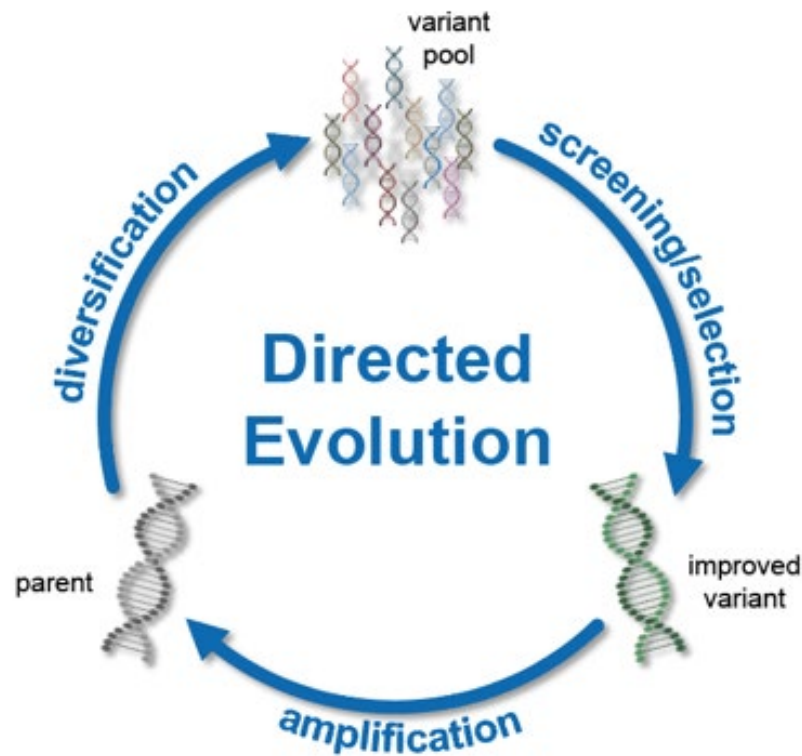


# Directed Evolution In Mammalian Cells

Yingjun Liu

27.04.2021

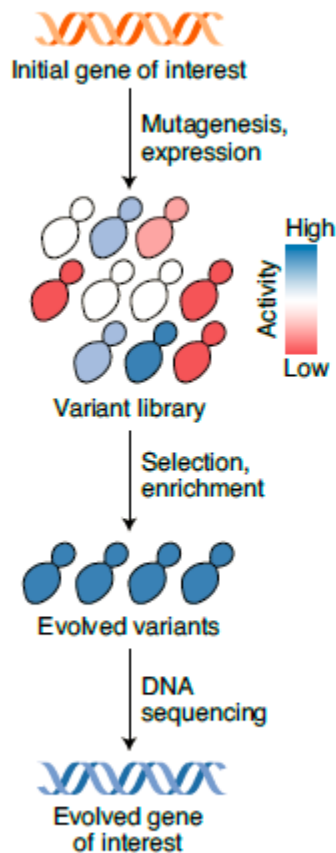
**Directed evolution** (DE) is a method used in protein engineering that mimics the process of natural selection to steer proteins or nucleic acids toward a user-defined goal.



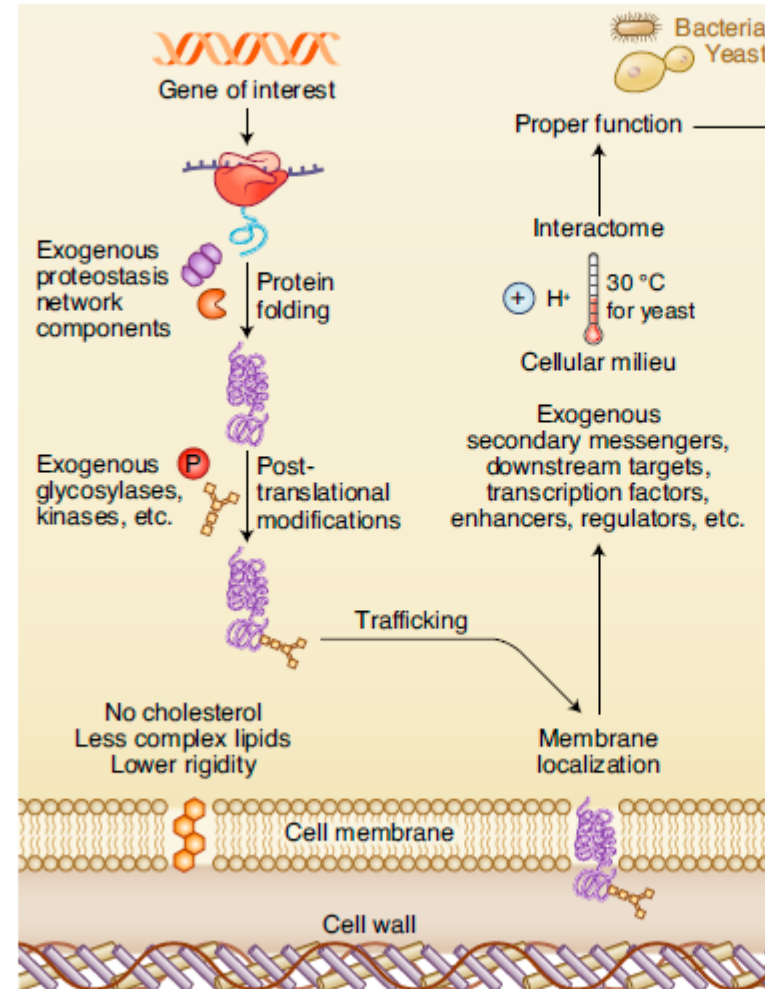
- Study the basic principles of evolution
- Generation of useful research tools (e.g. chemogenetics)
- Improving binding affinity of therapeutic antibodies (Affinity maturation) or the activity of de novo designed enzymes.
- Altering substrate specificity of existing enzymes
- .....

# Classical ways of directed evolution

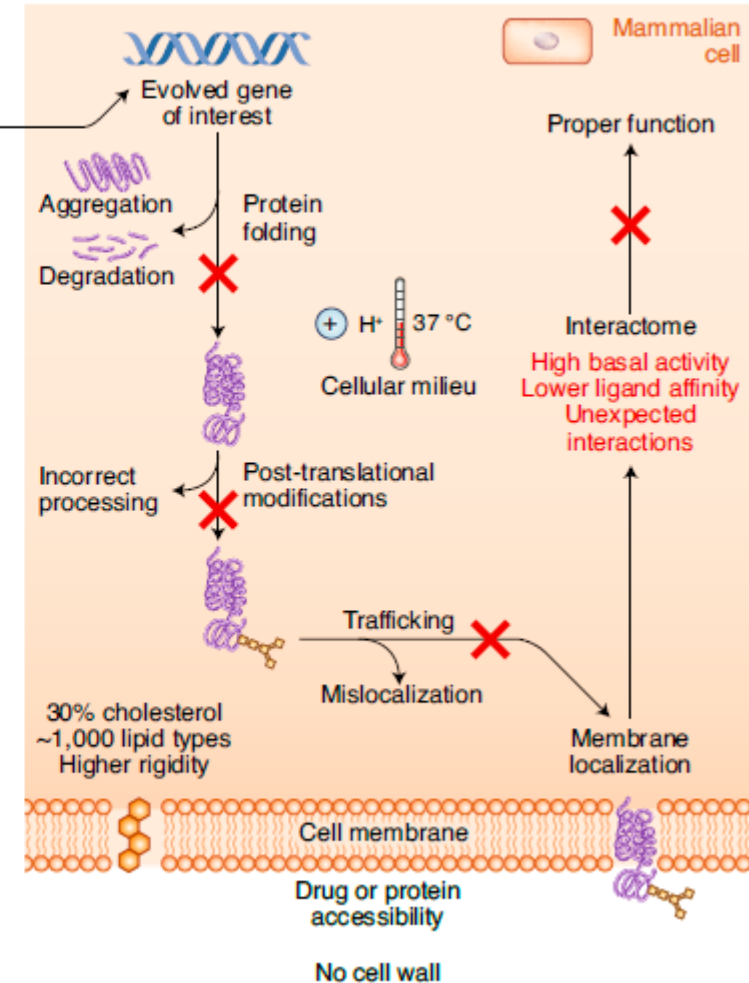
**a** Directed evolution is often performed in lower organisms or test tubes

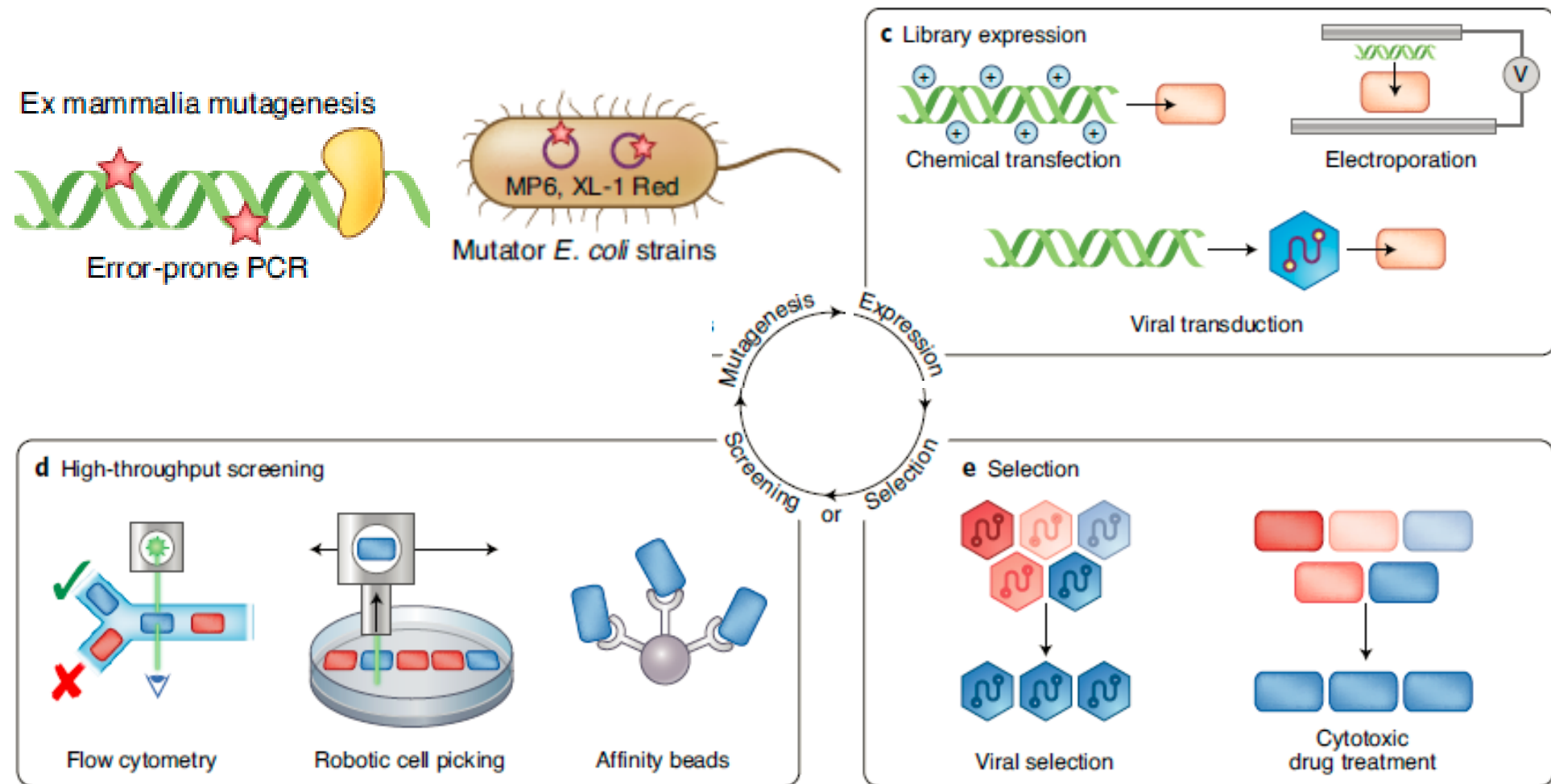


**b** Evolving genes in lower organisms often requires exogenous components

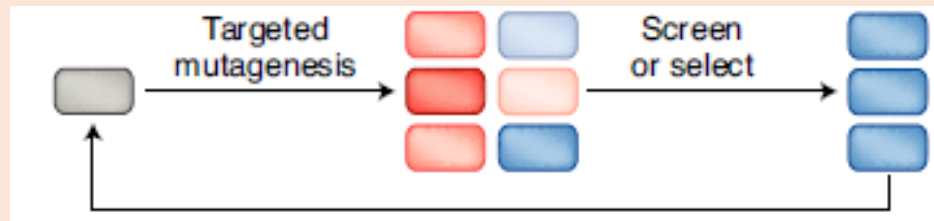


**c** But evolved variants often fail to function properly in mammalian cells



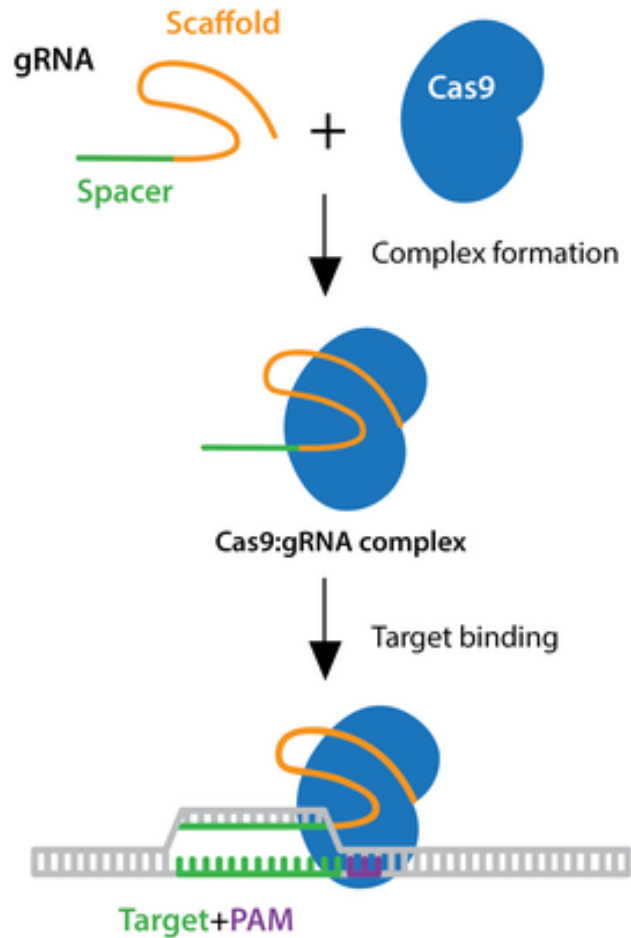


# Integrated approaches of directed evolution in mammalian cells???

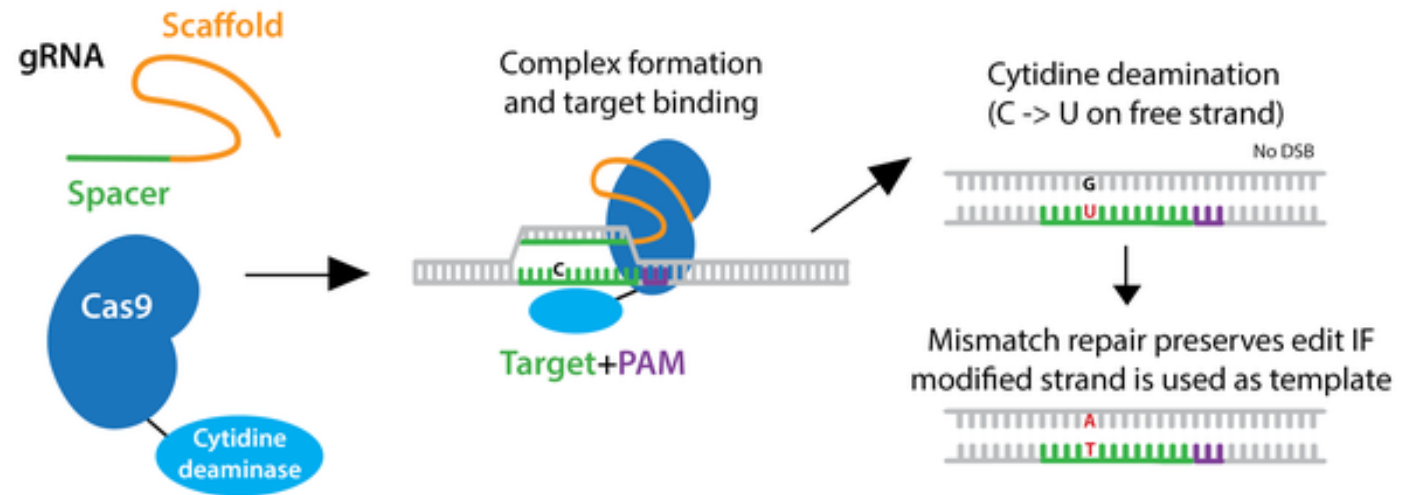


- CRISPR-CAS based approaches, e.g. **CRISPR-X** and EvolvR
- T7-RNA polymerase based approaches, e.g. MutaT7, **TRACE**
- **Virus based approaches**, e.g. mPACE and VEGAS

# The versatile CRISPR-CAS system

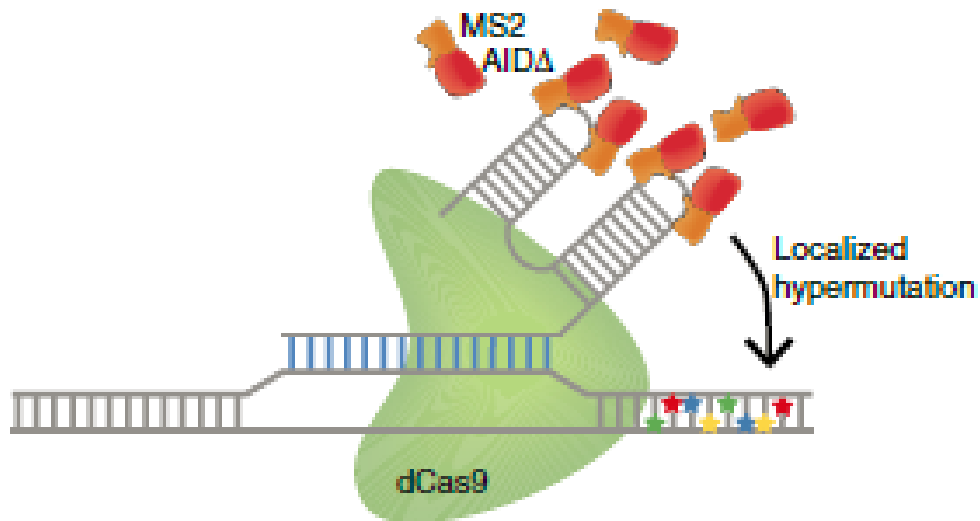


## CRISPR Base Editing

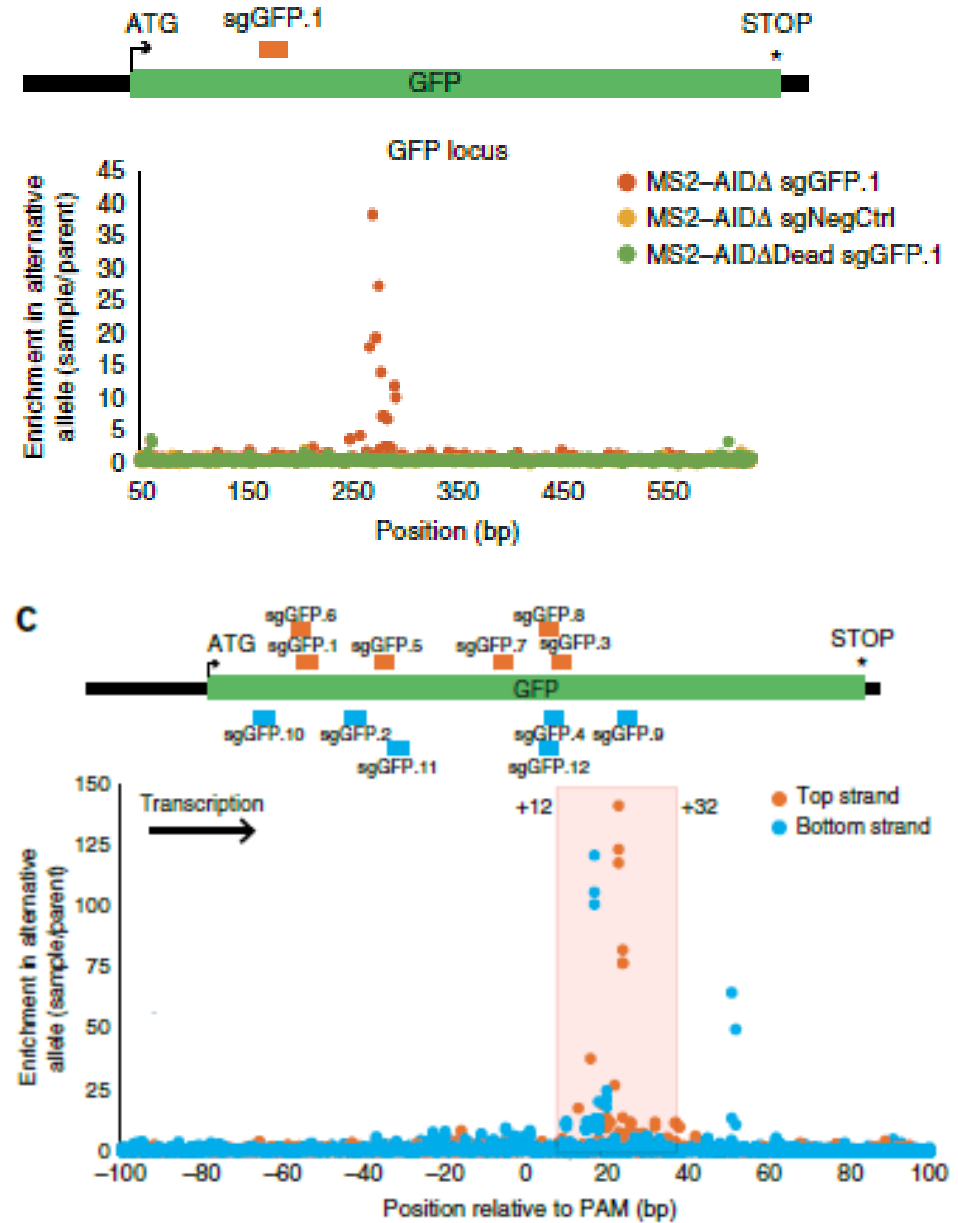


<https://www.addgene.org/guides/crispr/>

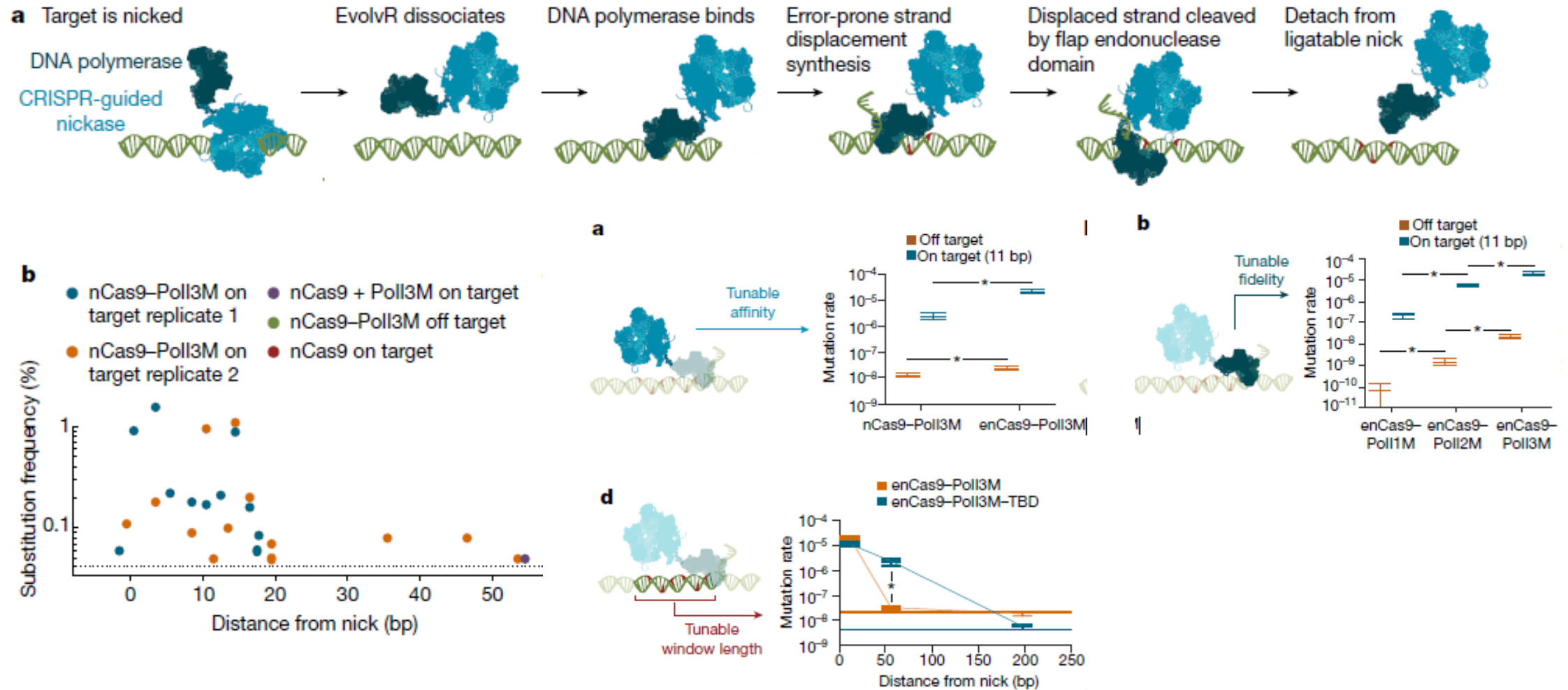
## The CRISPR-X strategy



Gaelen T Hess & Michael C Bassik et al., Nature Methods, 2016



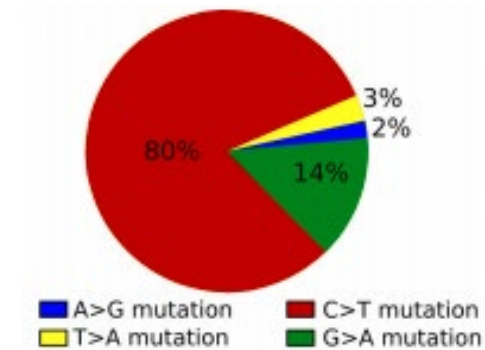
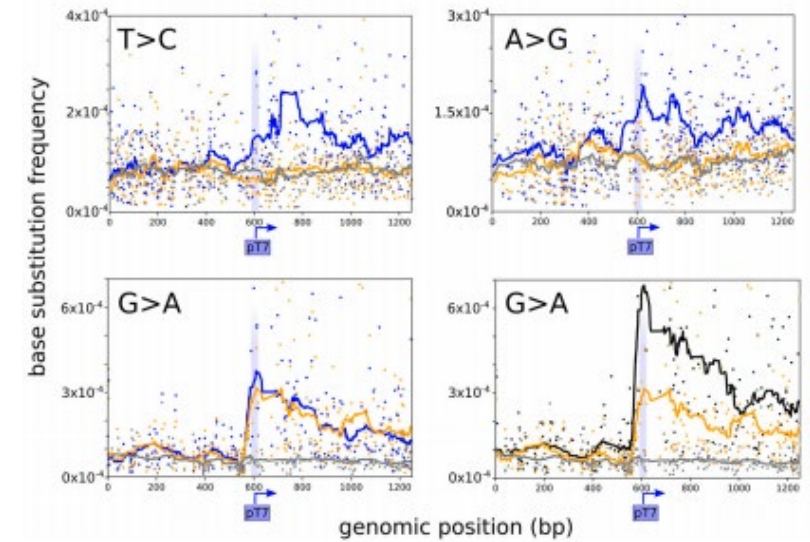
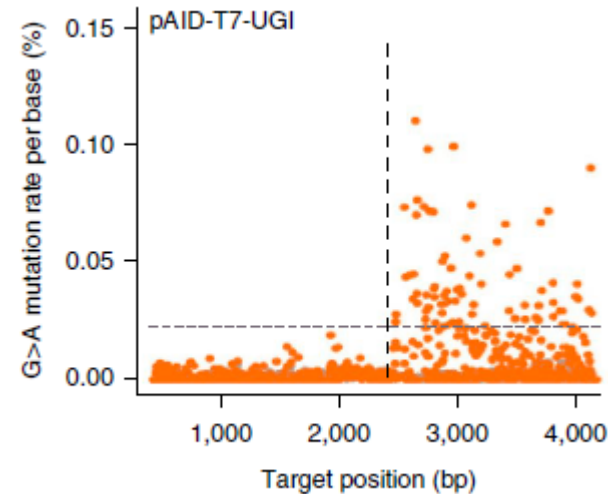
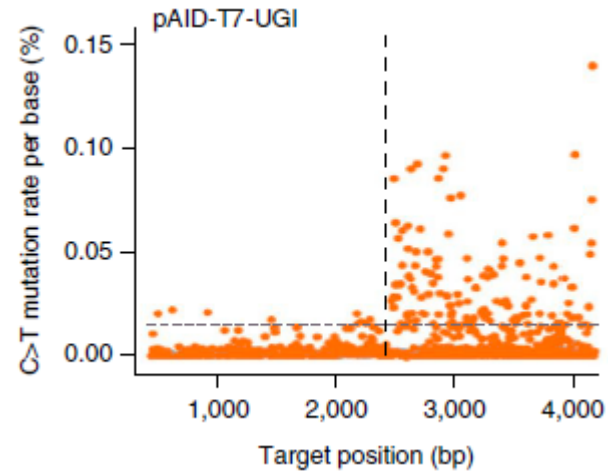
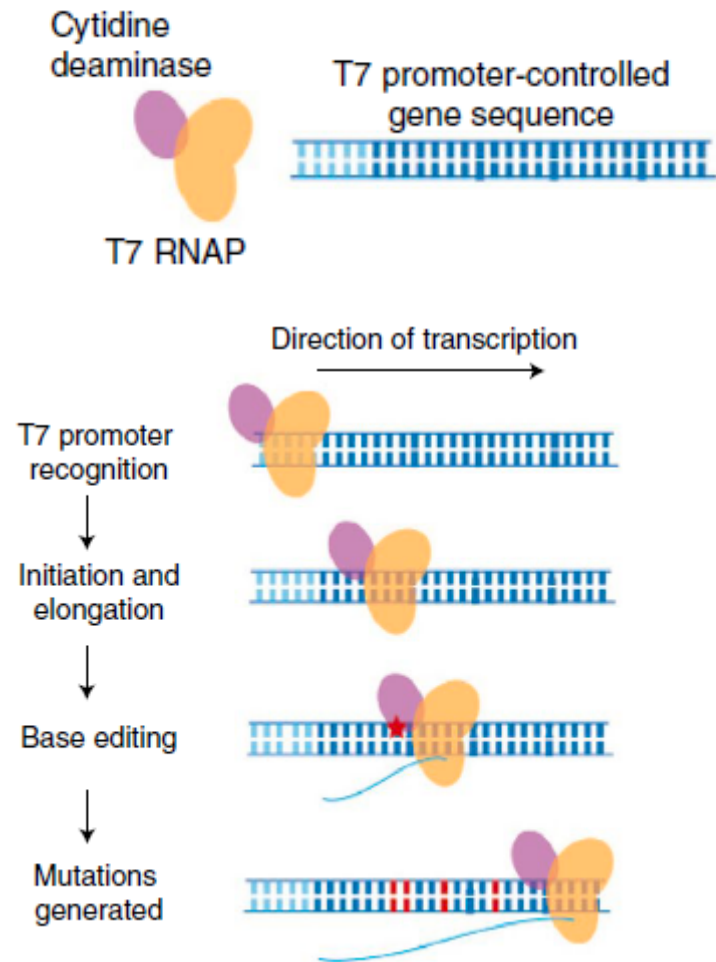
# The EvolvR strategy



Shaked O. Halperin, David V. Schaffer & John E. Dueber et al., Nature, 2018



# The T7-RNA polymerase based approaches



Haiqi Chen and Fei Chen et al., Nature Biotechnology, 2019

Aaron Cravens & Christina D. Smolke et al., Nature Communications, 2021

# The state of the art: Virus-based directed evolution systems in mammalian cells



Sindbis Virus-based

Resource

## VEGAS as a Platform for Facile Directed Evolution in Mammalian Cells

Justin G. English,<sup>1,5,\*</sup> Reid H.J. Olsen,<sup>1</sup> Katherine Lansu,<sup>1</sup> Michael Patel,<sup>2</sup> Karoline White,<sup>3</sup> Adam S. Cockrell,<sup>4</sup> Darshan Singh,<sup>1</sup> Ryan T. Strachan,<sup>1</sup> Daniel Wacker,<sup>1</sup> and Bryan L. Roth<sup>1,\*</sup>

AdenoVirus-based



Cite This: *J. Am. Chem. Soc.* 2018, 140, 18093–18103

Article

[pubs.acs.org/JACS](https://pubs.acs.org/JACS)

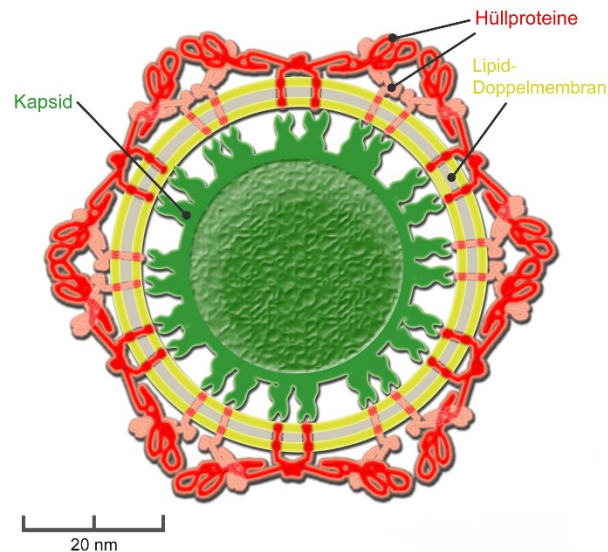
## An Adaptable Platform for Directed Evolution in Human Cells

Chet M. Berman,<sup>†,||,#</sup> Louis J. Papa, III,<sup>†,#</sup> Samuel J. Hendel,<sup>†,#</sup> Christopher L. Moore,<sup>†</sup> Patreece H. Suen,<sup>†</sup> Alexander F. Weickhardt,<sup>†</sup> Ngoc-Duc Doan,<sup>†</sup> Caiden M. Kumar,<sup>†</sup> Taco G. Uil,<sup>§,⊥</sup> Vincent L. Butty,<sup>‡</sup> Robert C. Hoeben,<sup>§</sup> and Matthew D. Shoulders<sup>\*,†,⊥</sup>

**Sindbis virus (SINV)** is an enveloped RNA virus of the genus *Alphavirus* in the virus family *Togaviridae*.

It was first isolated from *Culex* mosquitoes in 1952 in the Nile river delta in Egypt. The first human cases were described in Uganda in 1961, South Africa in 1963, and Australia in 1967. However, clinical SINV infection in humans has almost exclusively been reported in Northern Europe where it is endemic and where large outbreaks occur intermittently.

<https://www.ecdc.europa.eu/en/sindbis-fever/facts>



Fast replication (~ 24 hours per cycle)

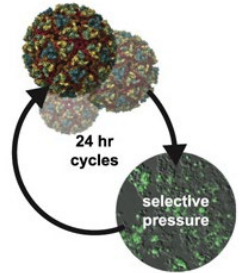
RNA viruses, such as Sindbis, are **highly mutagenic**, with no known proof-reading capability.

Has its' **own** RNA-dependent **RNA replicase** targeted to the viral genome by cis-acting, **conserved sequences**. These sequences are required to initiate replication and RNA templates, even those from related viral families, cannot be replicated by the Sindbis virus replicase, resulting in **high selectivity** between the replicase and the Sindbis virus genome

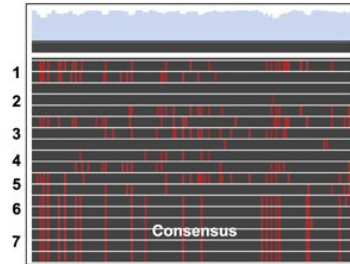
# The VEGAS strategy

## A Directed Evolution Platform for Mammalian Cell Culture

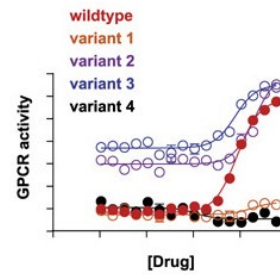
Evolve mutagenic virus  
in mammalian cells



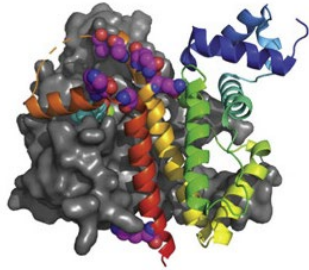
Isolate functional sequences  
from each cycle up to consensus



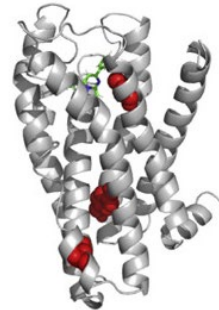
Assay for biological insight  
or tool-building performance



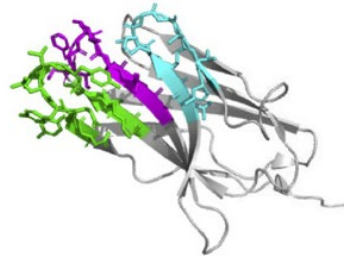
## Applied to Engineer Multiple Functional Protein Classes



Active Doxycycline Immune  
Tetracycline Response Element



Constitutively Active  
G-protein Coupled Receptor Mutants



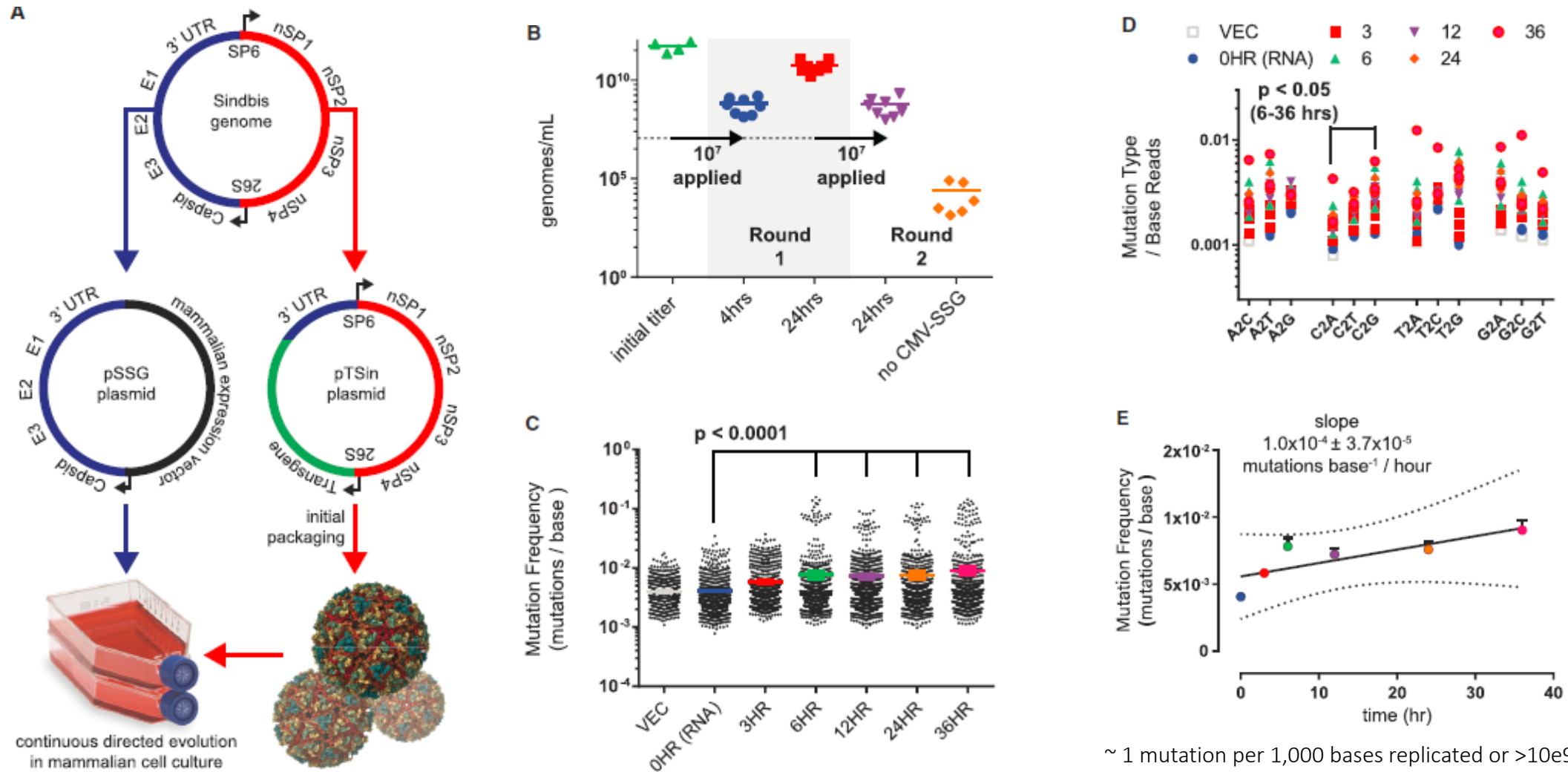
Allosteric Nanobodies Targeted  
to G-protein Coupled Receptors

## Highlights

- One day per round of directed molecular evolution in mammalian cells
- Mutation rates of  $10^{-3}$  from each round, surpassing many *in vitro* systems
- System does not require resetting or recycling of hits
- Three unique campaigns are presented, each succeeding in less than a week

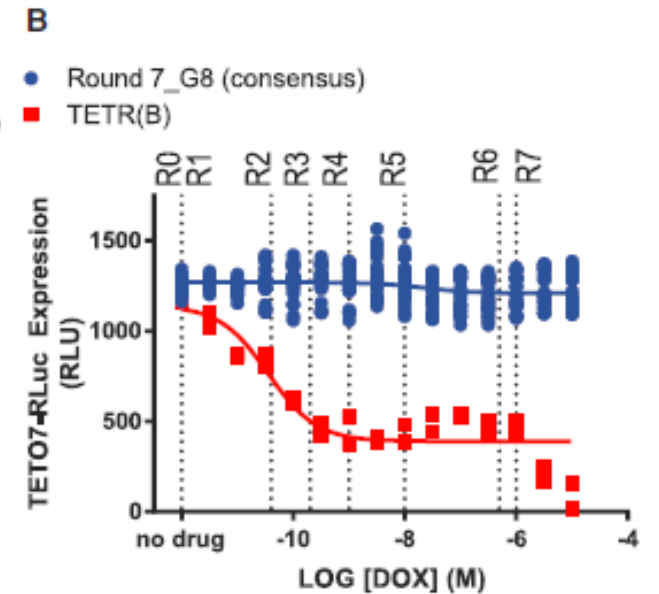
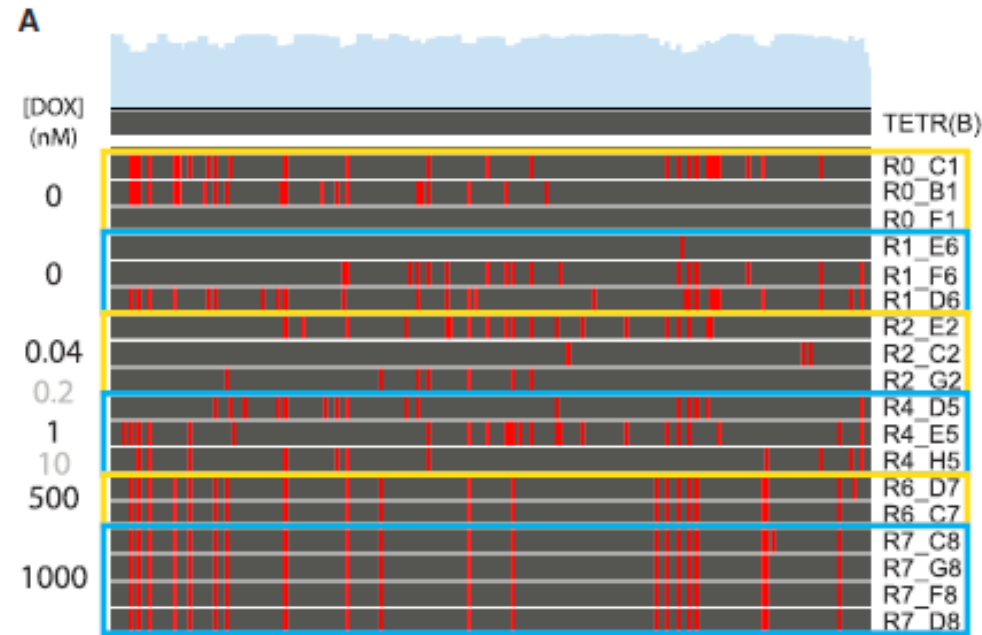
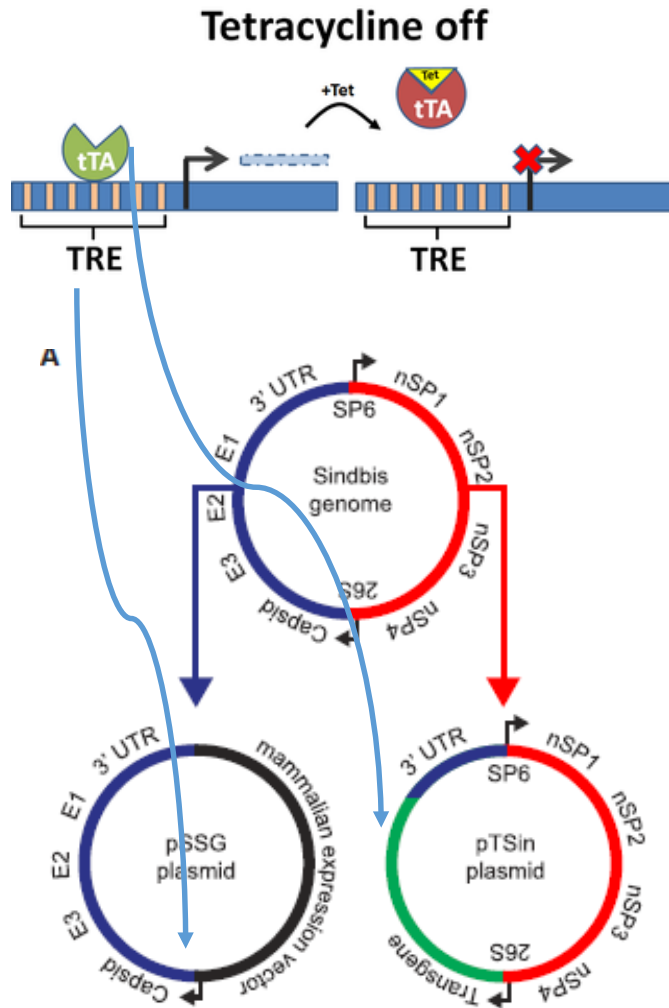


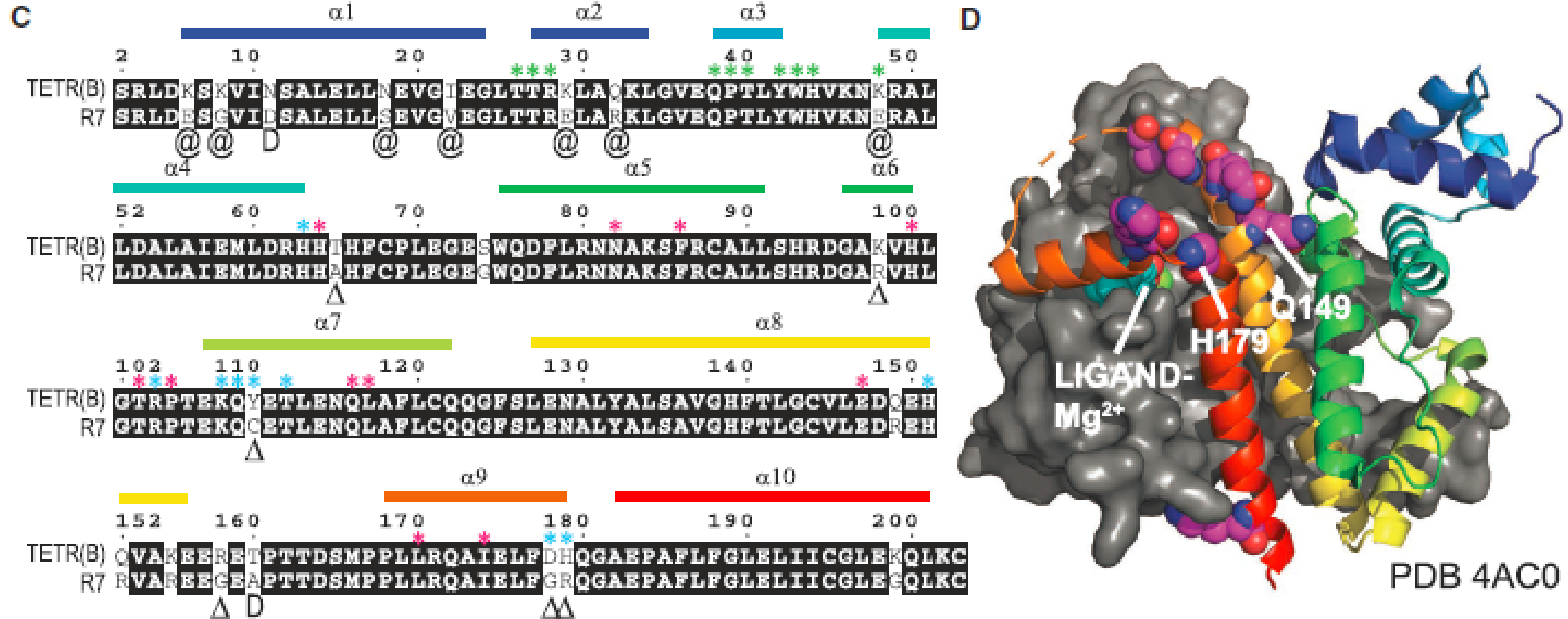
# Development of Sindbis virus for facile, mutagenic viral propagation in mammalian cell culture



~ 1 mutation per 1,000 bases replicated or >10e9 total mutations per day at the observed viral production rates.

Proof of concept: directed evolution of a doxycycline (DOX)-resistant variant of the transcription factor tTA.



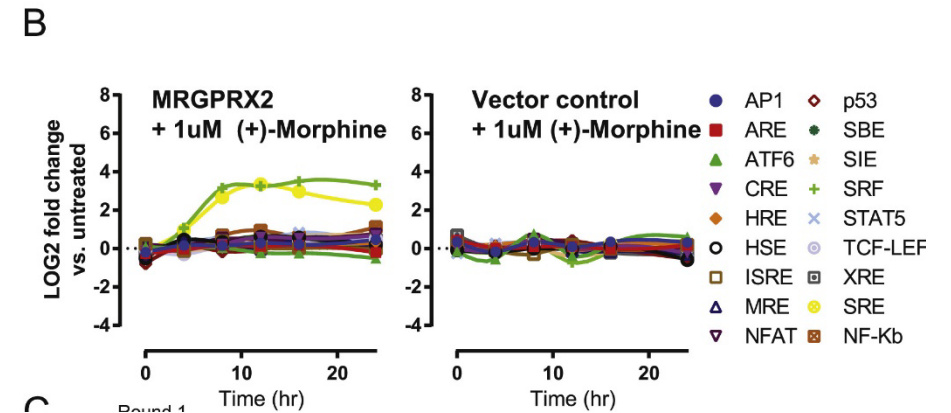
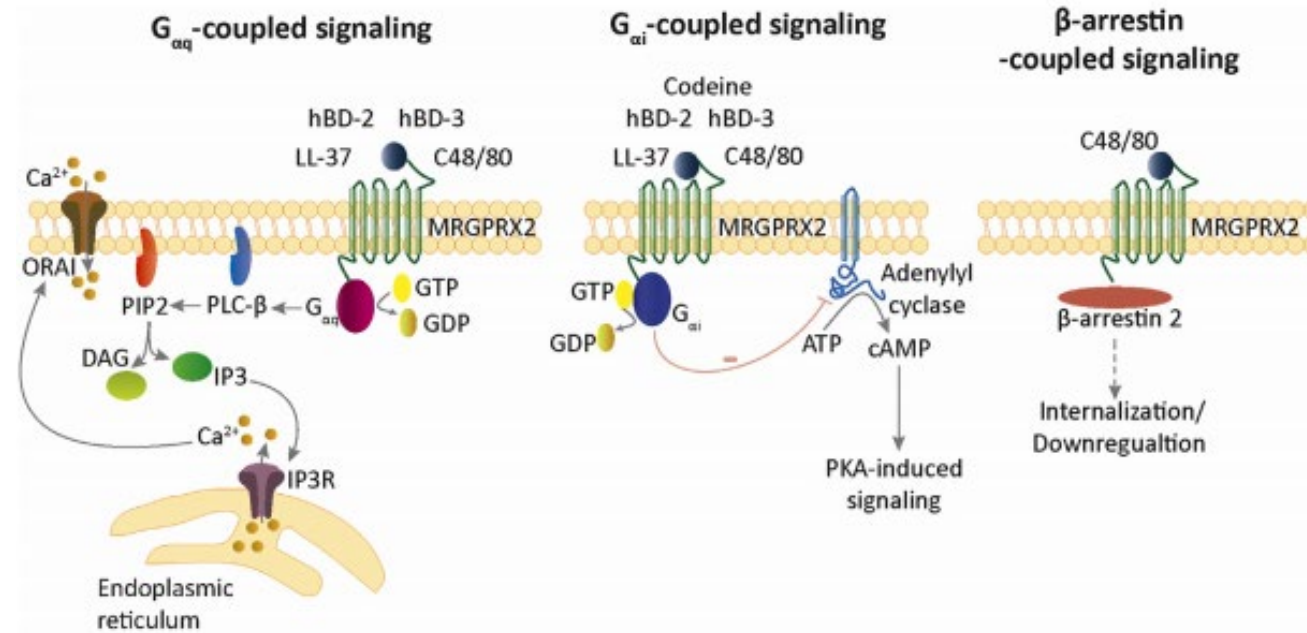


C. Peptide sequence alignment of TETR(B) and the R7 consensus. Exact residue ( $\Delta$ ), position (@), or subtype (D) substitutions previously published to enhance tTA activity in the presence of DOX. Residues (\*) with direct involvement in DNA binding (green), ligand binding (magenta), and ligand entry (cyan).

# Application of VEGAS for directed evolution of GPCRs

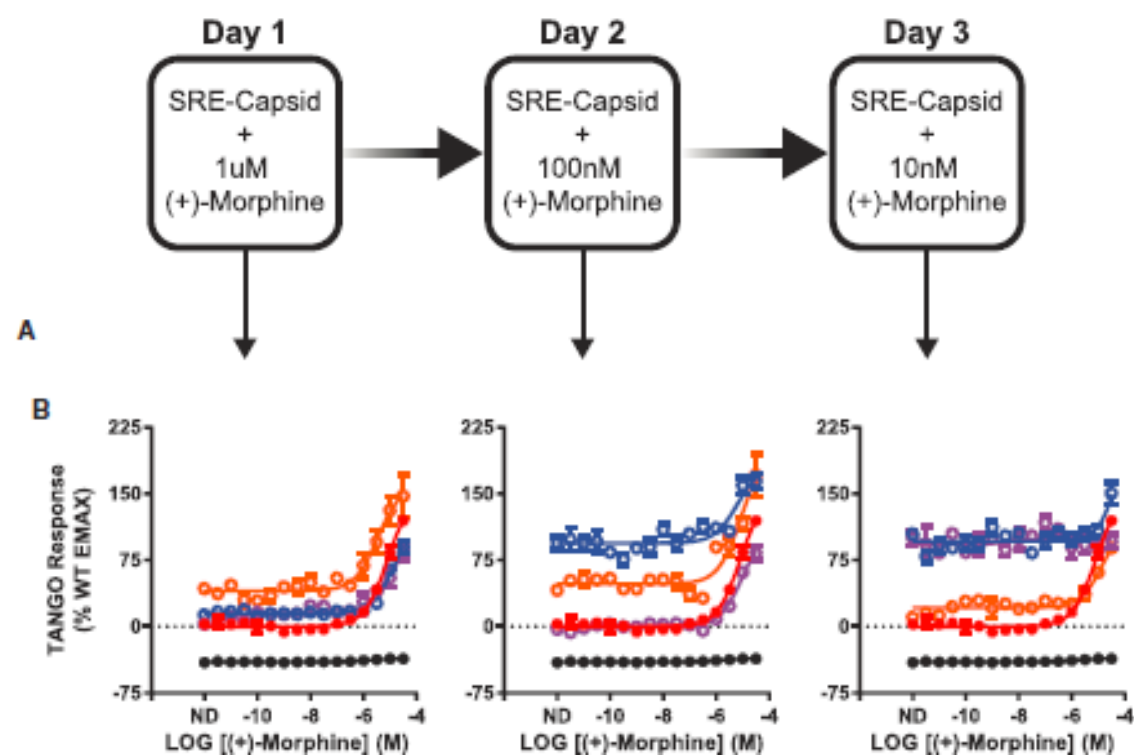
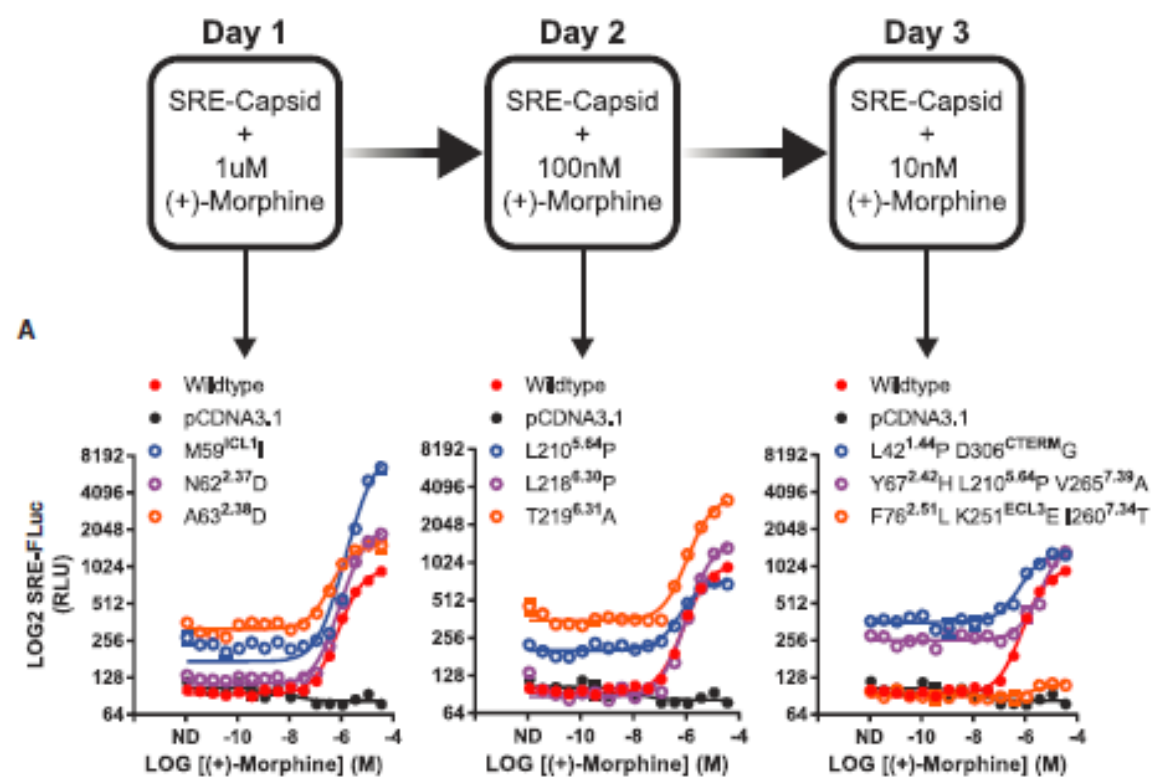
Mas-related G protein-coupled receptor X2 (MRGPRX2) is a primate-exclusive GPCR recently identified as an atypical opioid-recognition receptor, mainly expressed by neurons and mast cells.

Goal: Use VEGAS to develop constitutively active mutations (CAMs) of MRGPRX2 activated by (+)-morphine.

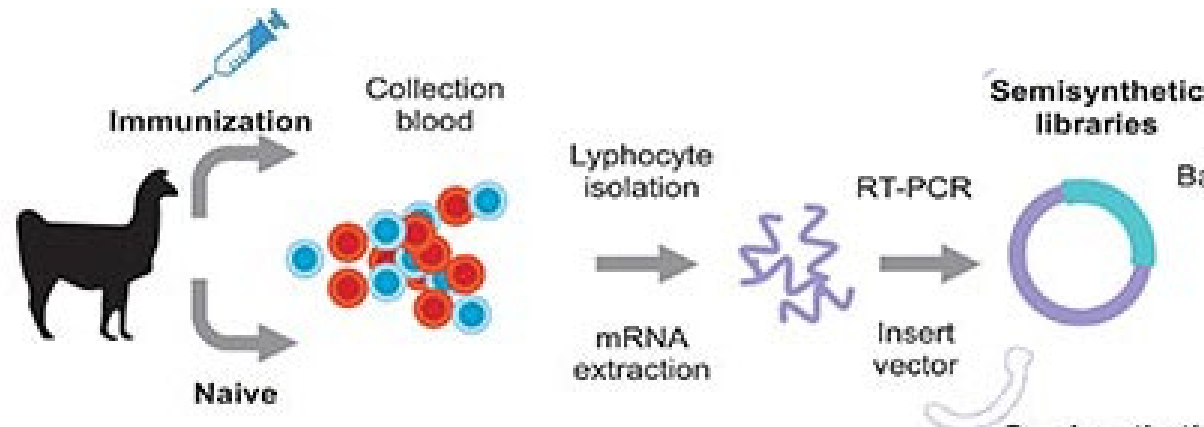
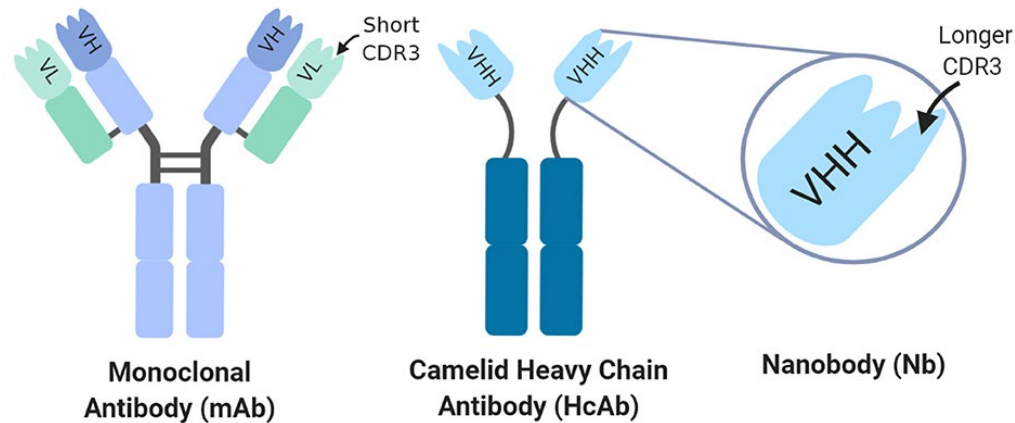


Helen Kuhn, Pavel Kolkhir, Andreas E. Kremer and Marcus Maurer et al., Journal of Allergy and Clinical Immunology, 2016

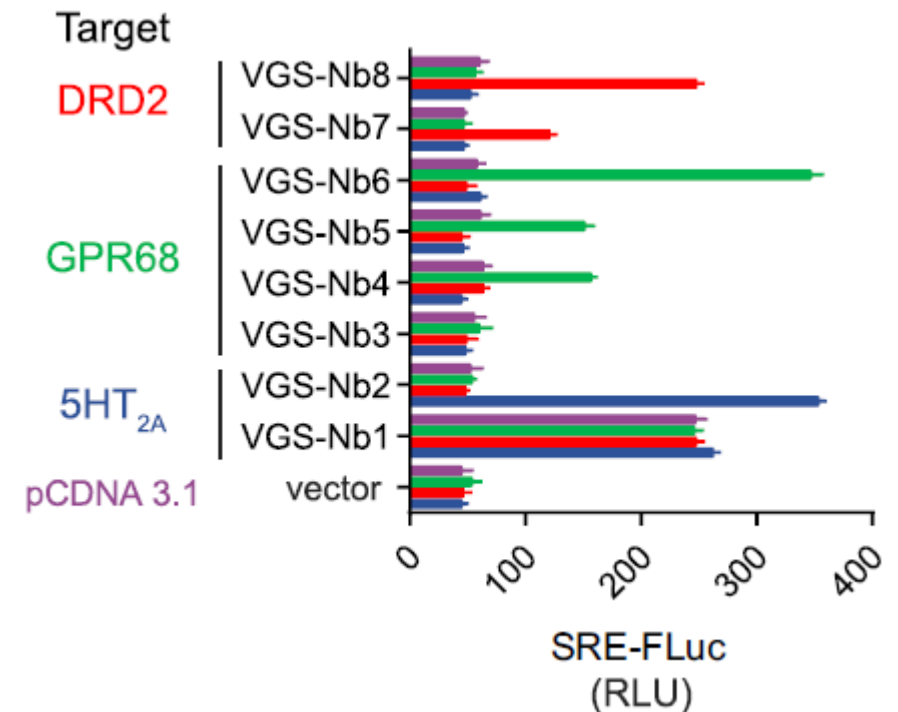


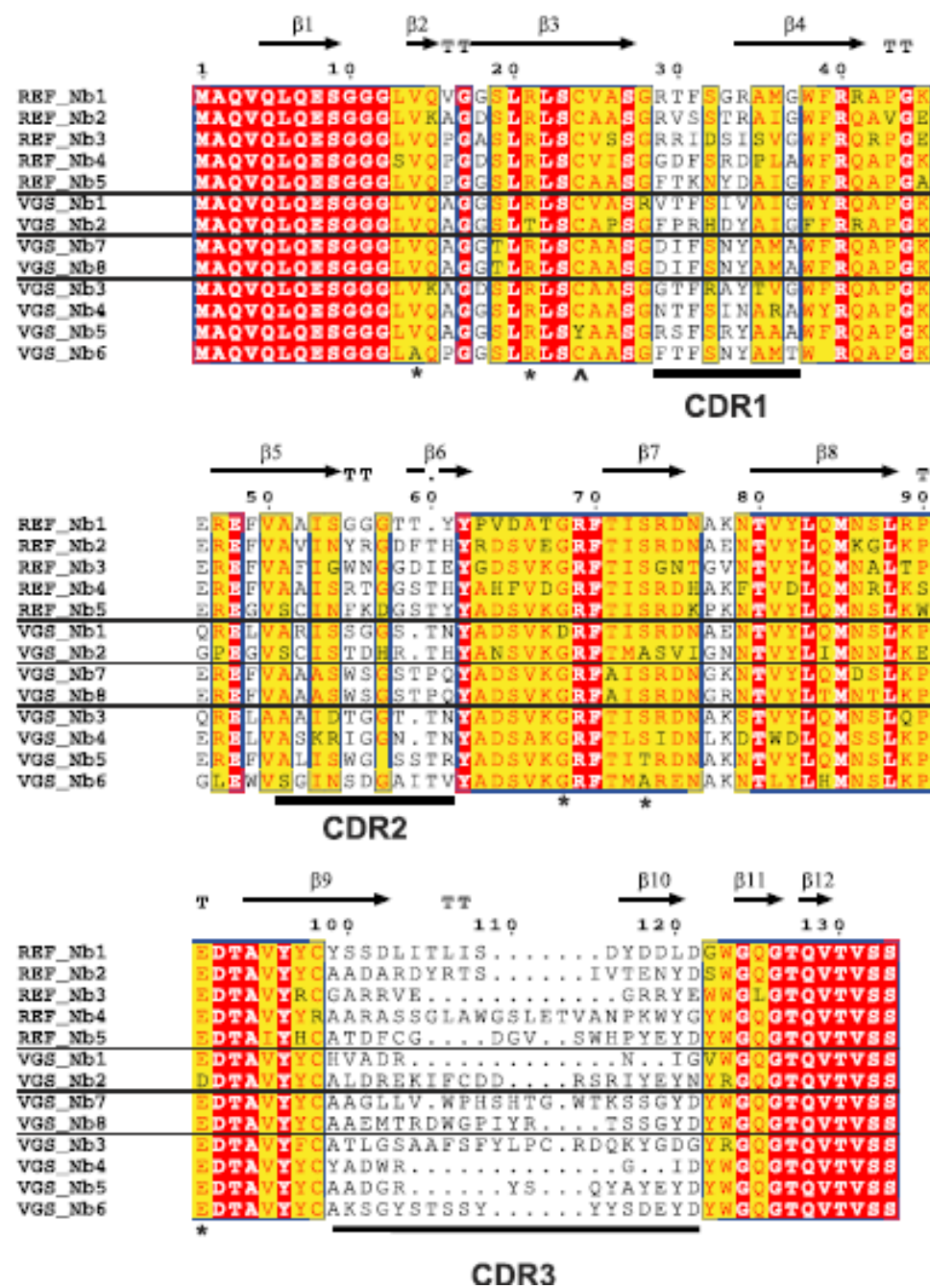
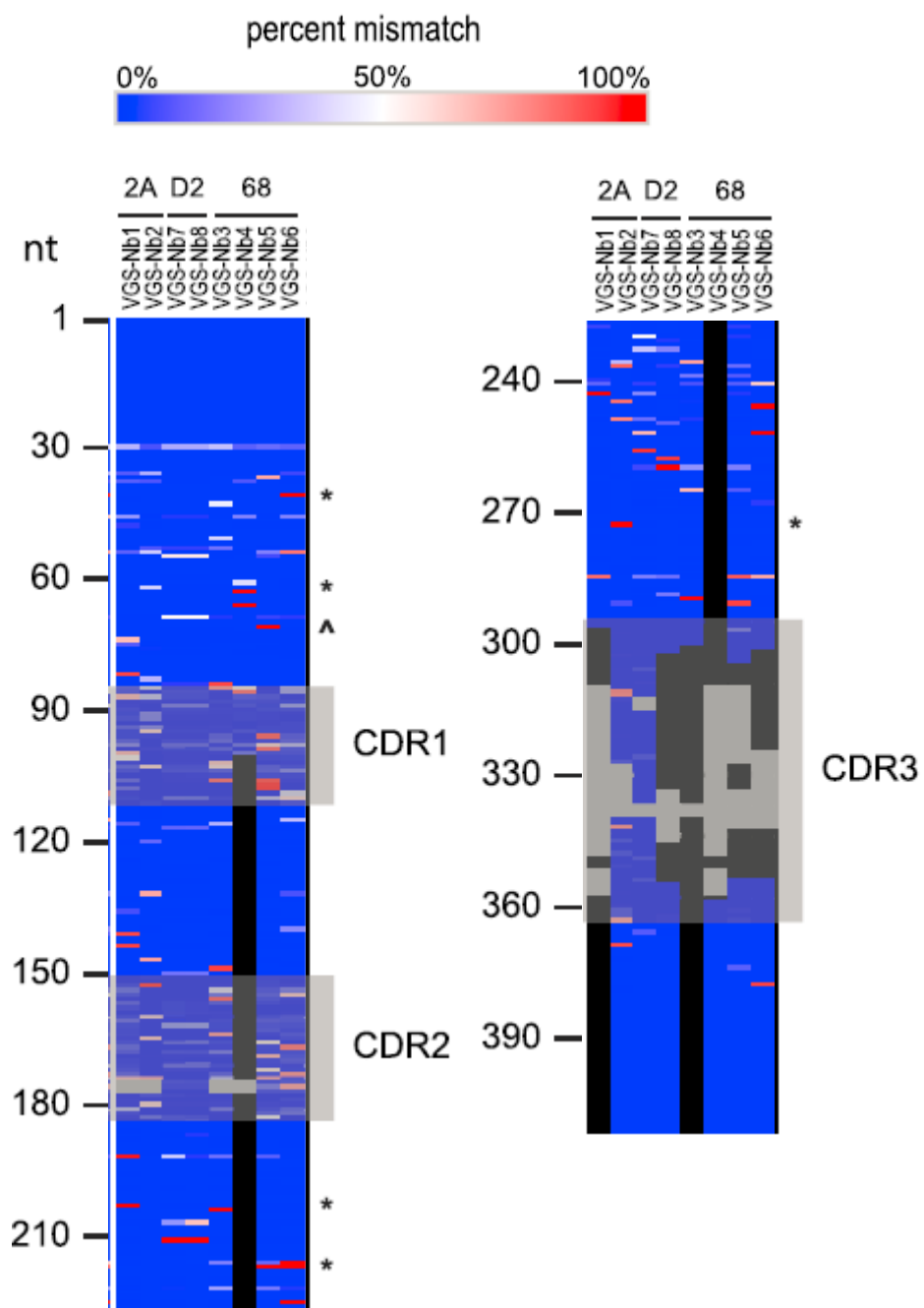


# VEGAS for the Evolution of Active-State Nanobodies

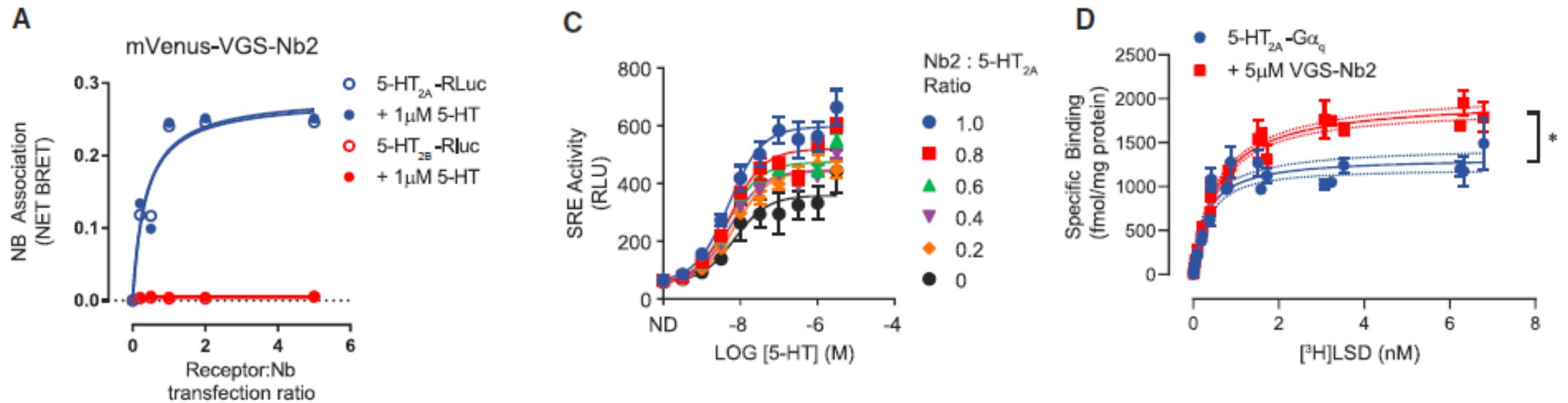


Directed evolution of 5HT<sub>2A</sub> nanobody library to three GPCR targets

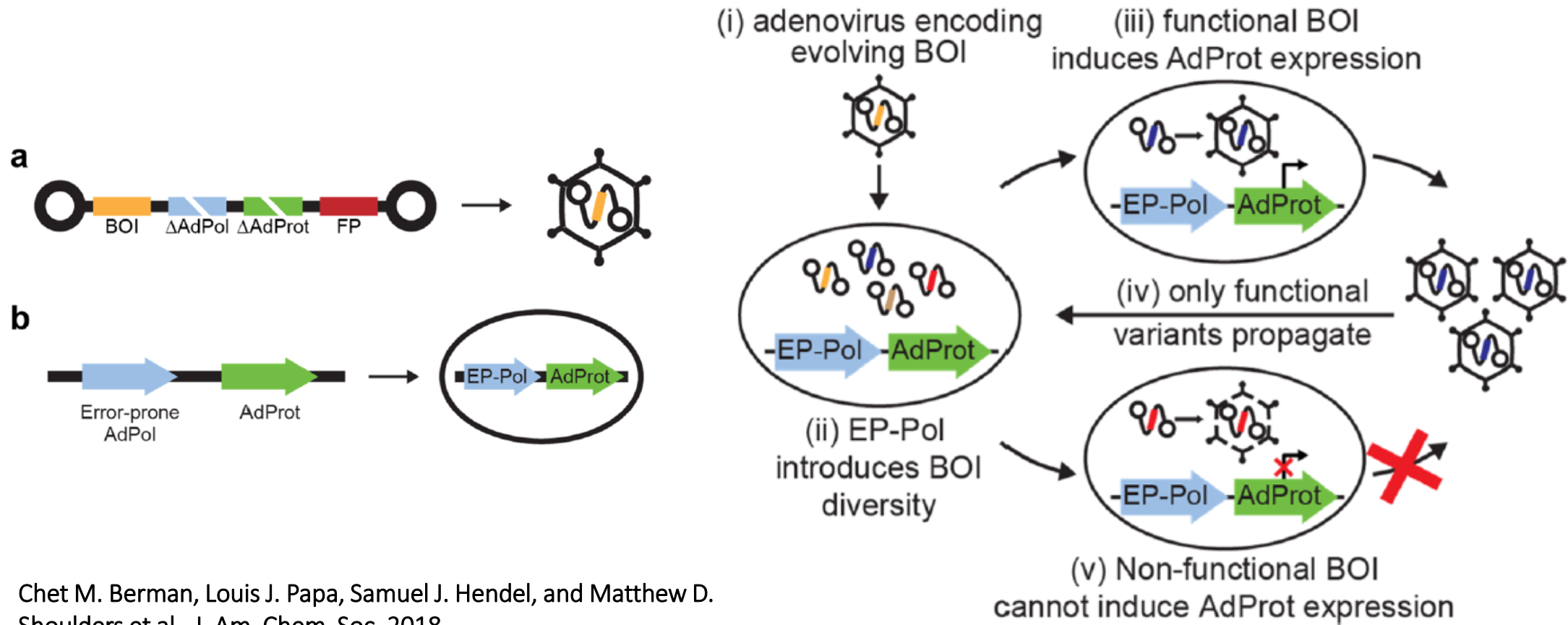




# Further characterization of evolved 5-HT<sub>2A</sub> nanobodies



# The adenovirus-based directed evolution strategy



Chet M. Berman, Louis J. Papa, Samuel J. Hendel, and Matthew D. Shoulders et al., J. Am. Chem. Soc. 2018

Thank you for your attention!

Questions?