome, ER

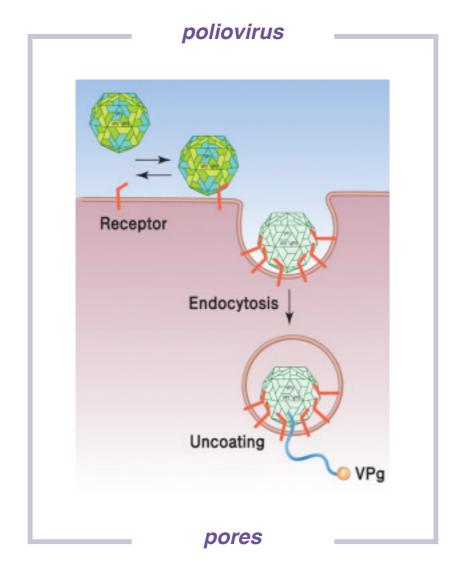
membrane fusion (enveloped virus)

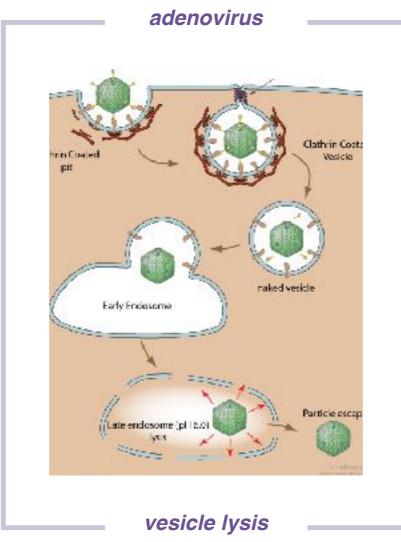
vacuole lysis

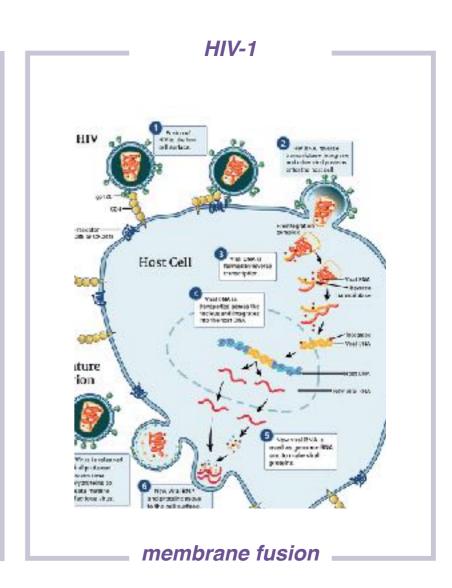
pore formation

ER associated degradation pathways

# Examples of Viral Penetration

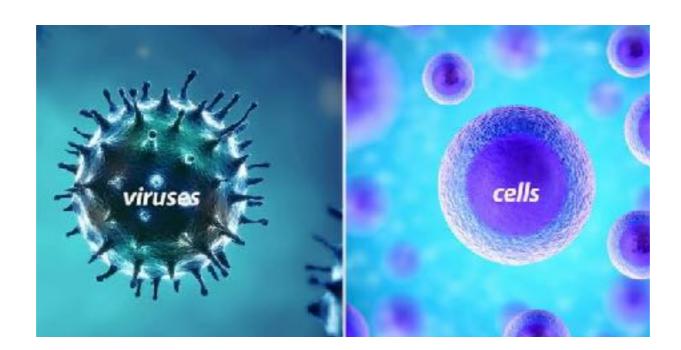






# A Thought

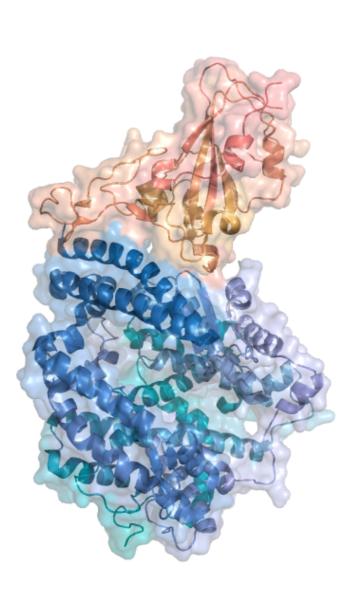
to understand a virus on must understand the cell that it infects



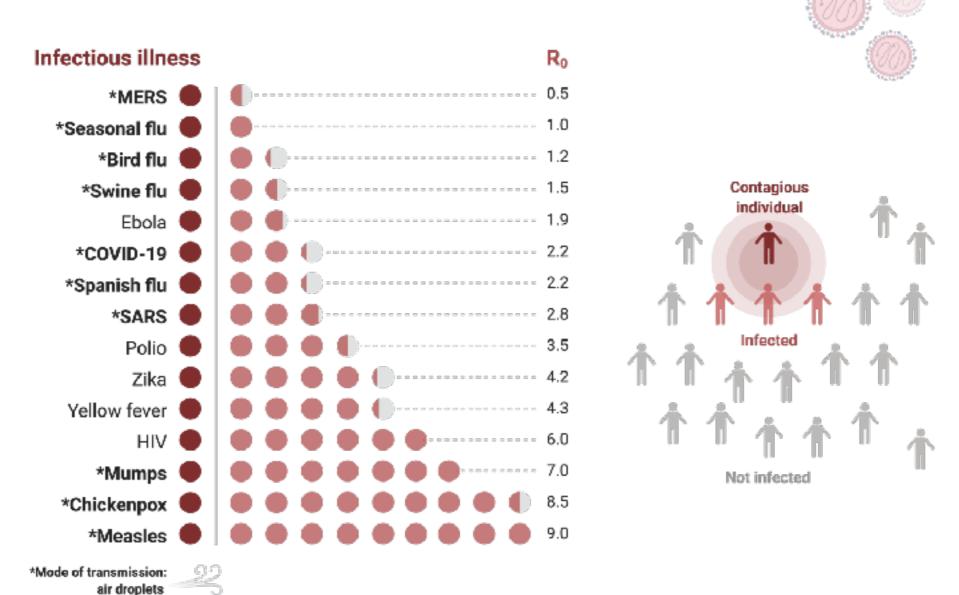
one can understand and learn about cells by studying viruses

## Outline

- Brief Overview of Viruses & Nomenclature
- General Mechanisms of Viral Entry
- Important Factors for Successful Viral Entry
  - ► Attachement
  - ► Signaling
  - ► Endocytosis
  - ► Penetration
  - ▶ Uncoating
- Details Associated Towards SARS-CoV-2 & Other Examples



#### Average Basic Reproduction Number (R<sub>0</sub>) of common viral infections



The **average basic reproduction number** (R₀) is an epidemiologic metric that describes the transmissibility of infectious agents. R₀ measures the expected number of secondary infections produced by a single infectious individual in a susceptible population during the mean infectious period.

AIDS (40 million HIV-1 infected, 25 million deaths)

Hepatitis B Virus (240 million chronically infected worldwide (2.2 million US) 25% will succumb to liver disease or cancer)

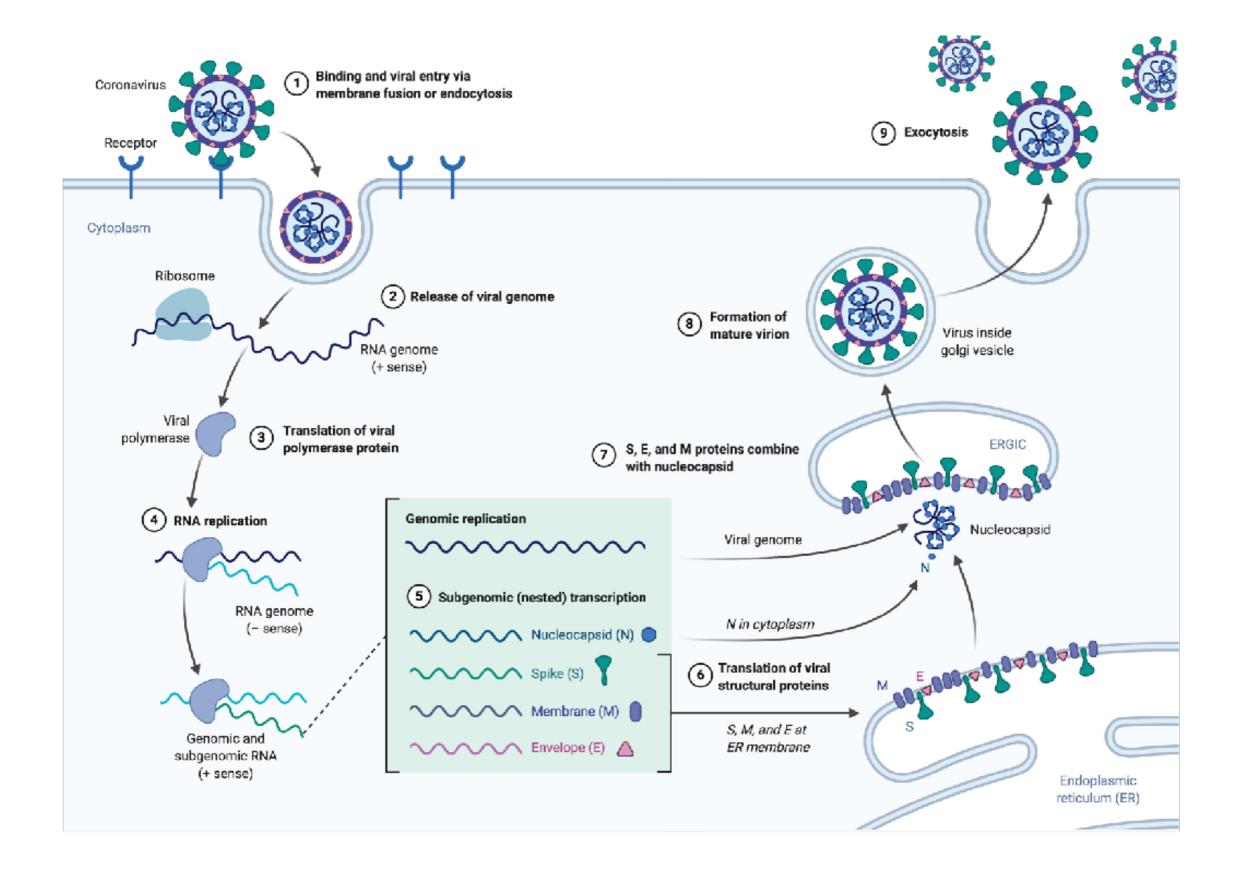
Rotavirus (> 200,000 children deaths yearly)

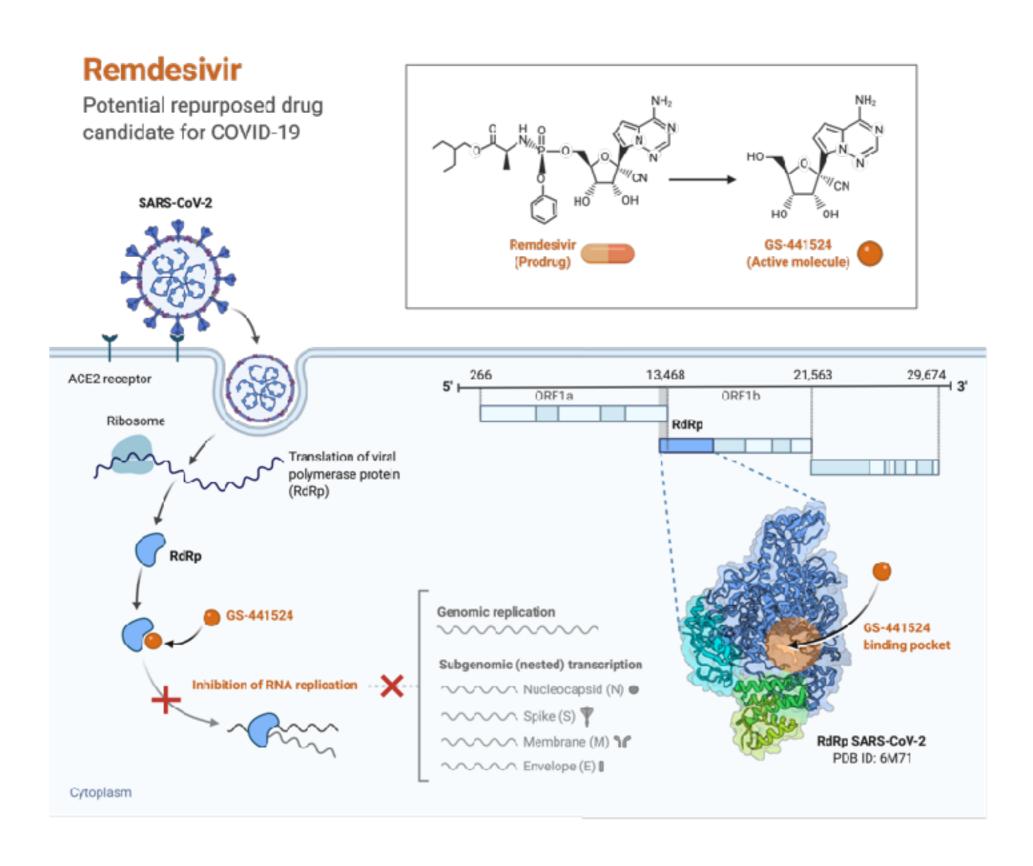
Influenza (> 39 million deaths, 1918–19)

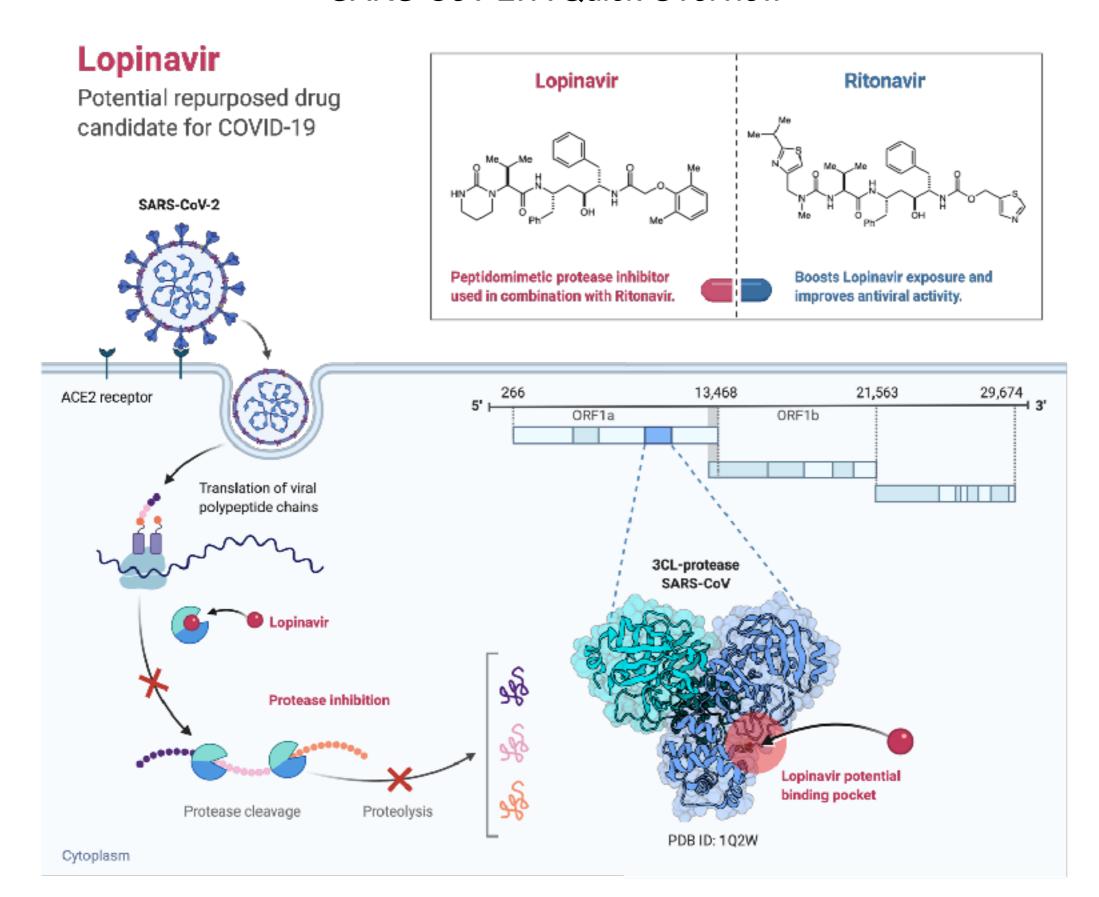
Avian Influenza (H5N1) (pandemic threat in 2005)

SARS-CoV-2 (3.5 million infected, 250,000 deaths, declared pandemic in 2020)

Disease	Flu	COVID-19	SARS	MERS
Disease Causing Pathogen	Influenza virus	SARS-CoV-2	SARS-CoV	MERS-CoV
R <sub>0</sub> Basic Reproductive Number  CFR Case Fatality Rate  Incubation Time	1. <b>3</b>	2.0 - 2.5 *	3	<b>0.3 - 0.8</b>
	0.05 - 0.1%	~3.4% *	9.6 - 11%	34.4%
	1 - 4 days	4 - 14 days *	2 - 7 days	6 days
Hospitalization Rate Community Attack Rate	2%	~19% <b>*</b>	Most cases	Most cases
	10 - 20%	30 - 40% <b>*</b>	10 - 60%	4 - 13%
Annual Infected (global)  Annual Infected (US)  Annual Deaths (US)	~ 1 billion	3.5 million (5/20)	8098 (in 2003)	420
	10 - 45 million	1.18 million (5/20)	8 (in 2003)	2 (in 2014)
	10,000 - 61,000	68,000 (5/20)	None	None







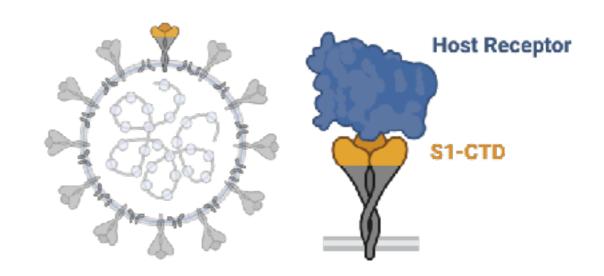
bioRxiv preprint doi: https://doi.org/10.1101/2020.03.22.002386. The copyright holder for this preprint (which was not peer-reviewed) is the author/funder. It is made available under a CC-BY 4.0 International license.

#### A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals Drug Targets and Potential Drug-Repurposing

David E. Gordon<sup>1,2,3,4</sup>, Gwendolyn M. Jang<sup>1,2,3,4</sup>, Mehdi Bouhaddou<sup>1,2,3,4</sup>, Jiewei Xu<sup>1,2,3,4</sup>, Kirsten Obernier<sup>1,2,3,4</sup>, Matthew J. O'Meara<sup>5</sup>, Jeffrey Z. Guo<sup>1,2,3,4</sup>, Danielle L. Swaney<sup>1,2,3,4</sup>, Tia A. Tummino<sup>1,2,6</sup>, Ruth Huettenhain<sup>1,2,3,4</sup>, Robyn M. Kaake<sup>1,2,3,4</sup>, Alicia L. Richards<sup>1,2,3,4</sup>, Beril Tutuncuoglu<sup>1,2,3,4</sup>, Helene Foussard<sup>1,2,3,4</sup>, Jyoti Batra<sup>1,2,3,4</sup>, Kelsey Haas<sup>1,2,3,4</sup>, Maya Modak<sup>1,2,3,4</sup>, Minkyu Kim<sup>1,2,3,4</sup>, Paige Haas<sup>1,2,3,4</sup>, Benjamin J. Polacco<sup>1,2,3,4</sup>, Hannes Braberg<sup>1,2,3,4</sup>, Jacqueline M. Fabius<sup>1,2,3,4</sup>, Manon Eckhardt<sup>1,2,3,4</sup>, Margaret Soucheray<sup>1,2,3,4</sup>, Melanie J. Bennett<sup>1,2,3,4</sup>, Merve Cakir<sup>1,2,3,4</sup>, Michael J. McGregor<sup>1,2,3,4</sup>, Qiongyu Li<sup>1,2,3,4</sup>, Zun Zar Chi Naing<sup>1,2,3,4</sup>, Yuan Zhou<sup>1,2,3,4</sup>, Shiming Peng<sup>1,2,6</sup>, Ilsa T. Kirby<sup>1,4,7</sup>, James E. Melnyk<sup>1,4,7</sup>, John S. Chorba<sup>1,4,7</sup>, Kevin Lou<sup>1,4,7</sup>, Shizhong A. Dai<sup>1,4,7</sup>, Wenqi Shen<sup>1,4,7</sup>, Ying Shi<sup>1,4,7</sup>, Ziyang Zhang<sup>1,4,7</sup>, Inigo Barrio-Hernandez<sup>8</sup>, Danish Memon<sup>8</sup>, Claudia Hernandez-Armenta<sup>8</sup>, Christopher J.P. Mathy<sup>1,9,10,2</sup>, Tina Perica<sup>1,2,9</sup>, Kala B. Pilla<sup>1,2,9</sup>, Sai J. Ganesan<sup>1,2,9</sup>, Daniel J. Saltzberg<sup>1,2,9</sup>, Rakesh Ramachandran<sup>1,2,9</sup>, Xi Liu<sup>1,2,6</sup>, Sara B. Rosenthal<sup>11</sup>, Lorenzo Calviello<sup>12</sup>, Srivats Venkataramanan<sup>12</sup>, Jose Liboy-Lugo<sup>12</sup>, Yizhu Lin<sup>12</sup>, Stephanie A. Wankowicz<sup>1,13,9</sup>, Markus Bohn<sup>6</sup>, Phillip P. Sharp<sup>4</sup>, Raphael Trenker<sup>14</sup>, Janet M. Young<sup>15</sup>, Devin A. Cavero<sup>3</sup>, Joseph Hiatt<sup>16,3</sup>, Theodore L. Roth<sup>16,3</sup>, Ujjwal Rathore<sup>3</sup>, Advait Subramanian<sup>1,17</sup>, Julia Noack<sup>1,17</sup>, Mathieu Hubert<sup>18</sup>, Ferdinand Roesch<sup>19</sup>, Thomas Vallet<sup>19</sup>, Björn Meyer<sup>19</sup>, Kris M. White<sup>20</sup>, Lisa Miorin<sup>20</sup>, Oren S. Rosenberg<sup>21,22,23</sup>, Kliment A Verba<sup>1,2,6</sup>, David Agard<sup>1,24</sup>, Melanie Ott<sup>3,21</sup>, Michael Emerman<sup>25</sup>, Davide Ruggero<sup>26,27,4</sup>, Adolfo García-Sastre<sup>20</sup>, Natalia Jura<sup>1,14,4</sup>, Mark von Zastrow<sup>1,1,4,28</sup>, Jack Taunton<sup>1,2,4</sup>, Alan Ashworth<sup>1,27</sup>, Olivier Schwartz<sup>18</sup>, Marco Vignuzzi<sup>19</sup>, Christophe d'Enfert<sup>29</sup>, Shaeri Mukherjee<sup>1,17</sup>, Matt Jacobson<sup>6</sup>, Harmit S. Malik<sup>15</sup>, Danica G. Fujimori<sup>1,4,6</sup>, Trey Ideker<sup>30</sup>, Charles S. Craik<sup>6,27</sup>, Stephen Floor<sup>12,27</sup>, James S. Fraser<sup>1,2,9</sup>, John Gross<sup>1,2,6</sup>, Andrej Sali<sup>1,2,6,9</sup>, Tanja Kortemme<sup>1,9,10,2</sup>, Pedro Beltrao<sup>8</sup>, Kevan Shokat<sup>1,4,7</sup>, Brian K. Shoichet<sup>1,2,6</sup>, Nevan J. Krogan<sup>1,2,3,4</sup>

# Receptor Binding Motifs (RBM)

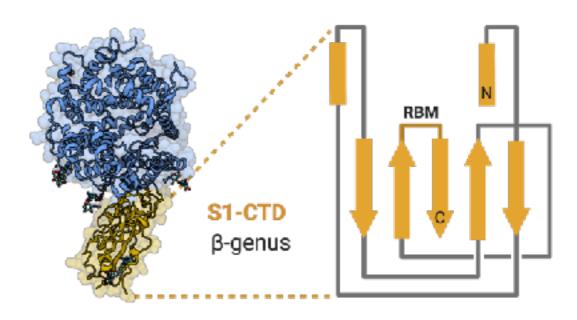
SARS-CoV-2 spike protein (S1-CTD)



# Host Receptor RBM2 RBM1 RBM3 RBM3 RBM3 RBM3

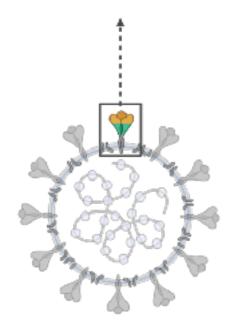
PDB ID: 3KBH PDB ID: 2AJF

#### **Host Receptor**

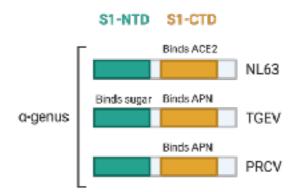


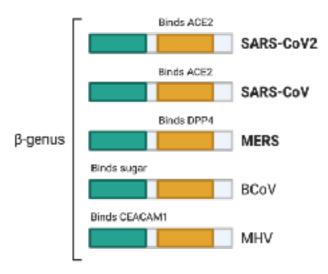
#### Schematic of spike-receptor binding mechanism

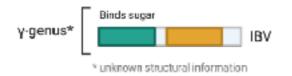
# Host Receptor S1-CTD S1-NTD RBD



#### Receptor Binding Domain (RBD)

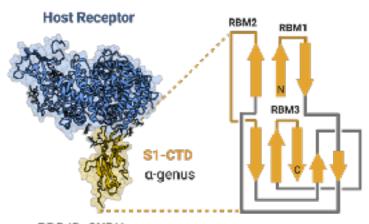




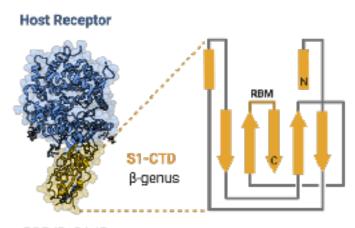


#### Receptor Binding Motifs (RBM)

Receptor binding motifs of S1-CTD bind to host receptor



PDB ID: 3KBH



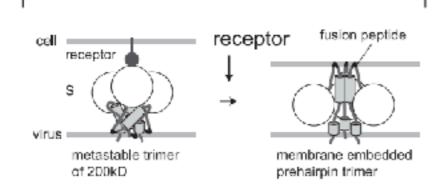
PDB ID: 2AJF

JOURNAL OF VIROLOGY, Nov. 2009, p. 11133–11141 0022-538X/09/\$12.00 doi:10.1128/JVI.00959-09 Copyright © 2009, American Society for Microbiology. All Rights Reserved. Vol. 83, No. 21

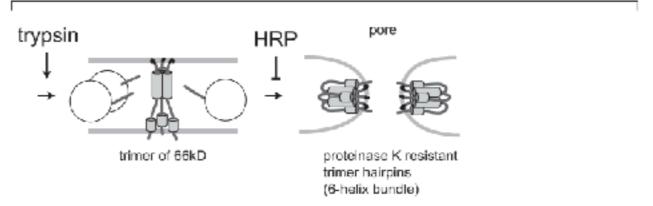
### 

Shutoku Matsuyama\* and Fumihiro Taguchi†

#### Step 1

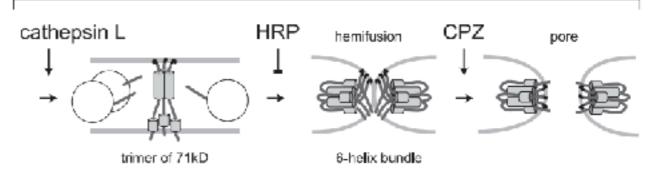


#### Step 2 triggered by trypsin



serine protease TMPRSS2 or cathepsin CTSL

#### Step 2 triggered by cathepsin L

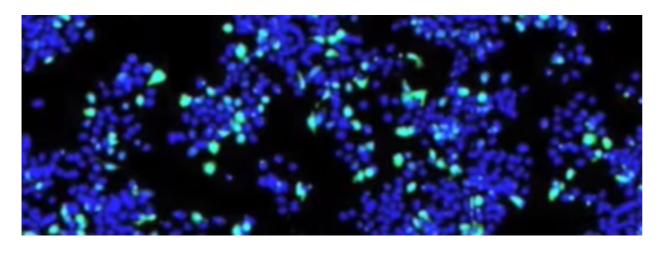


# Current State-of-the-Art for Understanding Systems Biology in Virology

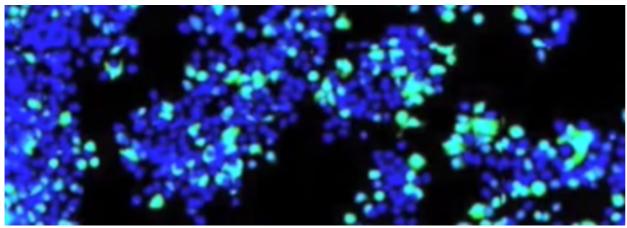
#### centered on siRNA silencing & high throughput experimentation

- ♦ 7000 druggable genes
- ◆ HTE using 384 well plates
- ◆ 3 siRNA per gene (testing in triplicate)
- ◆ mature viruses (MV) expressing GFP (green fluorescent protein)
- ◆ automated microscopy (hits contain no green)
- ♦ Hit = 2/3 or 3/3 siRNA causing 50% or less infection compared to controls

# Current State-of-the-Art for Understanding Systems Biology in Virology



control all normal human cell genes expressed



siRNA knockout of one gene increased viral replication (rare)

these genes are important for viral replication

siRNA knockout of one gene decrease in viral replication

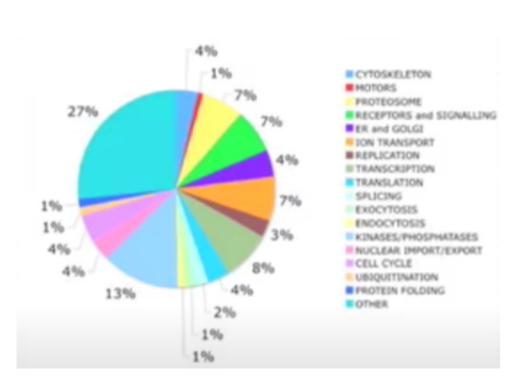
# Current State-of-the-Art for Understanding Systems Biology in Virology

#### results

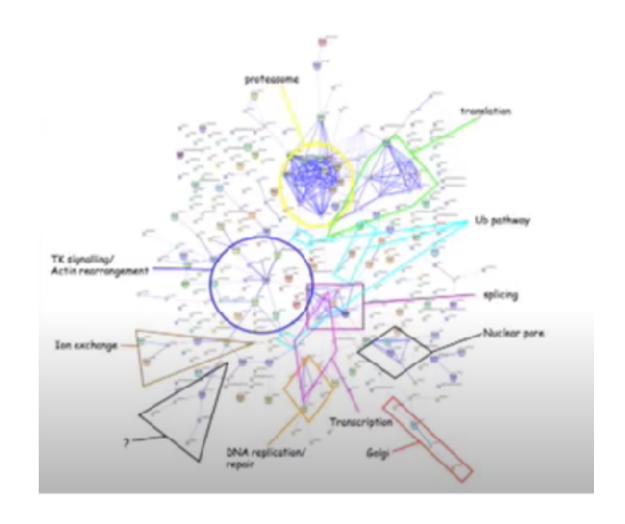
- ◆ 146 primary hits (3/3)
- ◆ 158 secondary hits (2/3)

#### total of 304 inhibit infection

- ◆ 4 increase infection
- ◆ string analysis of those genes





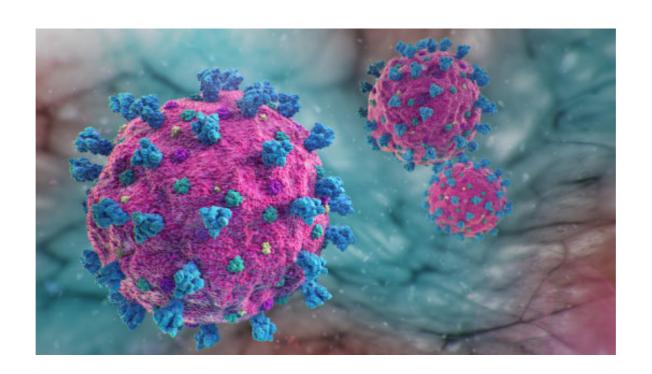


Mercer, J. et. al. Cell Reports 2, 1036-1047 (2012).

#### Additional Resources

- ♦ iBiology (video lecture series on many biology topics)
  - ◆ Virus Entry (Ari Helenius, ETH Zurich)
  - ◆ Virus Ecology & Evolution (Paul Turner, Yale)
  - ◆ Danger from the Wild: HIV (David Baltimore, Caltech)
  - ◆ Discovering Reverse Transcriptase (David Balitmore, Caltech)
  - ◆ Studying Coronavirus (Tracey Goldstein & Koen Van Rompay, UCD)
- ◆ BioRender ("ChemDraw" for biomolecules, Princeton License)

# Viral Entry



MacMillan Group Meeting May 04, 2020

Daniel Kim