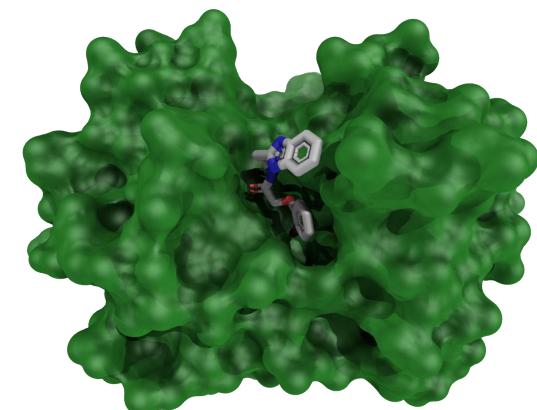
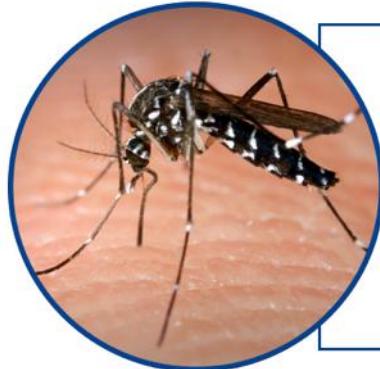


# *Targeting Flavivirus Non-structural Proteins For Drug Discovery*



*Andre S. Godoy*





# ZIKA VÍRUS

# 2015-16

Ministério confirma que novo vírus 'primo' da dengue foi encontrado por pesquisadores

Circulação da Febre Zika no País, no entanto, só será confirmada após testes feitos em laboratórios de referência

Fabiana Cambricoli, O Estado de S.Paulo  
05 Maio 2015 | 19h05

SIGA O ESTADÃO

## Surto de microcefalia em bebês faz País decretar emergência sanitária nacional

Foram notificados 141 casos no Nordeste; uma das suspeitas da equipe que investiga é a de ligação com o zika vírus

Lígia Formenti, O Estado de S. Paulo  
11 Novembro 2015 | 15h00

SIGA O ESTADÃO



**Le Monde**

Dimanche 10 Février 2016 - N° 18161 - Hors-série - 24€ - Tribune métropolitaine - [www.lemonde.fr](http://www.lemonde.fr) -  
Éditeur : Hubert Beuve-Méry - Directeur : Véronique Peugie

Zika : l'épidémie rouvre le débat sur l'avortement en Amérique latine

POLITIQUE  
NICOLAS SARKOZY  
VU ET RENOUER  
AVEC LE PFLPIF ?

HEALTH

The New York Times

## Zika Virus, a Mosquito-Borne Infection, May Threaten Brazil's Newborns

Global Health

By DONALD G. MCNEIL Jr. DEC. 28, 2015

# Zika cases



**January 2016**

- Confirmed
- Reported

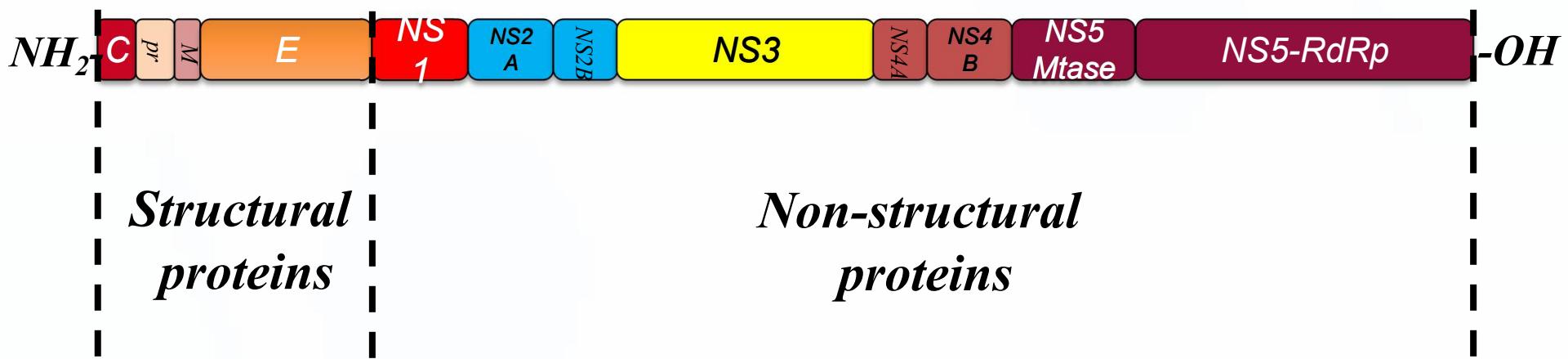
# Zika cases



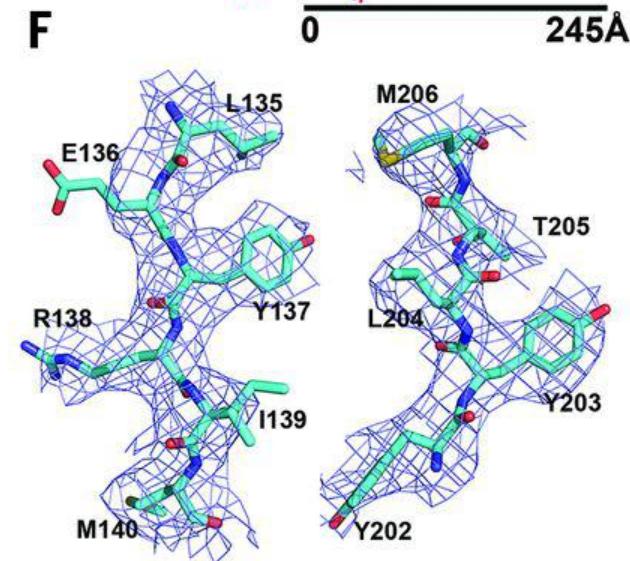
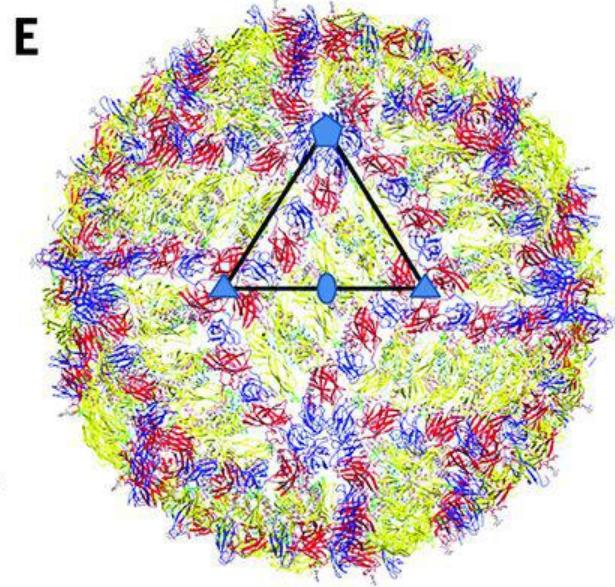
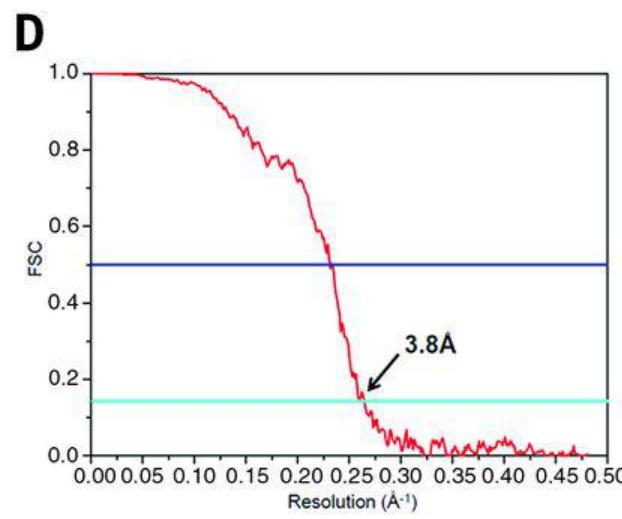
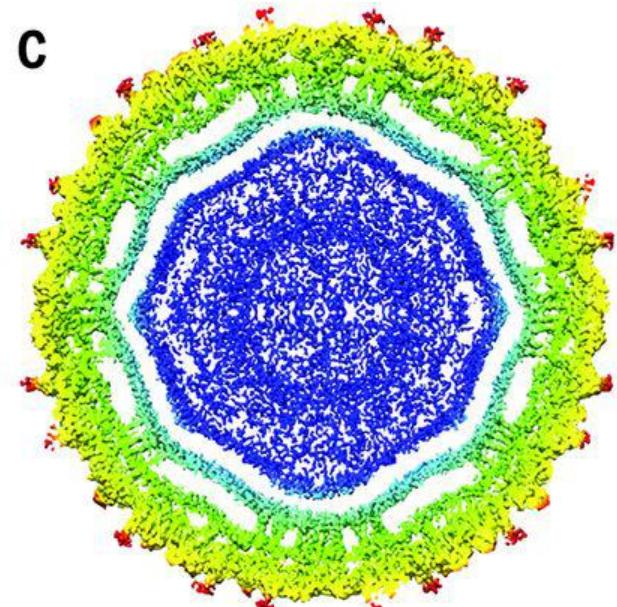
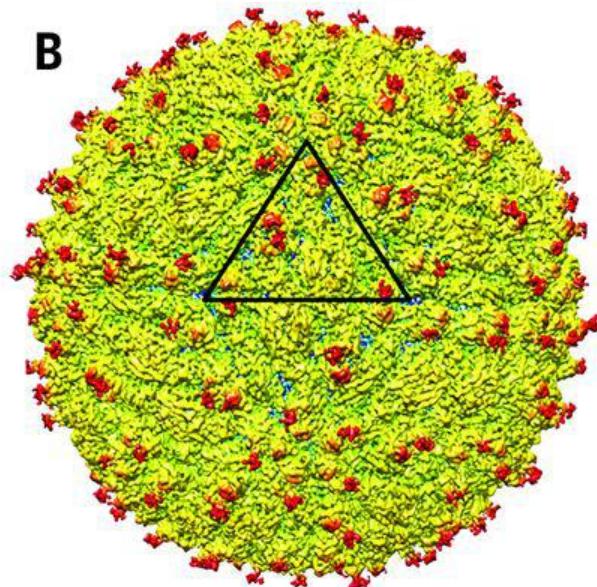
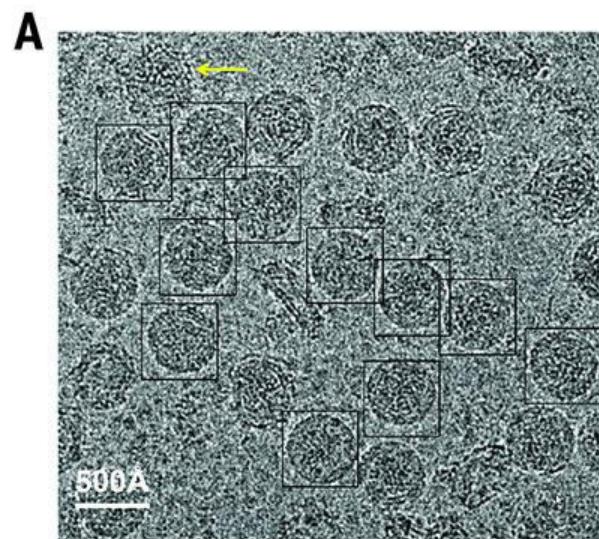
March 2016

Confirmed  
Reported

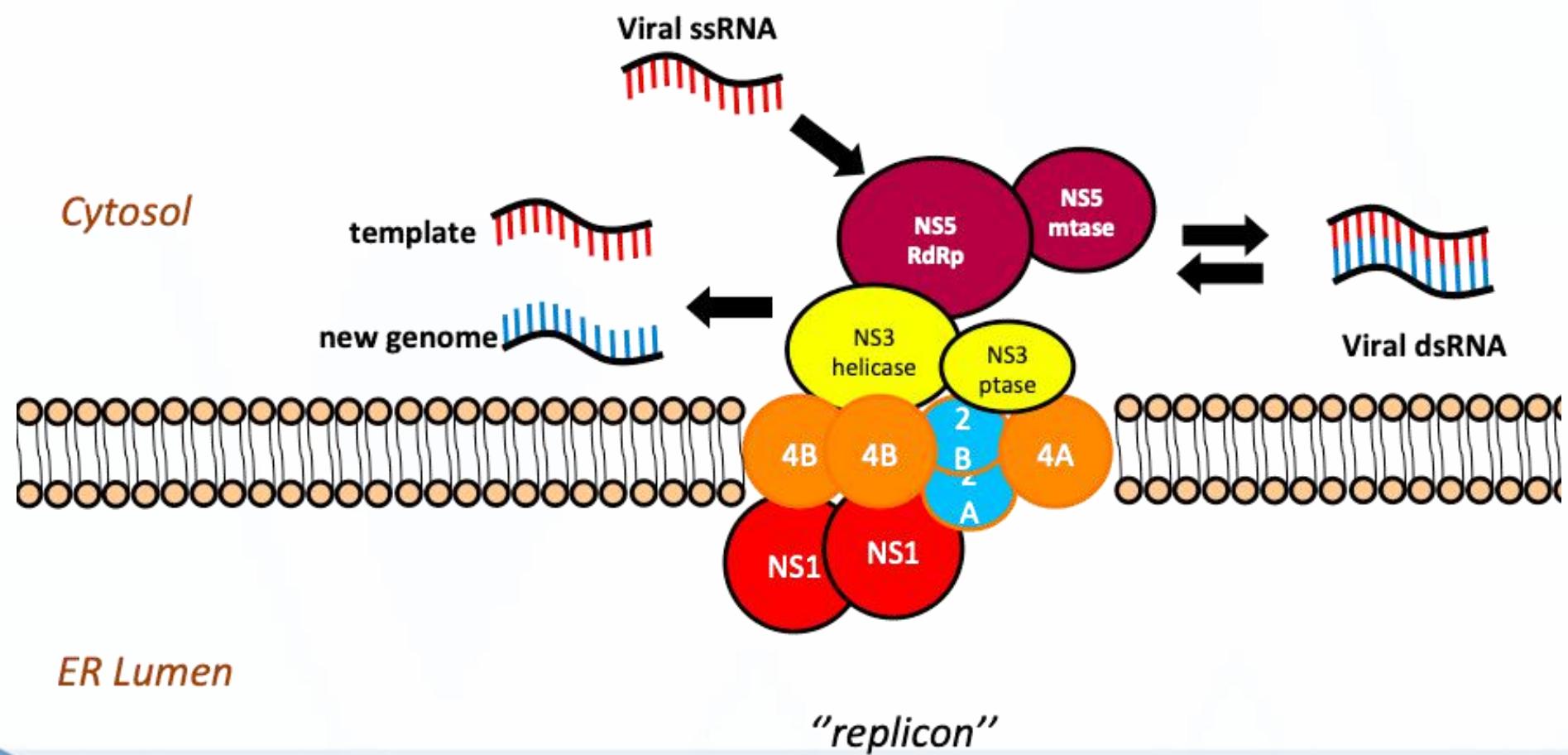
# Targeting Flavivirus Non-structural Proteins



# ZIKV Structural Proteins

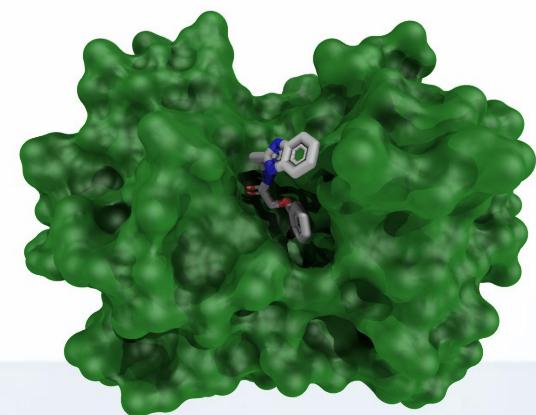


# Targeting Flavivirus Non-structural Proteins



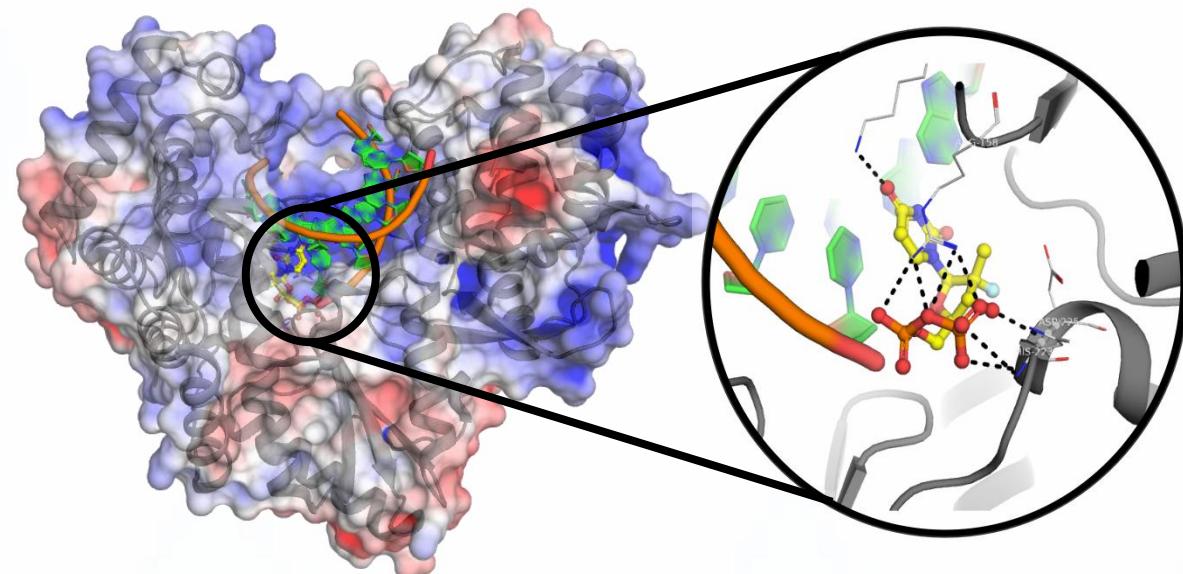
# **Structural Elucidation**

## **ZIKV NS5 RNA-dependent RNA polymerase**

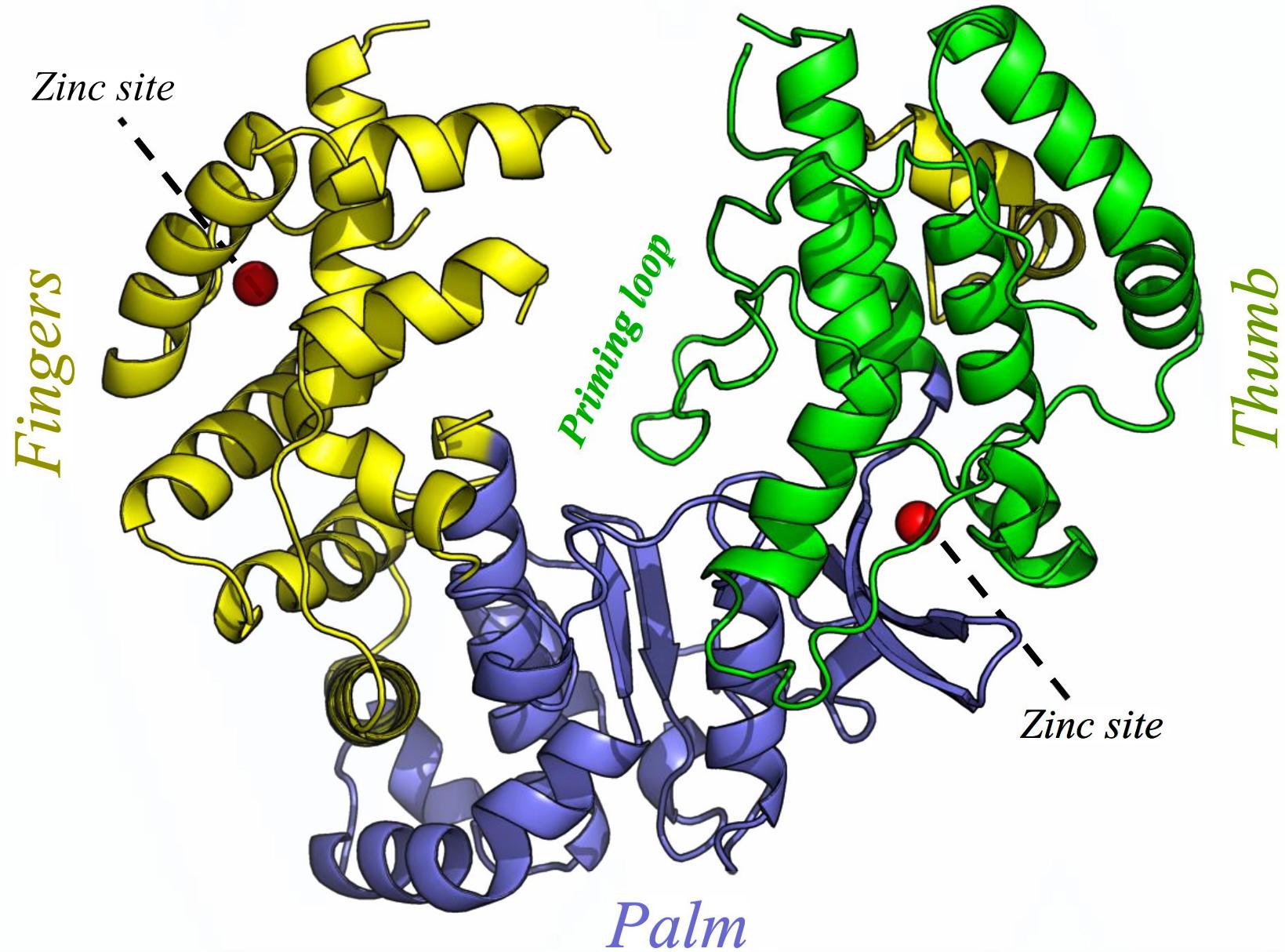


# ZIKV NS5 RdRp

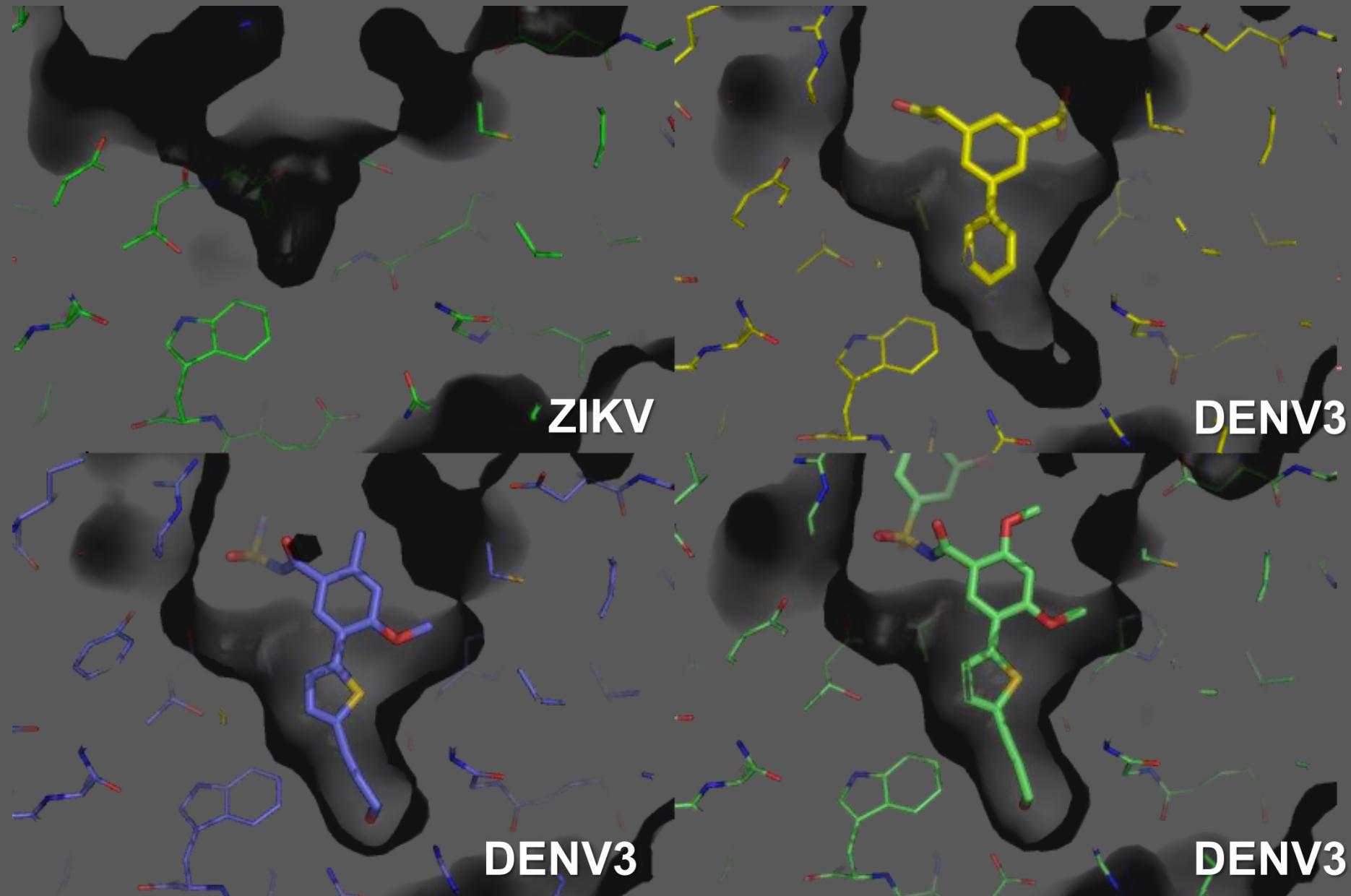
- *RNA-dependent RNA polymerase (RdRp) is an enzyme that catalyzes the replication of RNA*
- *Initiation is primer-independent (*de novo*)*
- *Essential for virus replication – exciting target !*



# ZIKV NS5 RdRp

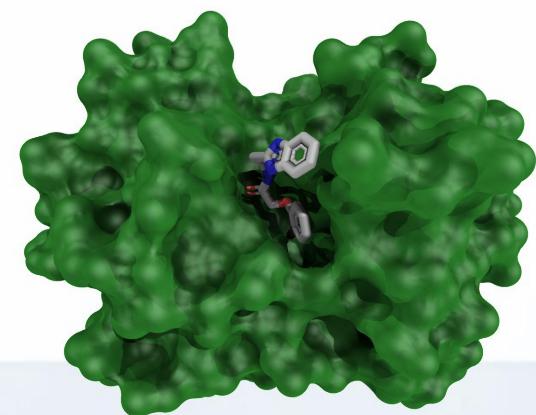


# ZIKV NS5 RdRp Priming loop

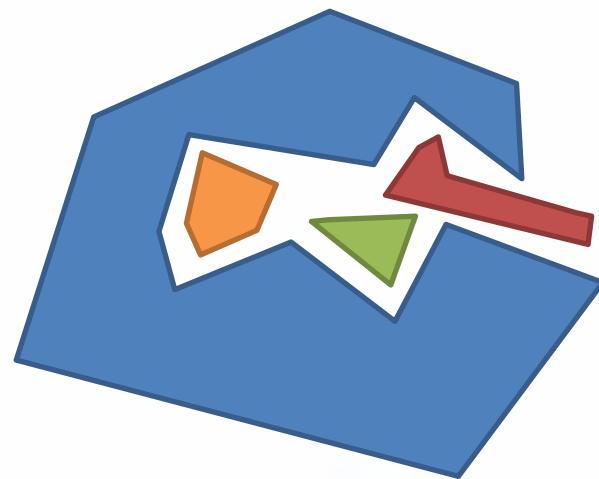
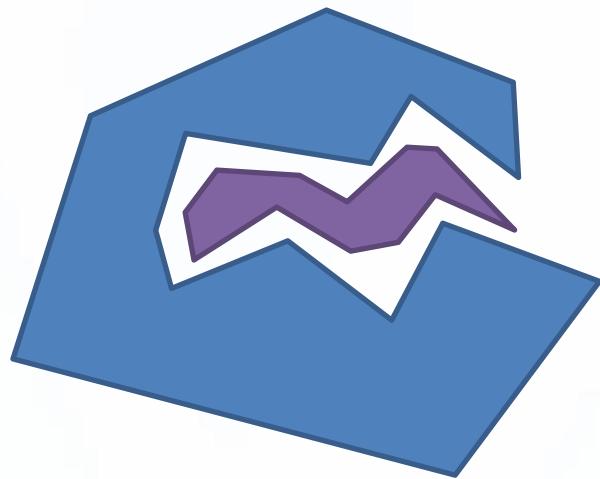


# **Fragment screening**

**Exploring NS3 Helicase domain**



- *Each heavy atom (HA) increases required Chemical Space (CS) by 8 fold*
- *$10^3$  molecules of MW 190 Da explore similar CS of  $10^{18}$  molecules of MW 440 Da*



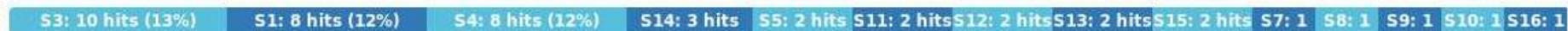
# PANDDA Inspect Summary

## Summary of Inspection of Datasets

### Fitting Progress



### Identified Ligands by Site



Datasets w. ligands: 41 (of 120)

Sites w. ligands: 14 (of 18)

Marked as interesting (unfitted): 0

Total number of events: 166

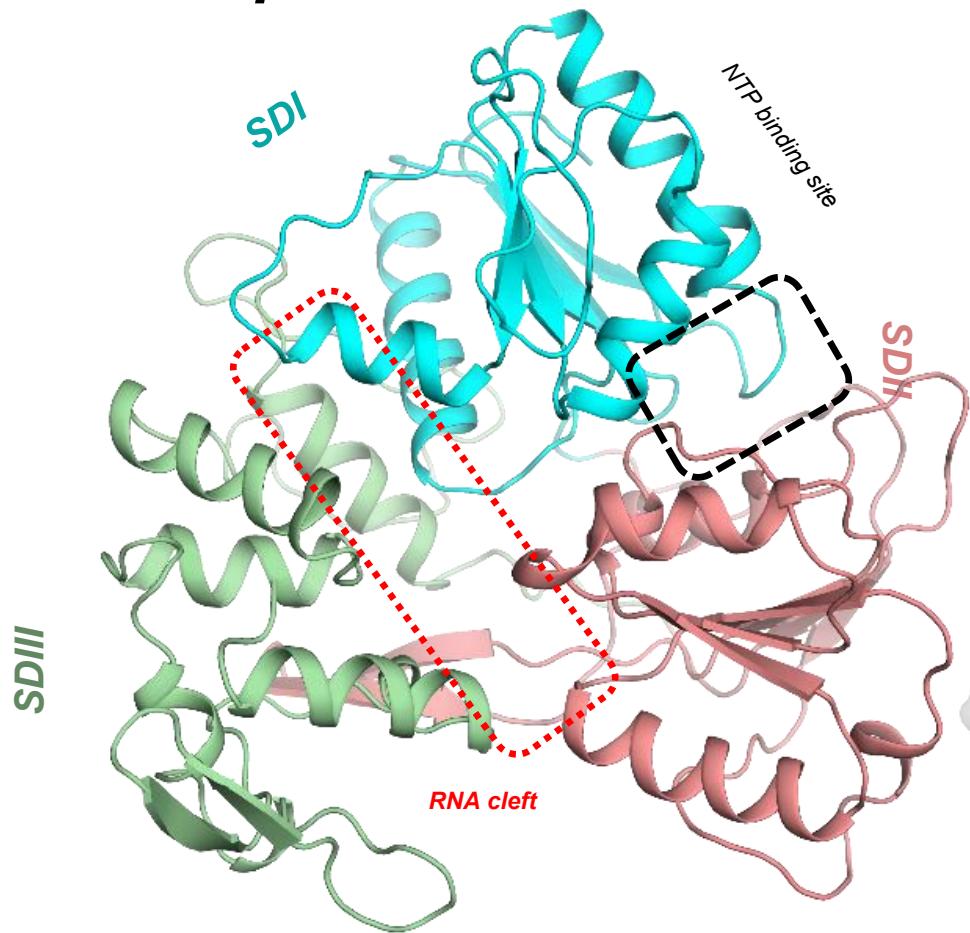
High confidence hits: 31

Medium confidence hits: 10

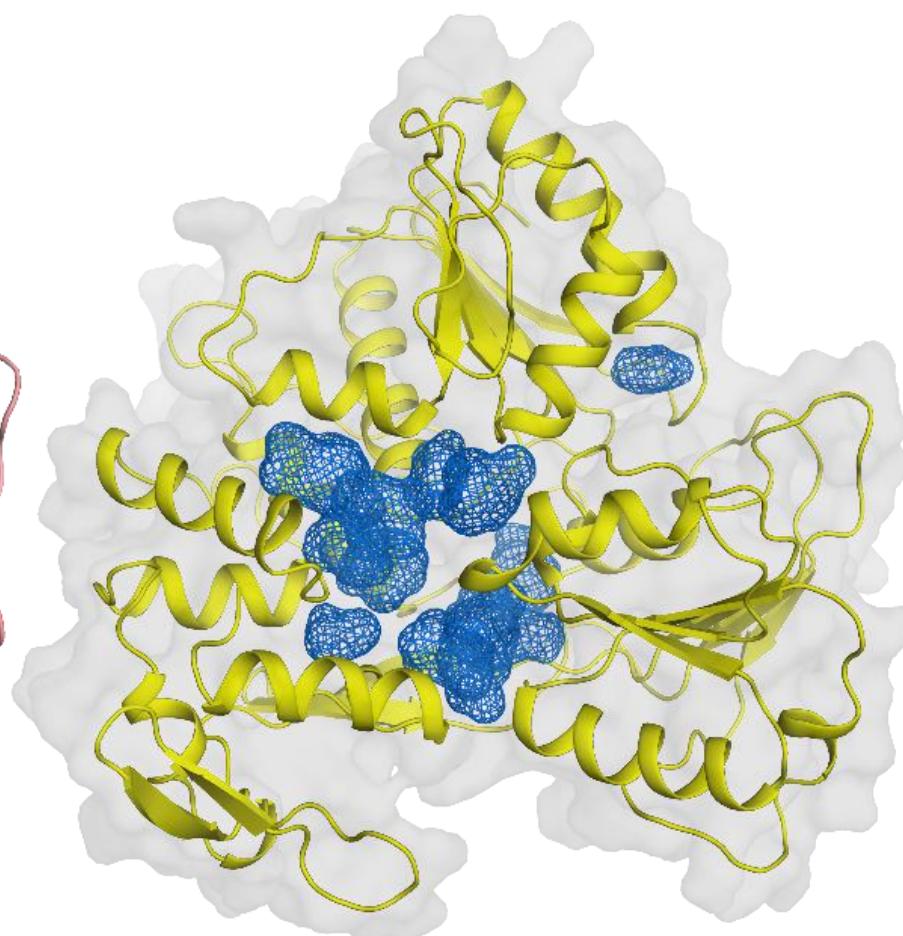
Low confidence hits: 3

- *500 fragments tested*
- *About 450 datasets collected and processed (From 1.3 – 3.0 Å)*
- *166 events (33%)*
- *about 16 sites (a lot in interfaces)*
- *44 reliable and on interesting sites (8%)*

- Several hits at the RNA binding site, previously unexplored

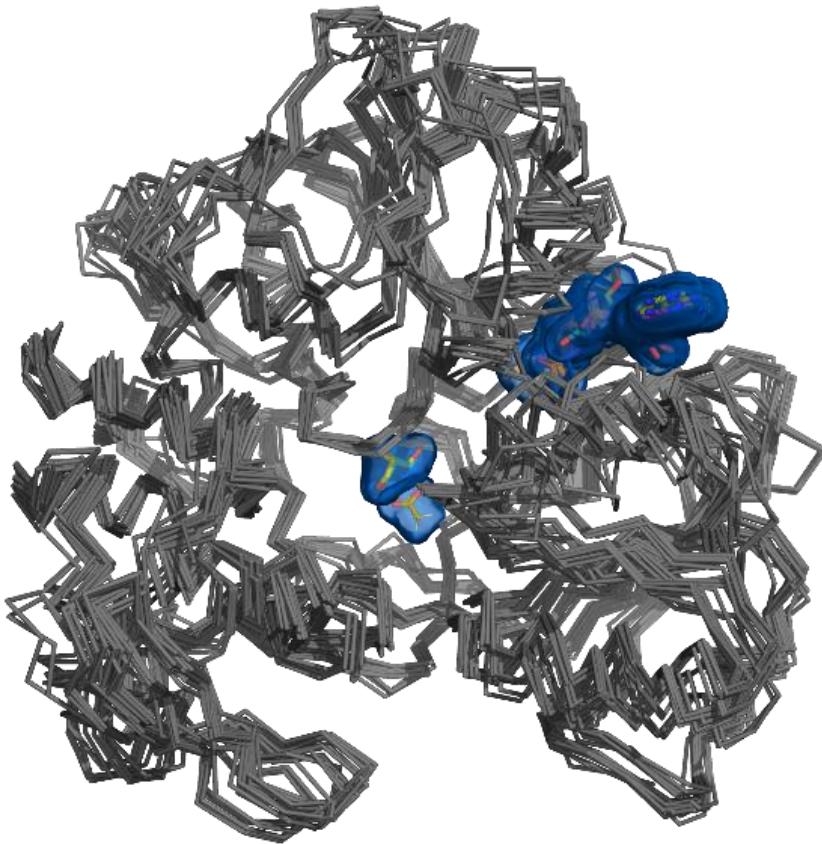


ZIKV NS3-HeI structure

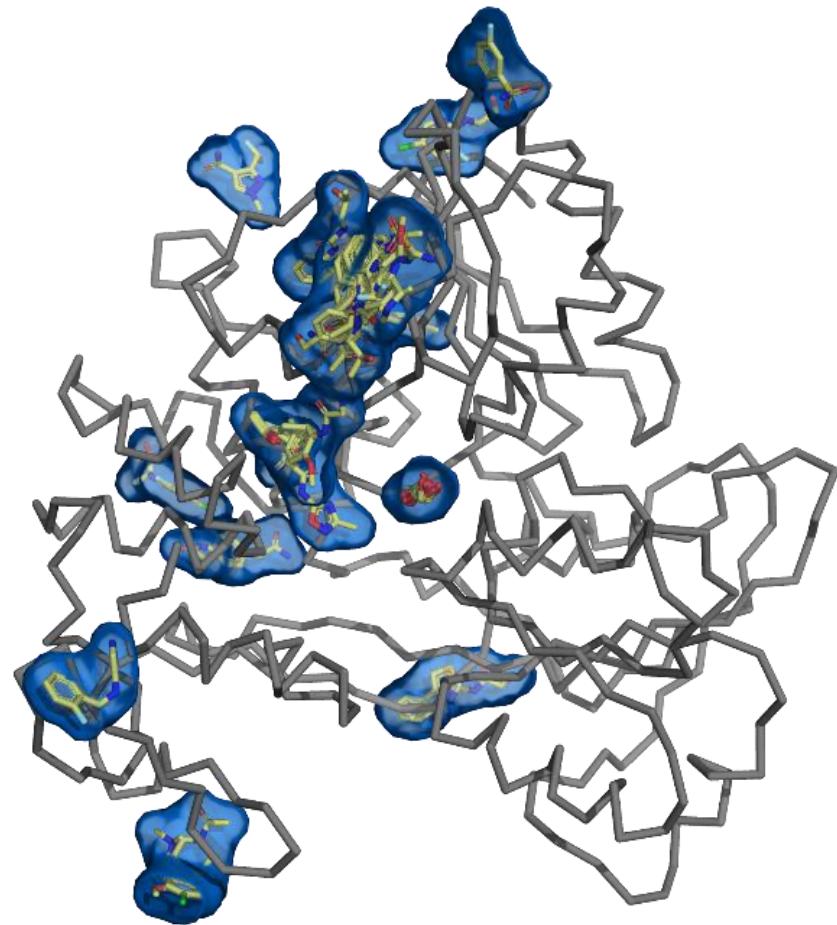


Theoretical predicted sites

- Several hits at the RNA binding site, previously unexplored



*protein ligand complexes for all  
flaviviral NS3-HeL in the PDB*

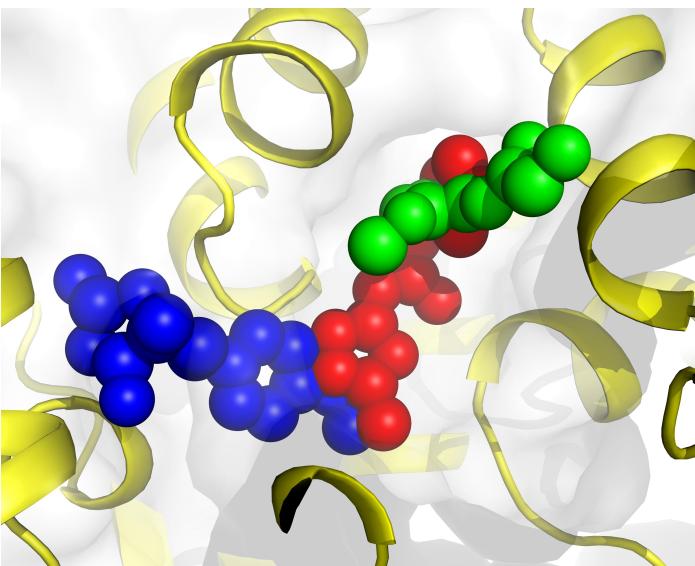
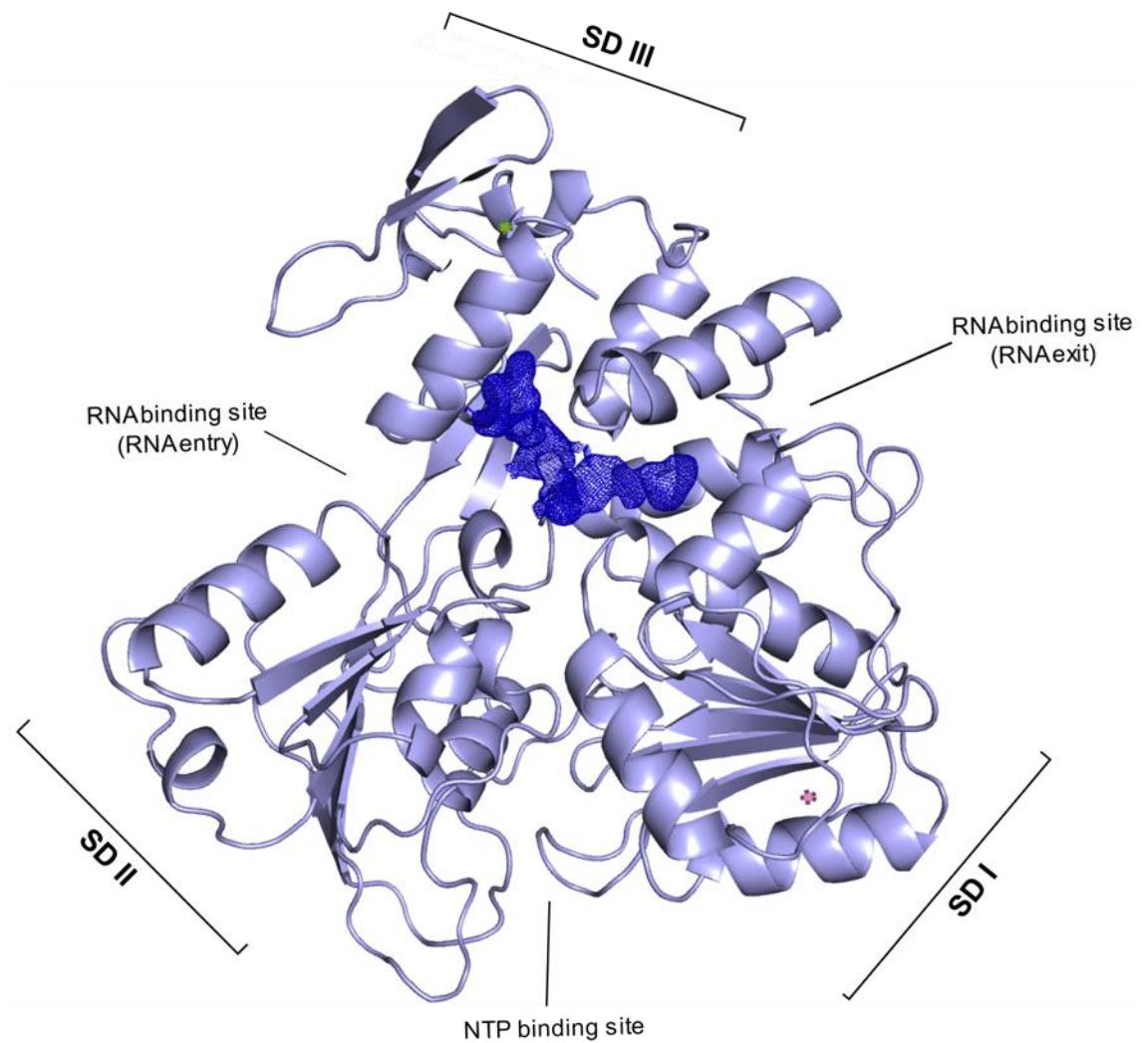


*Results from the X-Chem  
experiment*

# ZIKV NS3<sup>HE</sup> @ xChem Diamond

CIBFar

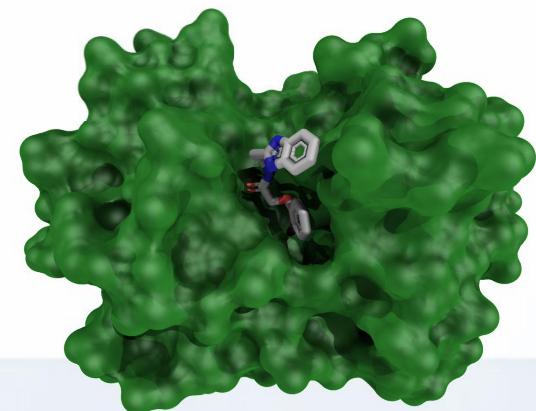
- Three fragments close within binding distance at the RNA binding site



*under development...*

# **Replicons**

**Cell based assays using  
non-infectant clones**



# Cell lines expressing reporter containing viral replicons

## FLAVIVIRIDAE

A



B



## TOGAVIRIDAE

A

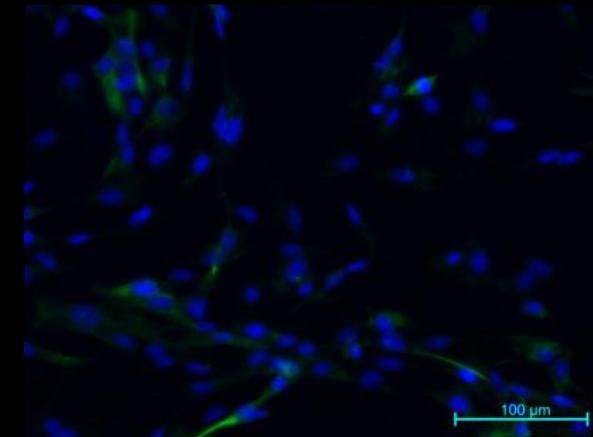
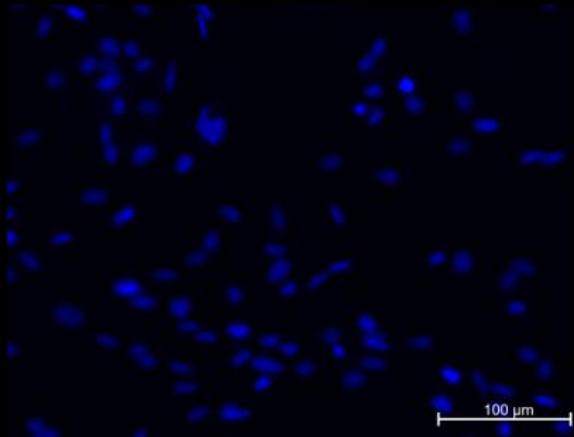
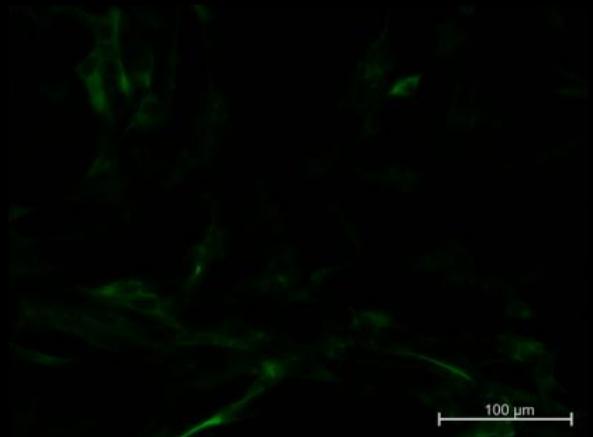


B

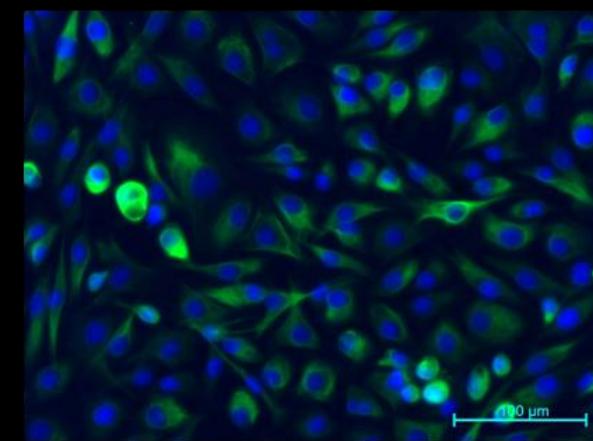
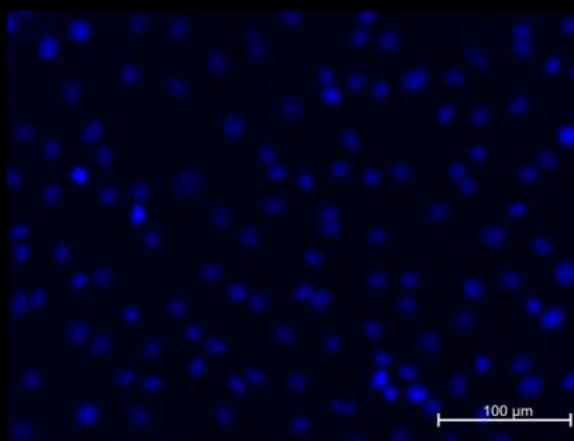
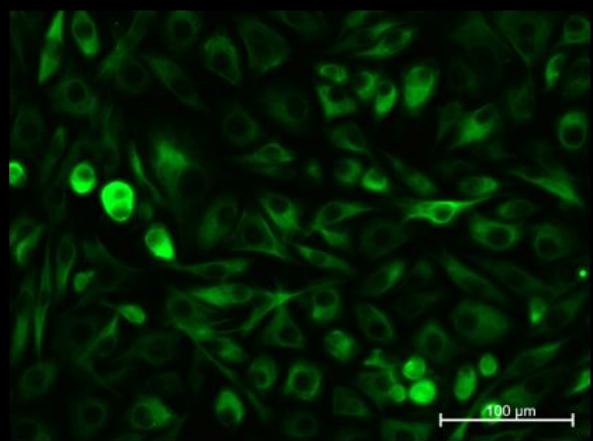


# Flaviviral Replicons

BHK-21



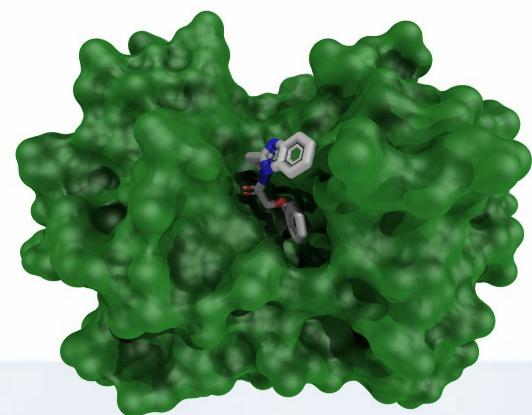
BHK-21-RepYFV7D-LUC



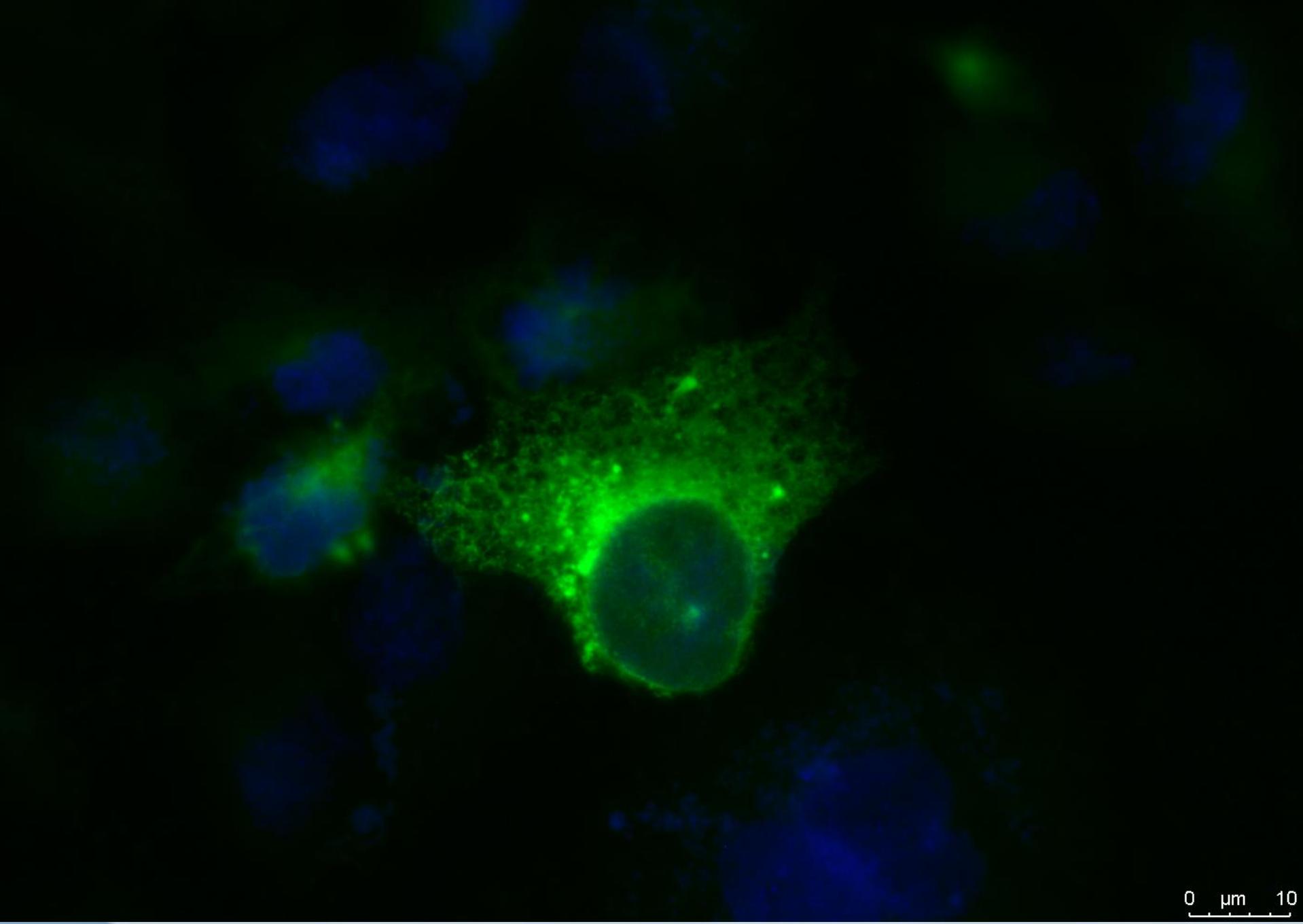
**Antiviral assay using BHK-21 cell line expressing YFV reporter replicon.** Indirect immunofluorescence assay (IFA). NS1 protein expression was evidenced using a monoclonal primary antibody (*mAbF2*) antibody and FITC-conjugated secondary antibody.

# **Viral assembly**

## **Replication complex**

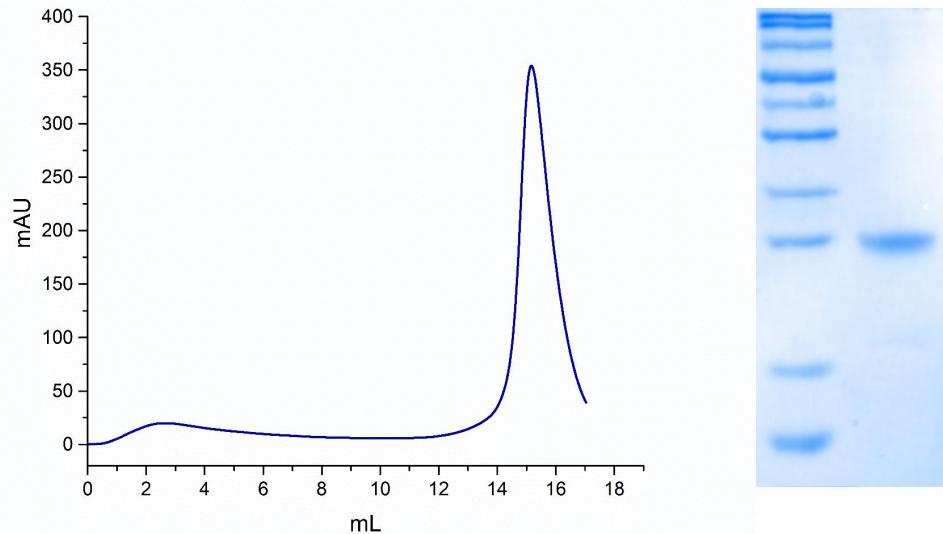
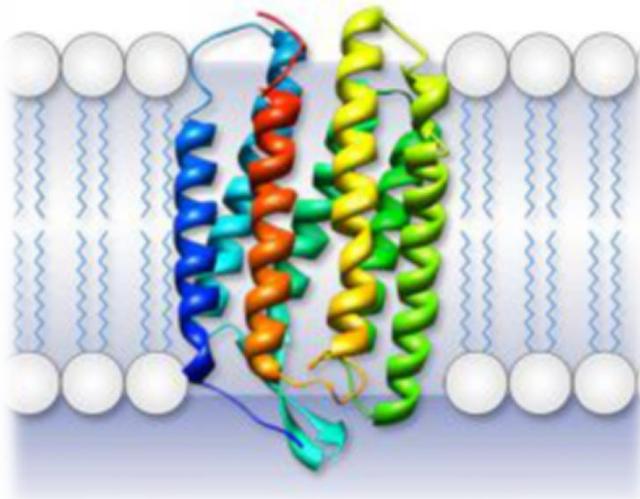


# Transmembrane viral complex

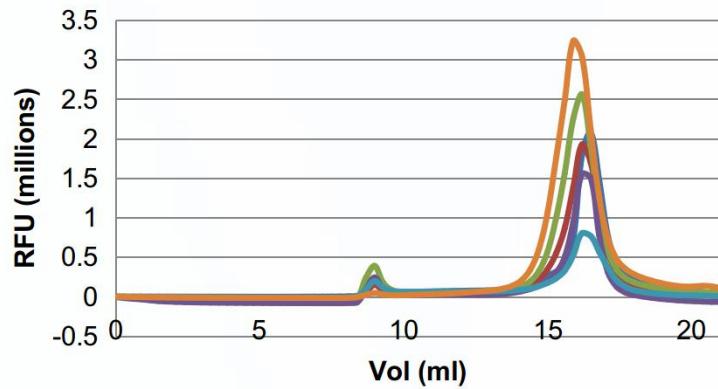


0  $\mu\text{m}$  10

# Transmembrane viral complex

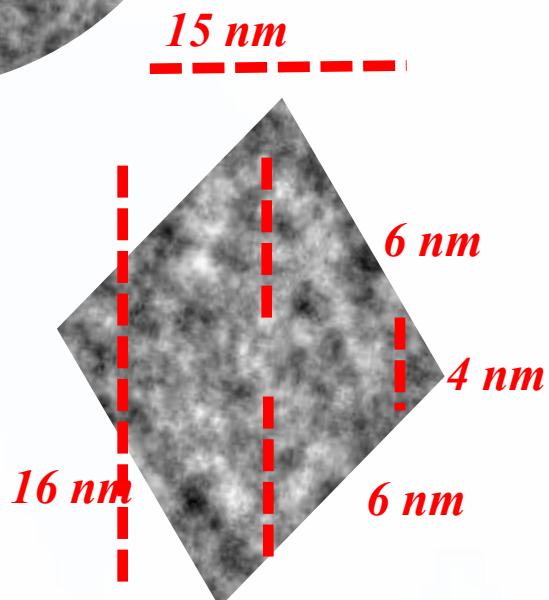
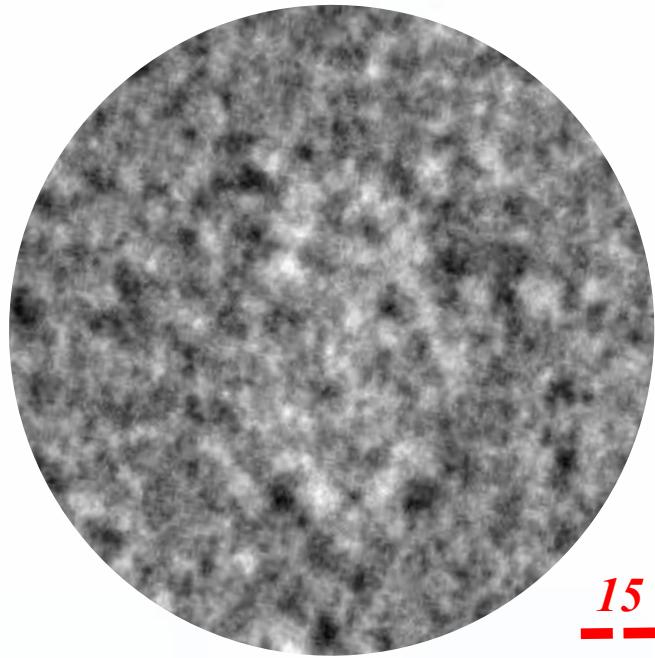


## FSEC - Detergents

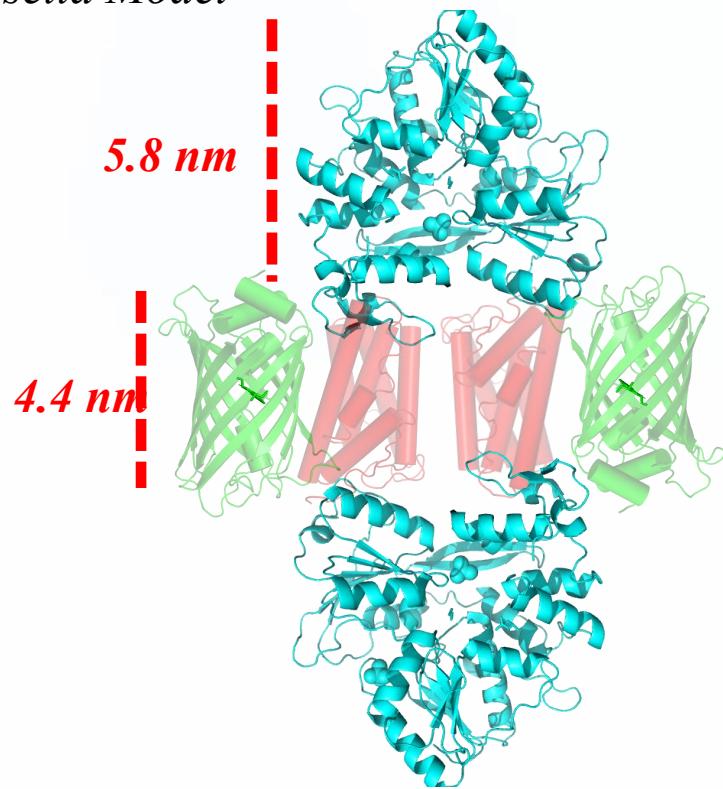


Ms. Edwin Quesnay  
Profa. Andre Ambrosio

# Transmembrane viral complex



- NS3 PDB 6HM3
- NS4B Rosetta Model
- GFP



# Resurgence of Yellow Fever in Brazil/2017

MINAS GERAIS 

## Sete mortes por febre amarela são confirmadas em Minas Gerais

Ministro da Saúde, Ricardo Barros, vai participar de videoconferência com autoridades do estado e do Espírito Santo para discutir casos da doença.

Por G1 MG — Belo Horizonte  
18/01/2017 09h55 - Atualizado há 2 anos



## Casos de febre amarela põem cidades do litoral paulista em alerta no feriado

Quem ainda não se vacinou deve, ao menos, passar repelente e evitar áreas de mata



William Cardoso

SÃO PAULO | AGORA O registro de mortes por [febre amarela em cidades do litoral paulista](#) põe em alerta quem pretende passar o feriado de 7 de

# SCIENTIFIC REPORTS

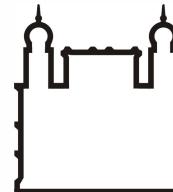
OPEN

## Phylogenetics of Yellow Fever Virus in the Americas: new insights into the origin of the 2017 Brazilian outbreak

Received: 4 May 2017  
Accepted: 30 June 2017  
Published online: 07 August 2017

Daiana Mir<sup>1</sup>, Edson Delatorre<sup>1</sup>, Myrna Bonaldo<sup>2</sup>, Ricardo Lourenço-de-Oliveira<sup>3</sup>, Ana Carolina Vicente<sup>4</sup> & Gonzalo Bello<sup>1</sup>

Yellow fever virus (YFV) strains circulating in the Americas belong to two distinct genotypes (I and II) that have diversified into several concurrent enzootic lineages. Since 1999, YFV genotype I has spread outside endemic regions and its recent (2017) reemergence in non-endemic Southeastern Brazilian states fuels one of the largest epizootic of jungle Yellow Fever registered in the country. To better understand this phenomenon, we reconstructed the phylogenetics of YFV American genotypes using sequences from nine countries sampled along 60 years, including strains from Brazilian 2017 outbreak. Our analyses reveals that YFV genotypes I and II follow roughly similar evolutionary and demographic dynamics until the early 1990s, when a dramatic change in the diversification process of the genotype I occurred associated with the emergence and dissemination of a new lineage (here called modern). Trinidad and Tobago was the most likely source of the YFV modern-lineage that spread to Brazil and Venezuela around the late 1980s, where it replaced all lineages previously circulating. The modern-lineage caused all major YFV outbreaks detected in non-endemic South American regions since 2000, including the 2017 Brazilian outbreak, and its dissemination was coupled to the accumulation of several amino acid substitutions particularly within non-structural viral proteins.



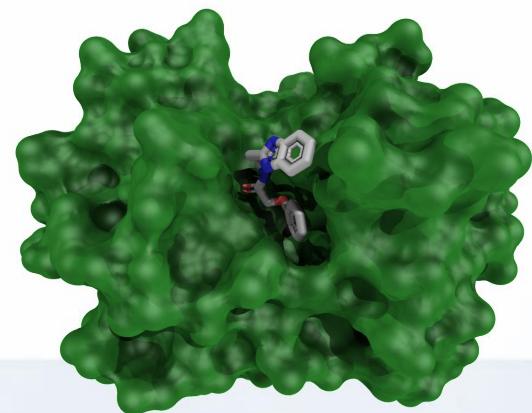
Ministério da Saúde

FIOCRUZ  
Fundação Oswaldo Cruz

Gabriela Noske  
Victor Oliveira  
Ms. Nathalya Furtado  
Dr. Myrna Bonaldo

# **Structural elucidation**

**YFV NS3 protease domain**



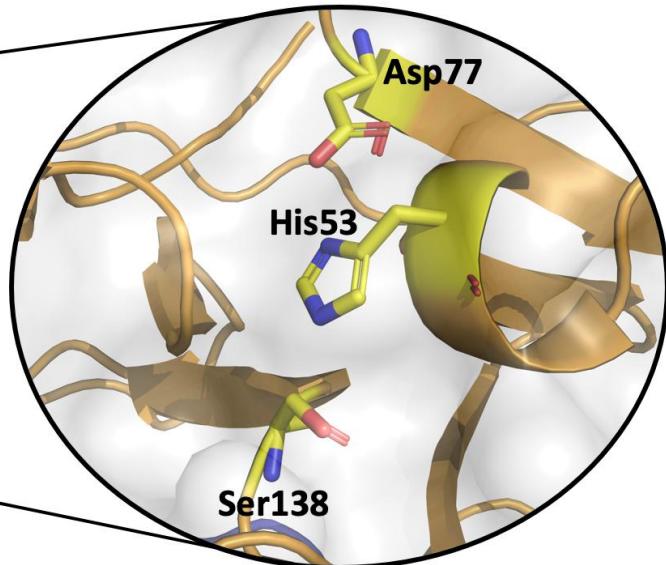
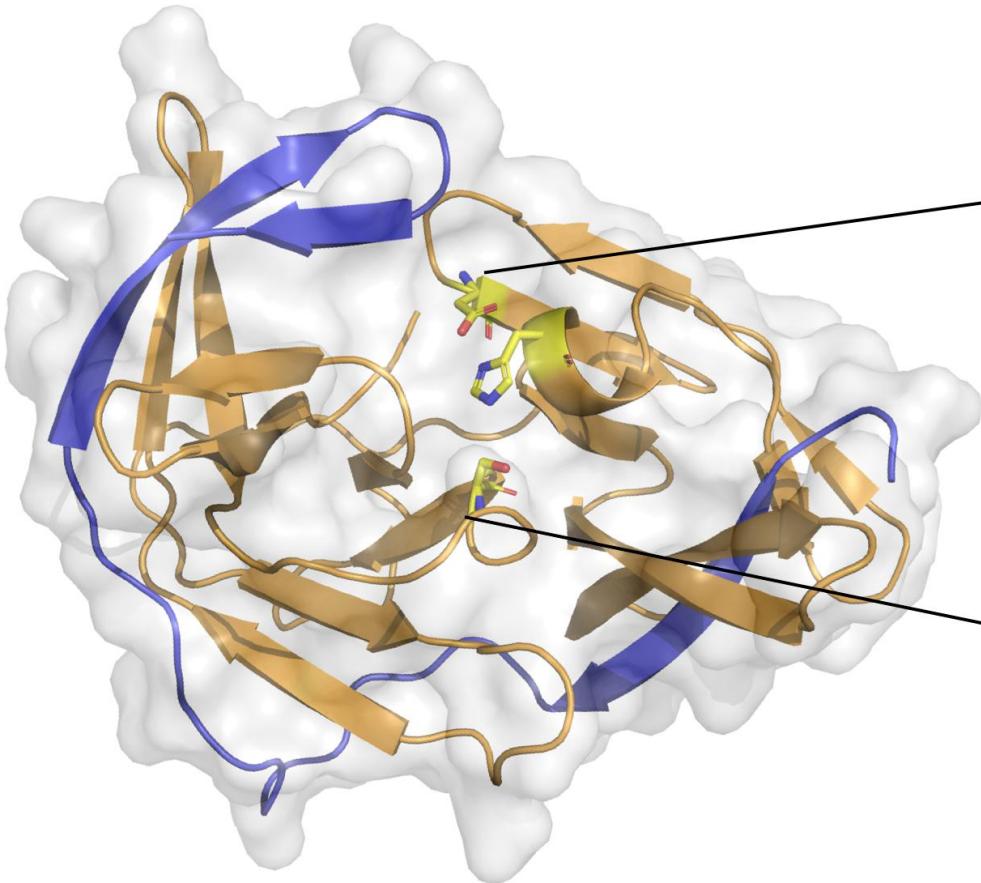
# YFV NS2B-NS3 protease– to be published

CIBFar

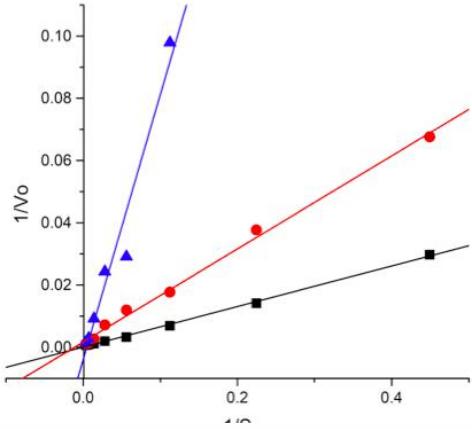
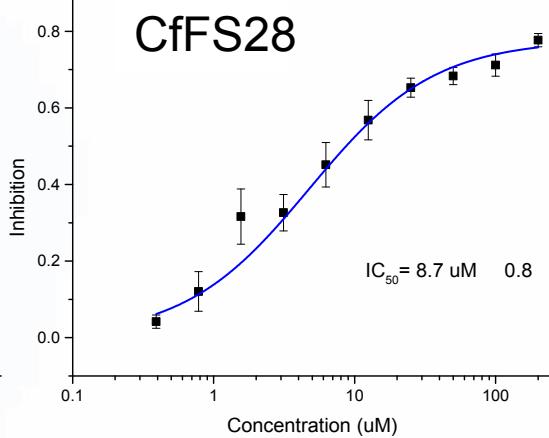
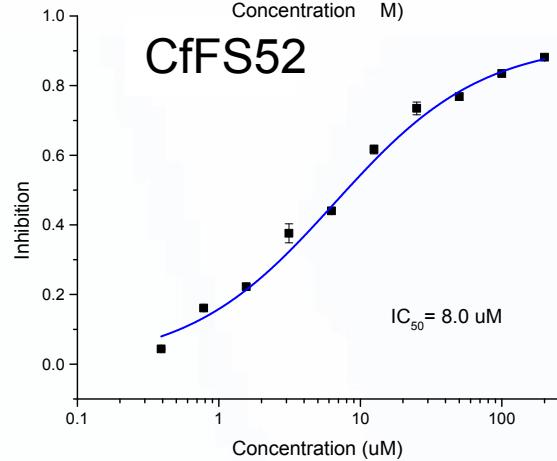
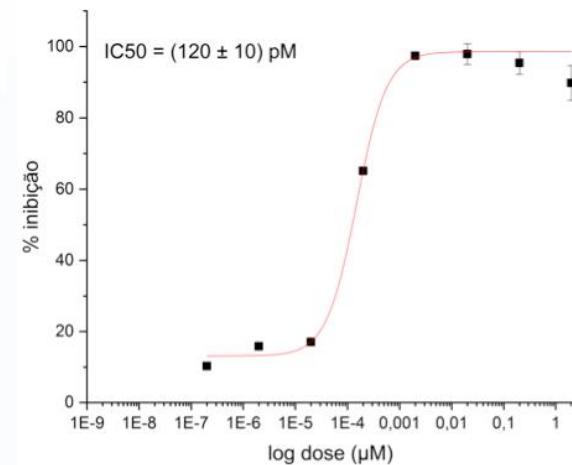
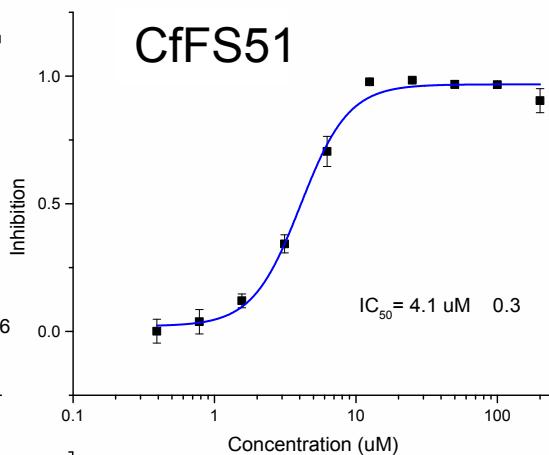
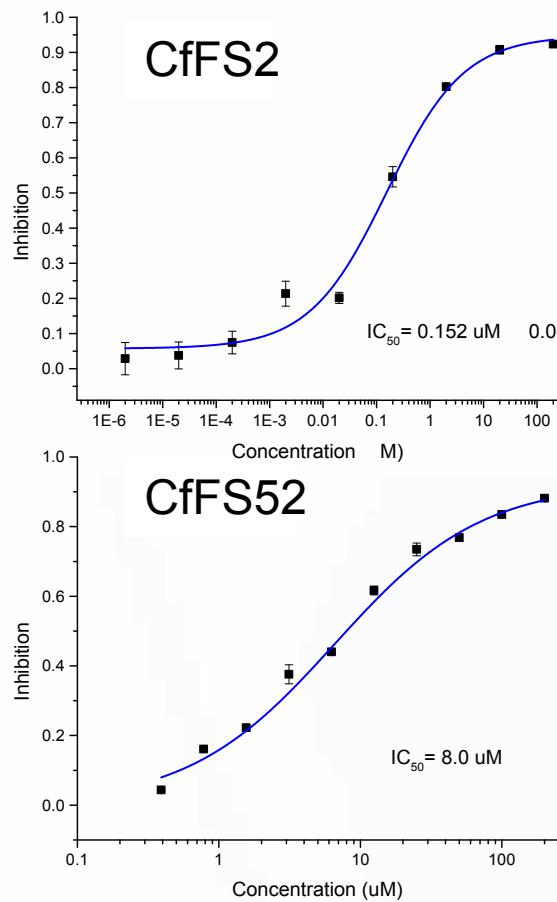


NS2B

NS3 protease



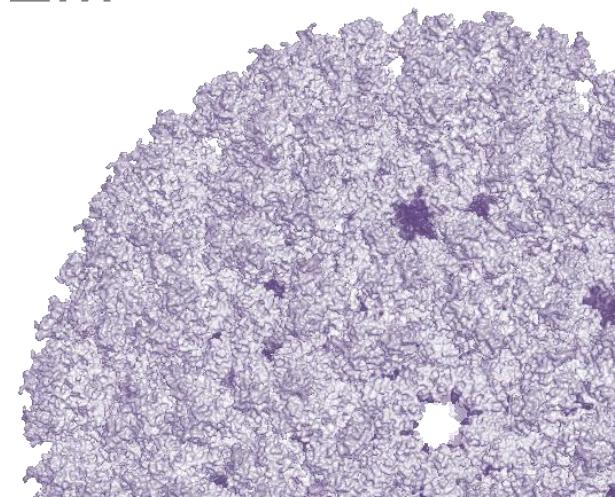
# IS2B-NS3protease YFV



Enzyme kinetics of YFV  
protease versus synthetic  
peptide

compounds series examples  
(about 1,000 tested so far)

- Zika Virus
  - Recombinant proteins
  - Enzyme assays
  - Biochemical assays
  - Cell-based assays
  - X-ray XTAL
  - Cryo-EM
- Yellow Fever Virus
- Chikungunya Virus
- Mayaro Virus



# Acknowledgements



## People @ IFSC/USP



Dr. Rafael V C Guido



André Godoy



Nathalya Mesquita



Rafaela Fernandes



Renata Vieira



Bruna Macedo



Victor Oliveira.



Ketllyn Oliveira



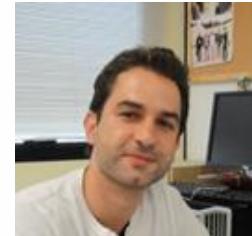
Gabriela Noske



Marjorie Freire



Gustavo Lima



Andre Ambrósio



*Congratulations and thank you !*