

# *Structural studies of viral envelope proteins and insight for vaccine design*



GIVRF, March 15, 2016

Félix Rey

Institut Pasteur, Paris

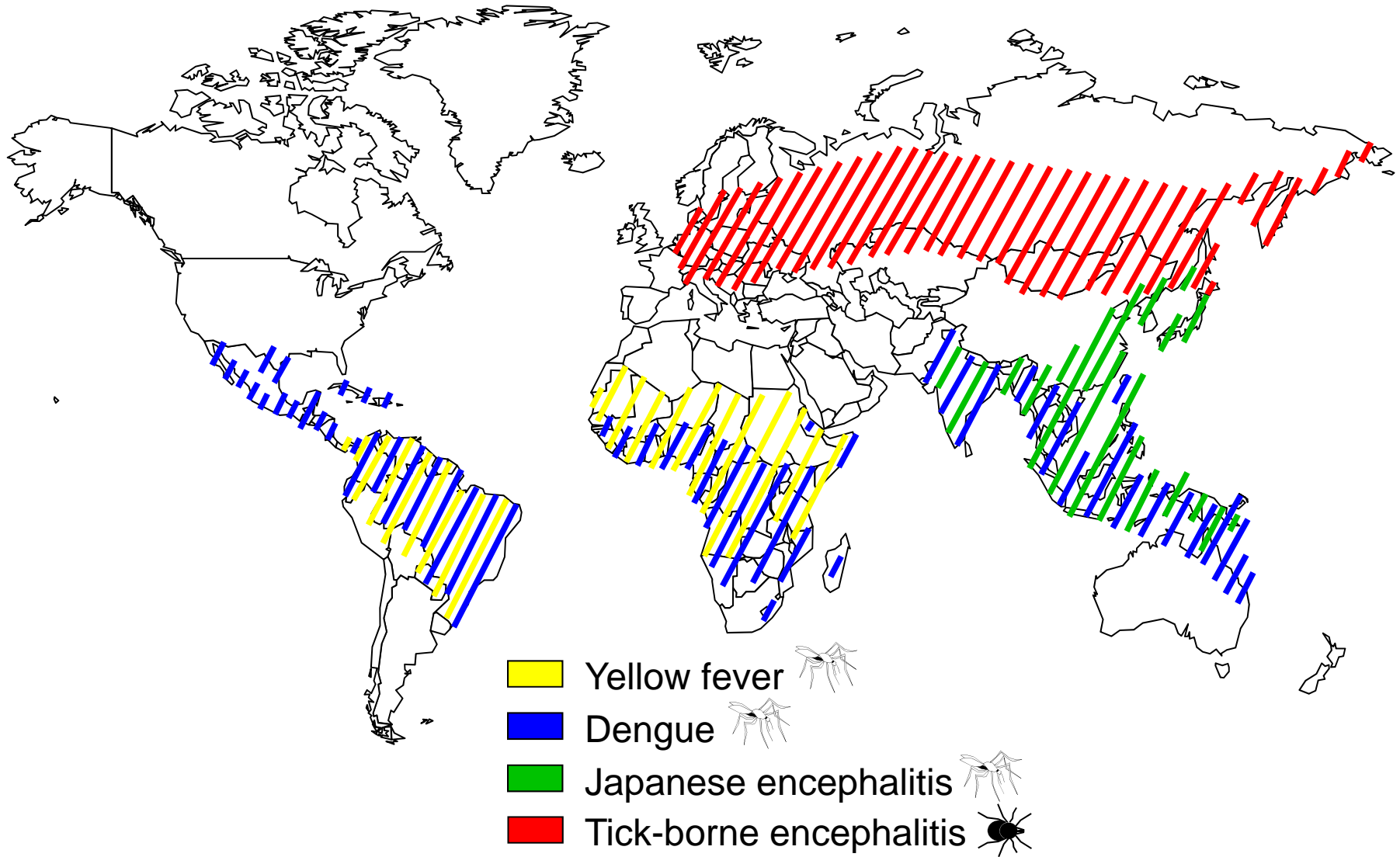
# Dengue virus

- There are four different dengue viruses: serotypes 1-4
- The envelope protein E is the sole target of neutralizing antibodies. It shares 65% aa sequence identity between the most distant serotypes
- Infection by one serotype leads to life-long immunity against that serotype, but infection by other serotypes can be more serious
- Macrophages can become infected via Fcγ receptors through non-neutralizing antibodies bound to viral particles (ADE).

# Flaviviruses

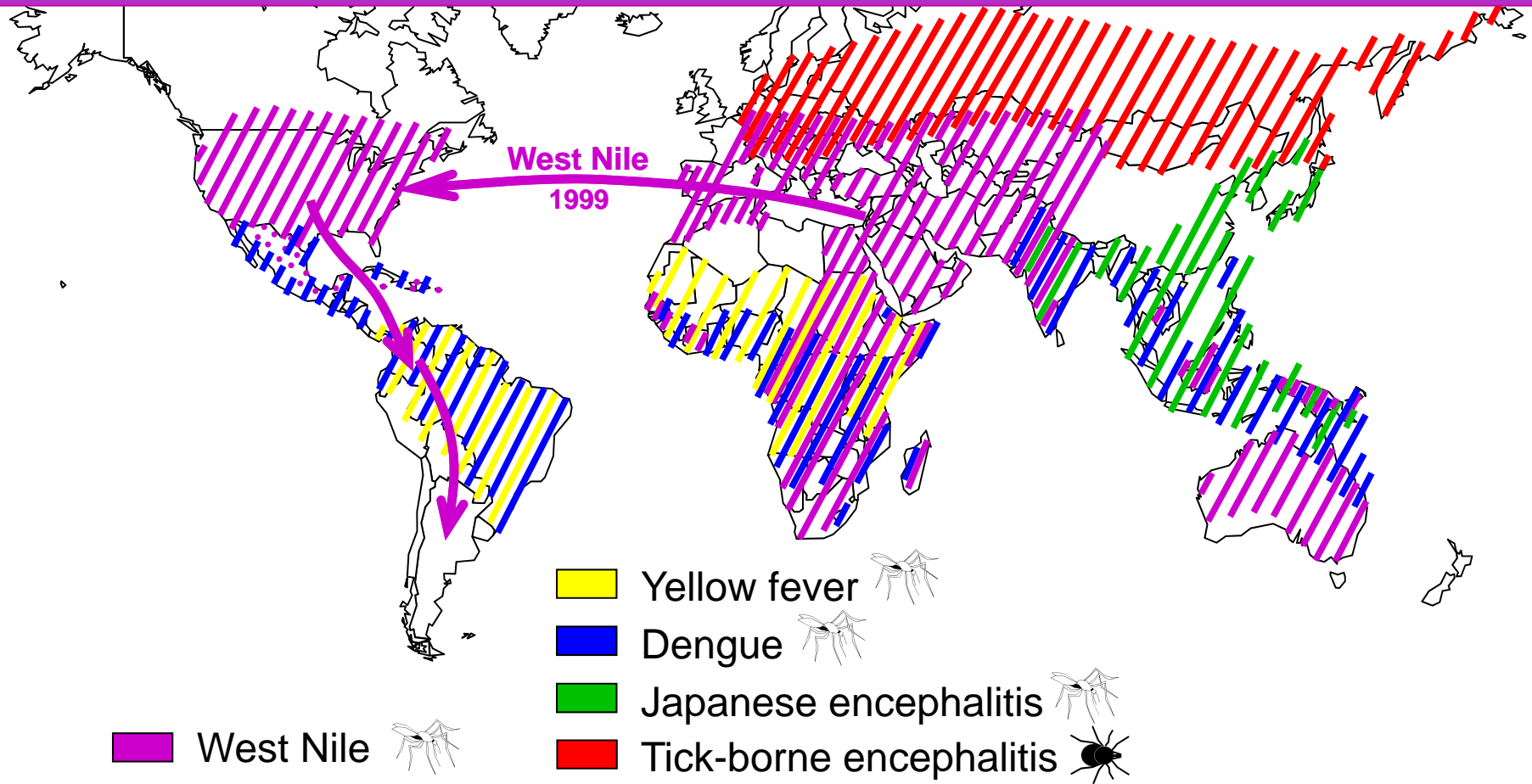
- Group of small enveloped viruses with a positive-sense, single stranded RNA genome, encoding a single polyprotein precursor to all viral proteins
- They cause serious disease and are of global concern. These include encephalitis, fevers, hemorrhagic fevers.
- The geographic distribution generally follows the distribution of the arthropod vector (insects or ticks)

# Flaviviruses

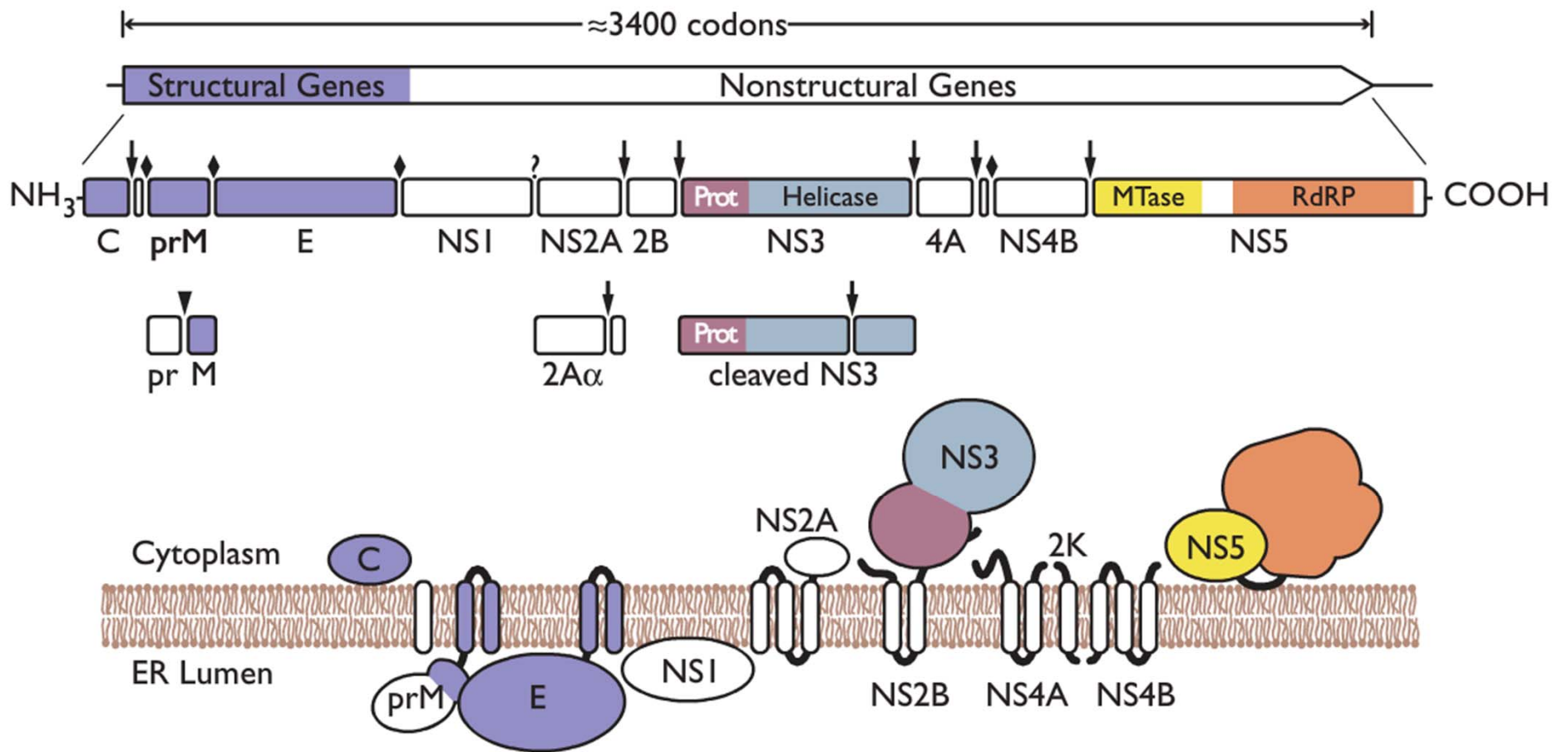


# Flaviviruses

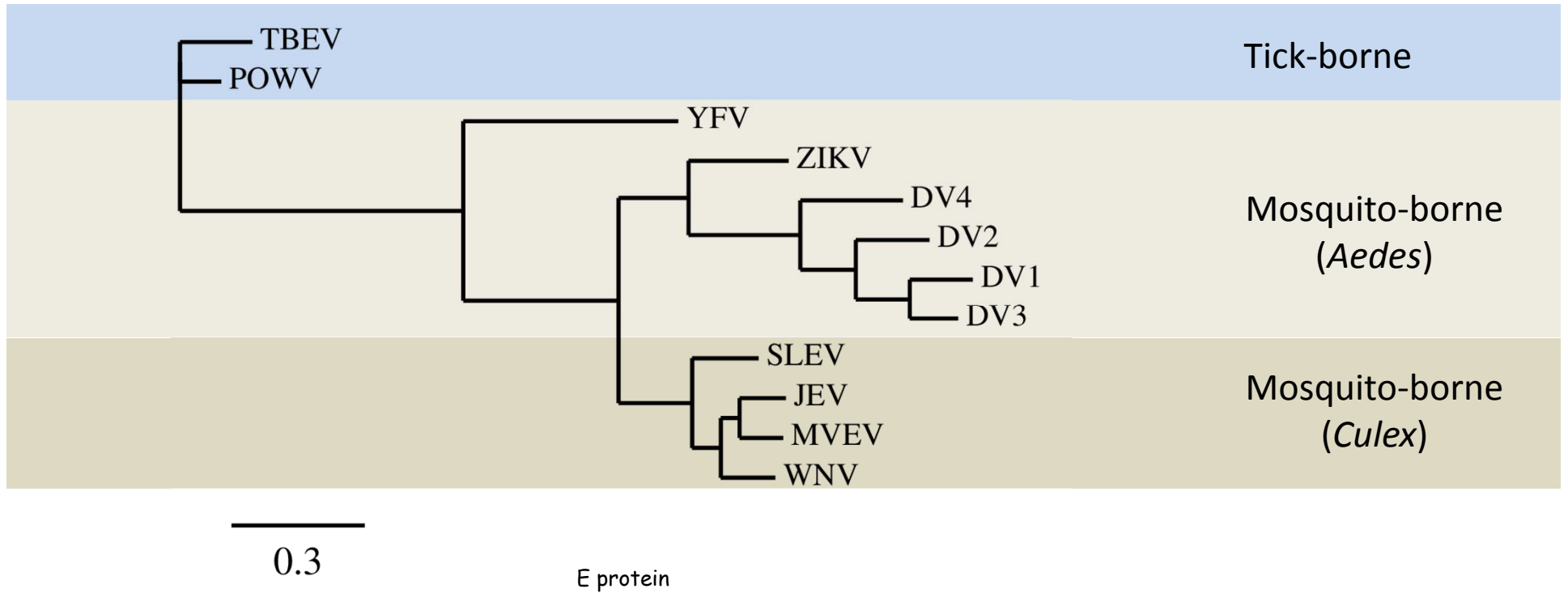
Similarly, now zika virus appeared in South America and is expanding toward the Caribbean islands, after having initially spread from Africa to South East Asia and then to Polynesia



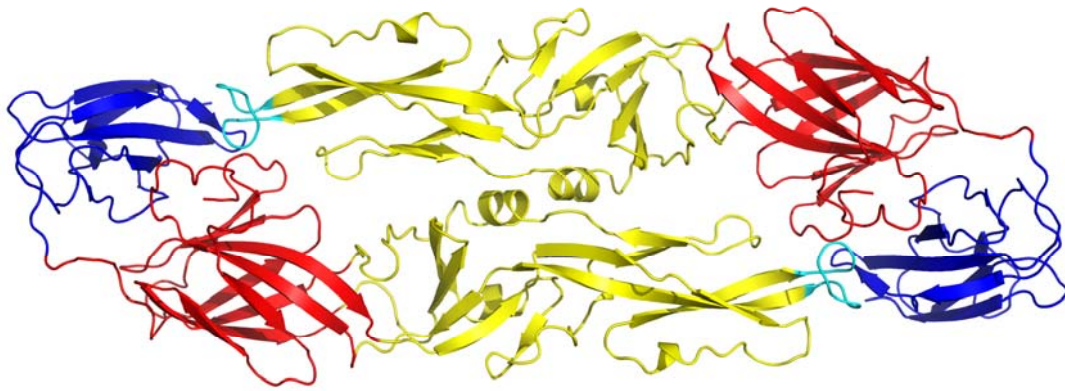
# Flavivirus Genomic Organization:



# Flaviviruses: phylogenetic tree based on protein E



## The main antigen of dengue virus: protein E



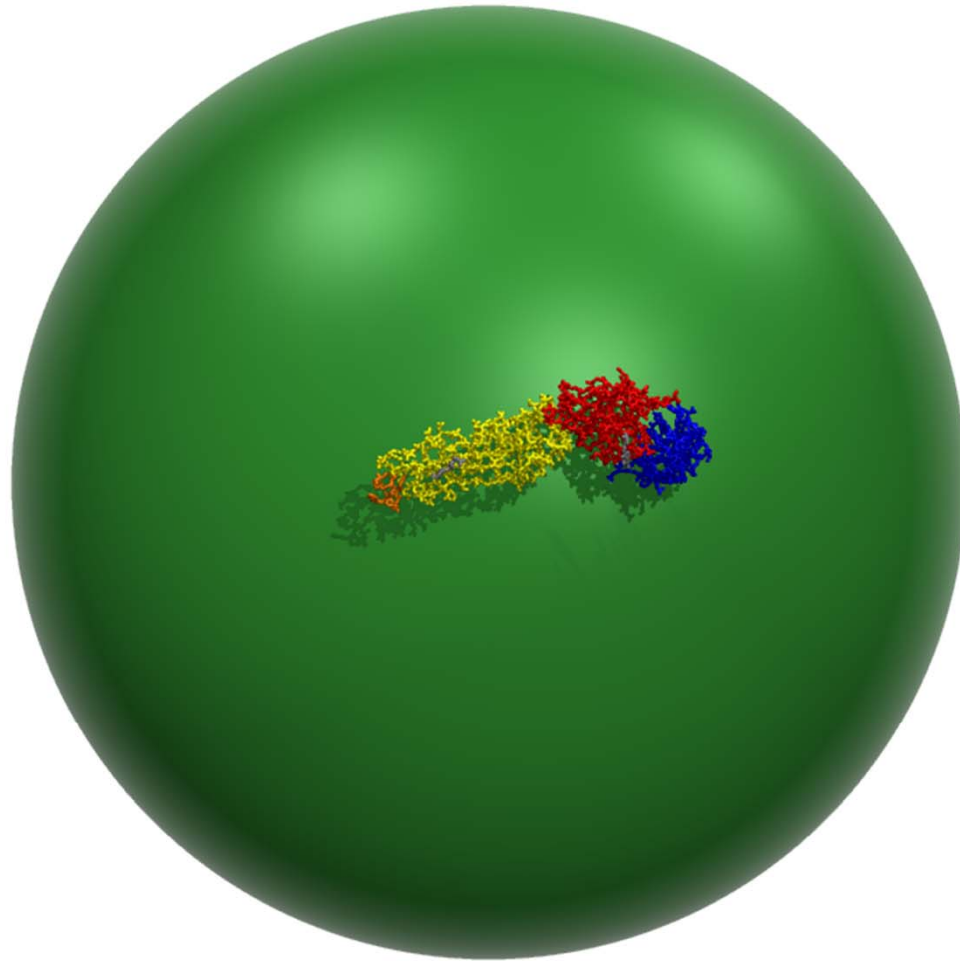
### **Pre-fusion form (dimer)**

Modis et al, 2003

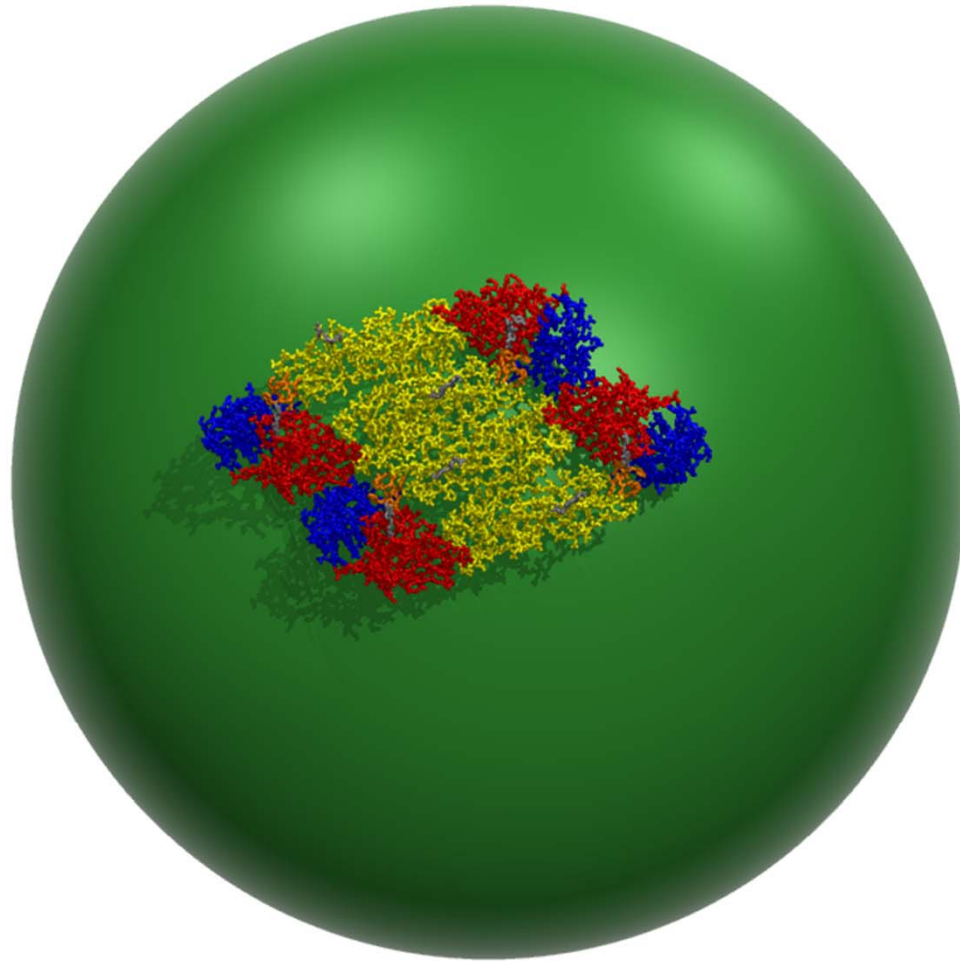
Rey et al, 1995



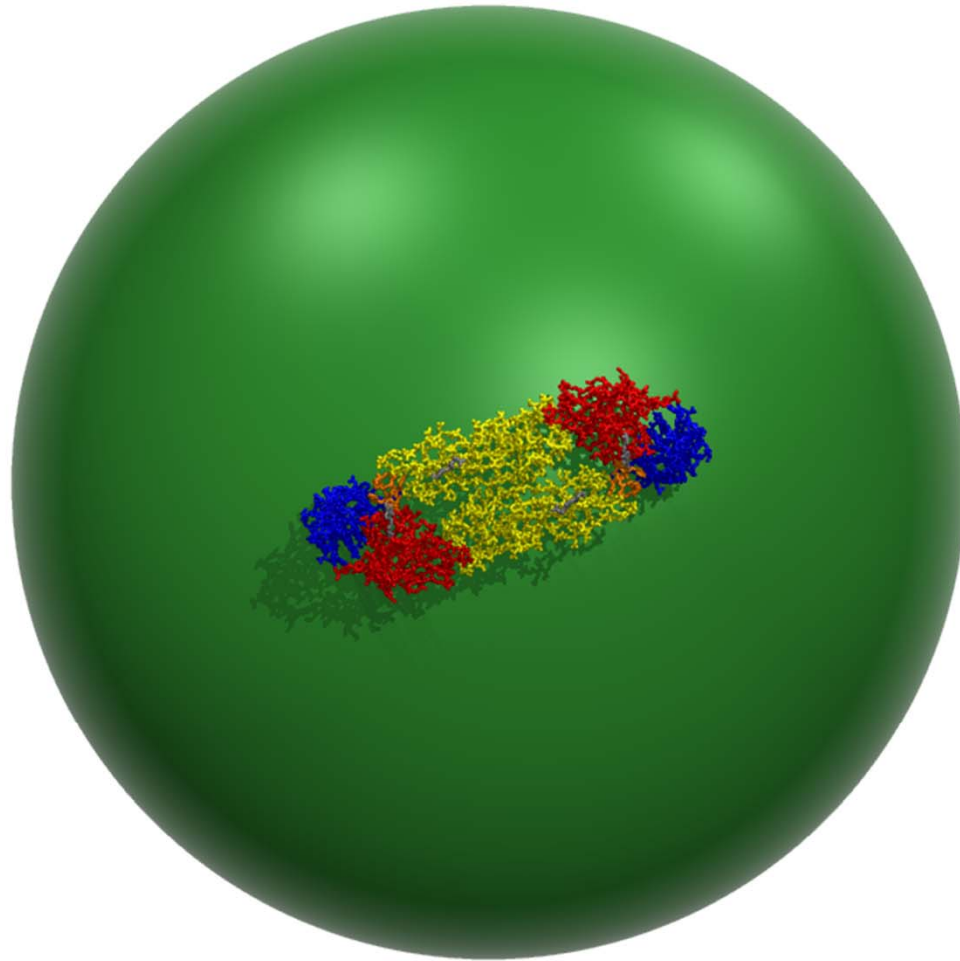
Mature flavivirus particle:



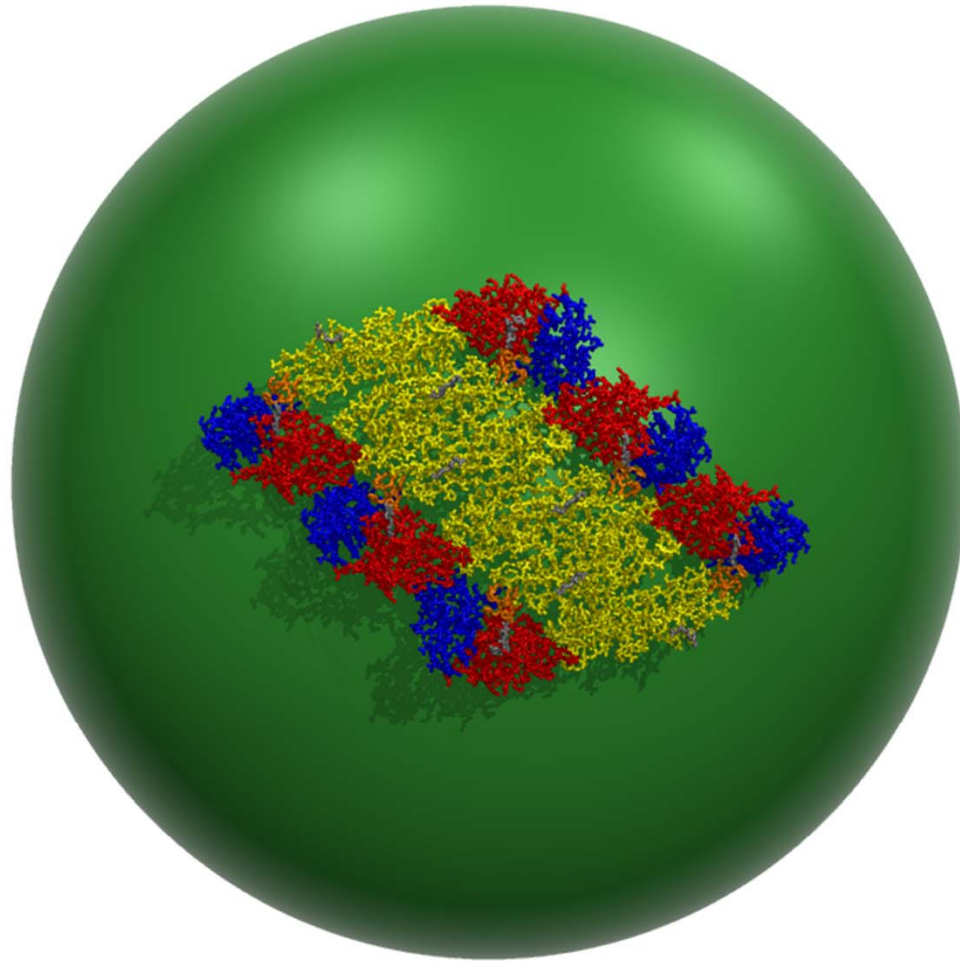
Mature flavivirus particle:



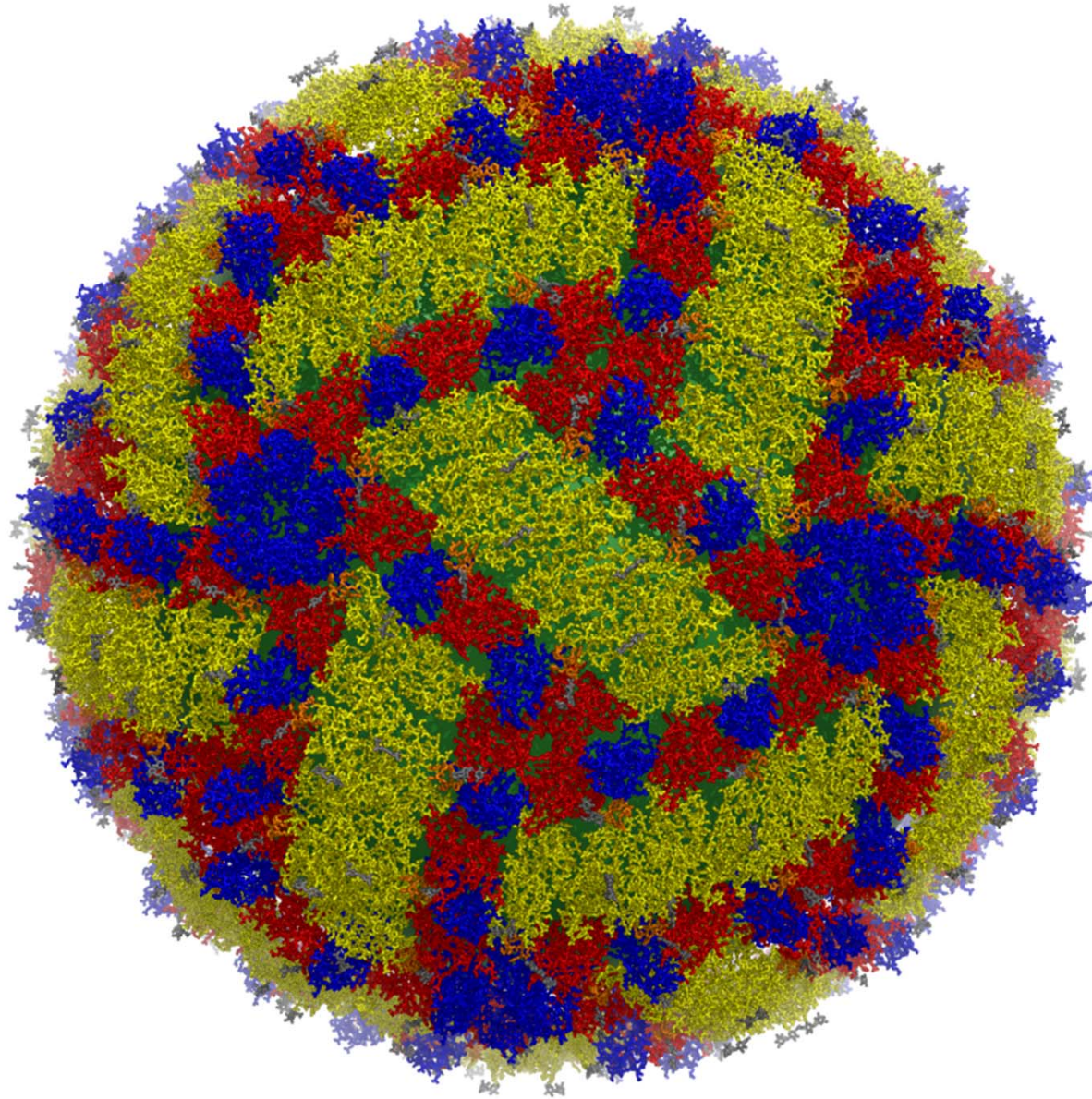
Mature flavivirus particle:



Mature flavivirus particle:



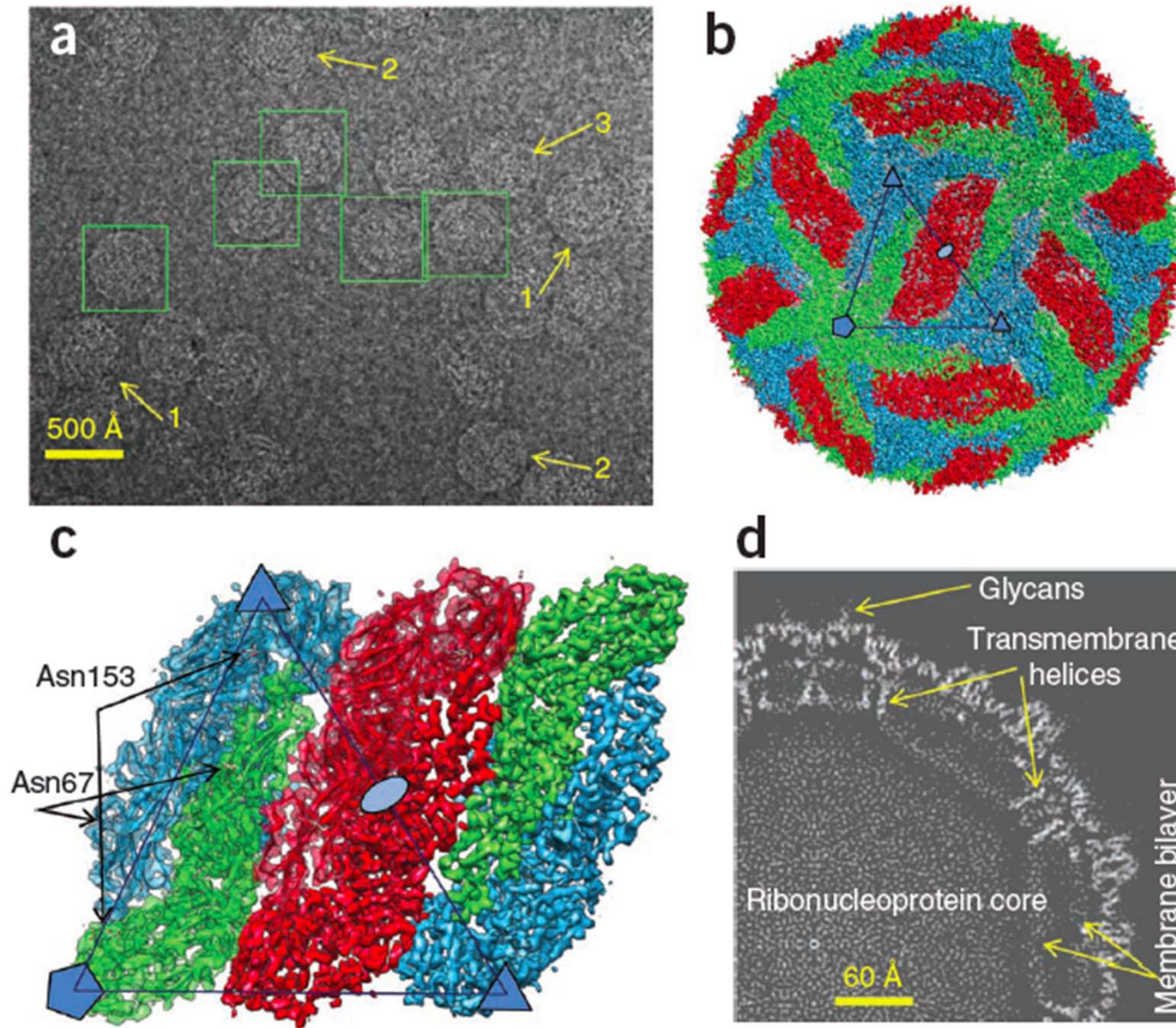
Mature flavivirus particle:



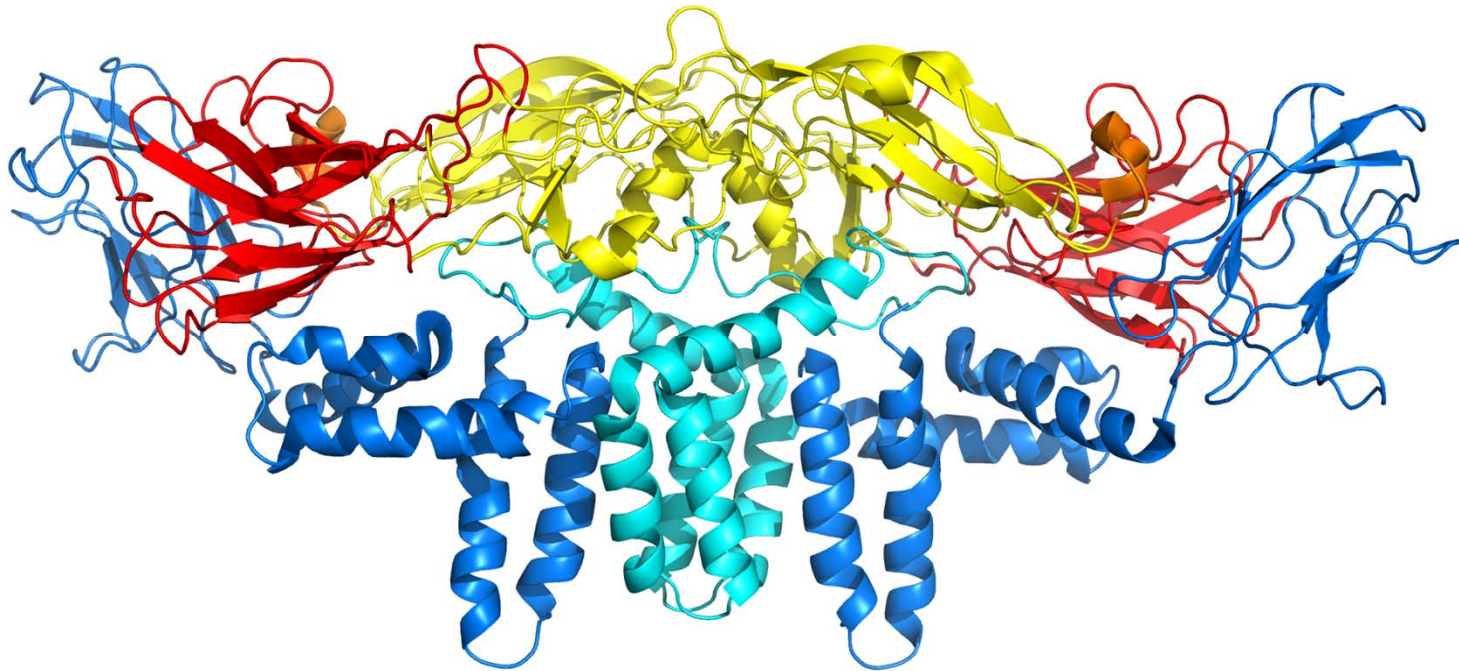
# Cryo-EM structure of the mature dengue virus at 3.5-Å resolution

Xiaokang Zhang<sup>1-5,9</sup>, Peng Ge<sup>1-3,9</sup>, Xuekui Yu<sup>1-3</sup>, Jennifer M Brannan<sup>3,8</sup>, Guoqiang Bi<sup>4,5</sup>, Qinfen Zhang<sup>6</sup>, Stan Schein<sup>2,7</sup> & Z Hong Zhou<sup>1-5</sup>

NSMB 2013



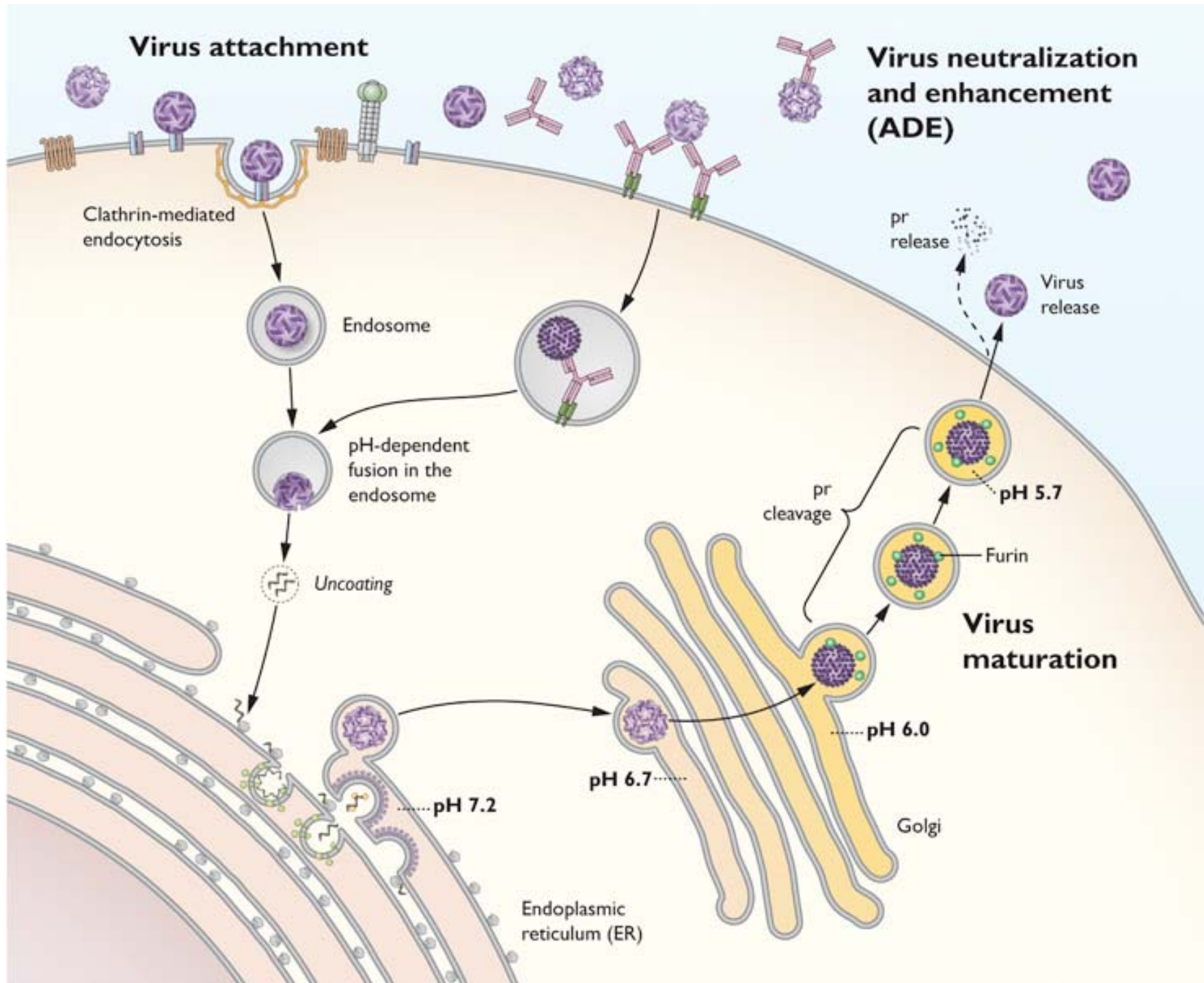
mature DENV-2 M-E dimer  
(3J2P)

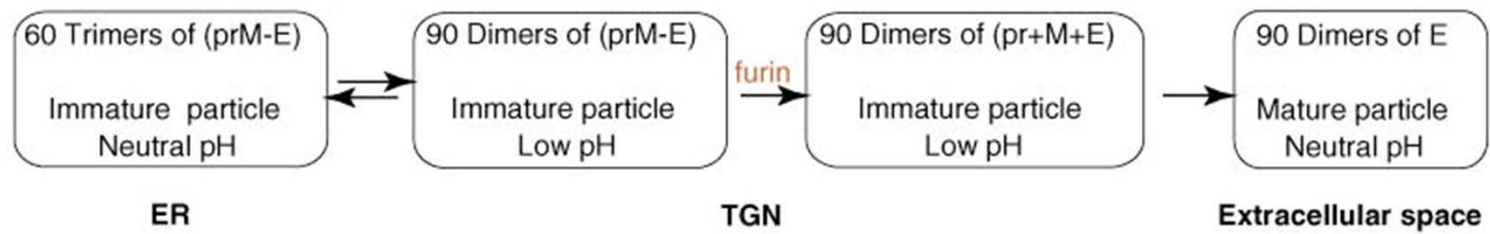
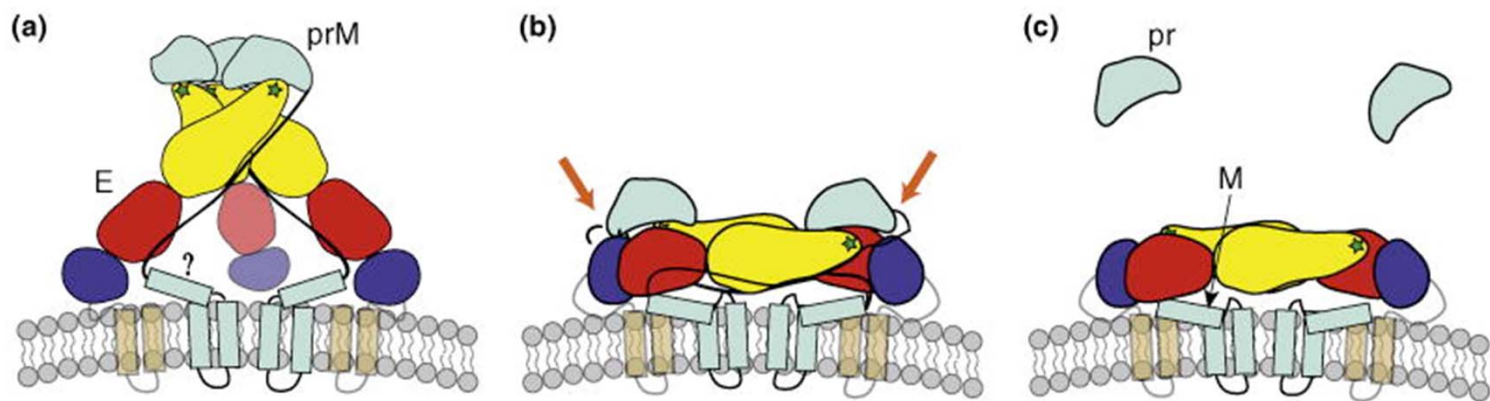


cryo-EM structure at 3.6 Å resolution  
(Zhang *et al*, NSMB, 2012)

- **DENV buds as immature particles in the ER of the infected cell**
- **Immature DENV particles contain a heterodimer between the envelope protein E and the precursor membrane glycoprotein (prM)**
- **These particles have 60 trimeric spikes with prM/E subunits**

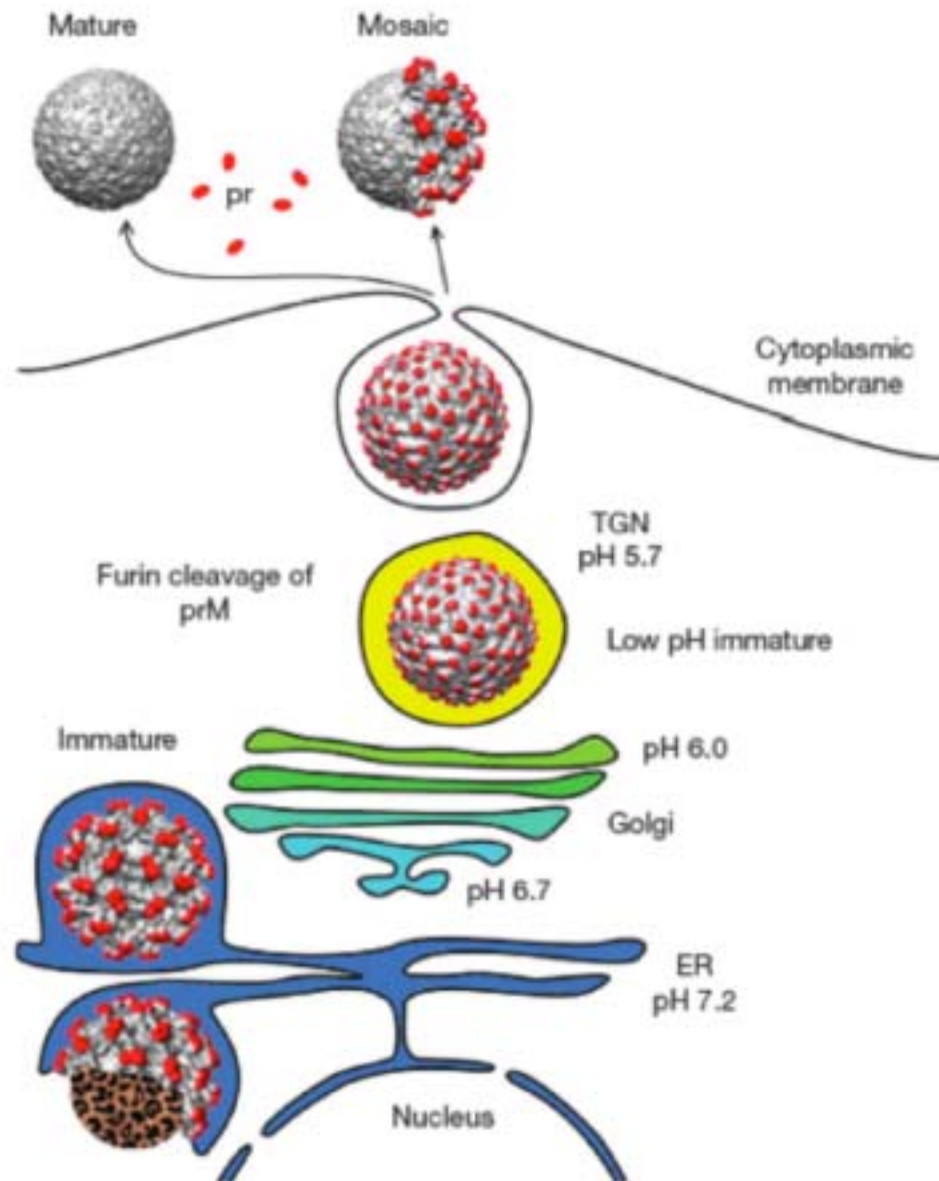






Structure of maturation-deficient dengue virus

*P. Plevka et al*



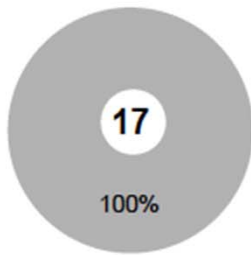
- **The extent of maturation depends on cell type.**
- **In some cells, the amount of unprocessed prM is more than 60%.**
- **This means that dengue virus is presented to the immune system in a very heterogeneous way.**
- **Antibodies against prM are non-neutralizing, and can be strong enhancers of the infection (ADE)**
- **The epitopes of the neutralizing antibodies produced in humans have been a matter of debate.**

- **The structure of the mature virion, displaying dimers tightly packed, is only a medium (or time-average) structure**
- **Mature dengue particles show a highly dynamic behavior**
- **This behavior is a consequence of the metastability of the protein, which needs to undergo a major conformational change to induce fusion.**
- **In addition, about 1000 to 10000 particles are needed in average for an infection event**
- **The vast majority of dengue particles displays regions that are buried in functional, well structured dimers required for entry into cells.**

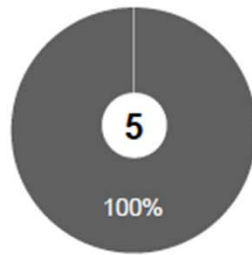
- The challenge is to protect against all four dengue viruses simultaneously
- The Sreaton and Mongkolsapaya laboratories at Imperial College recently isolated antibodies out of plasmablasts from dengue patients, following a cohort in Thailand

# Abundance of conformational Abs in select patients

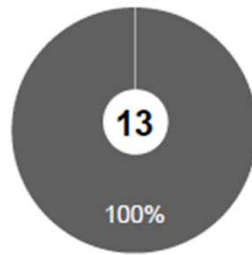
Patient # 747



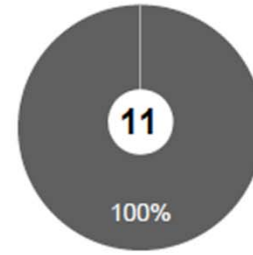
749



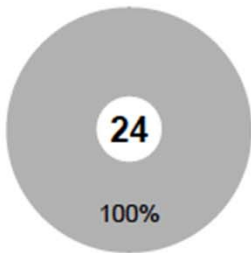
750



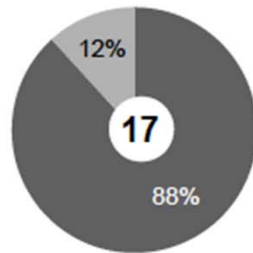
751



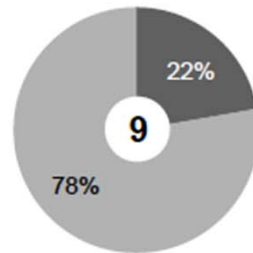
752



753

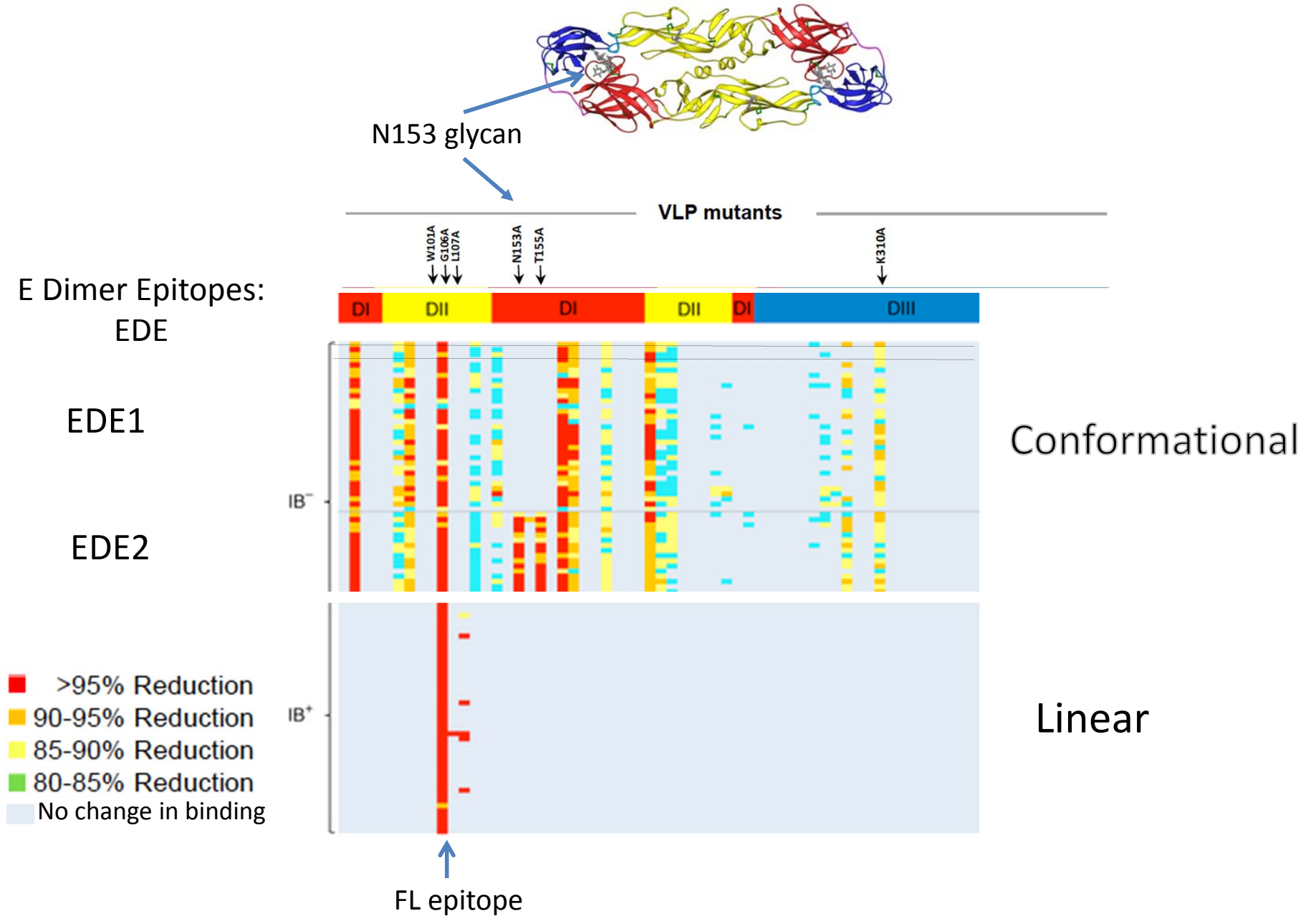


758



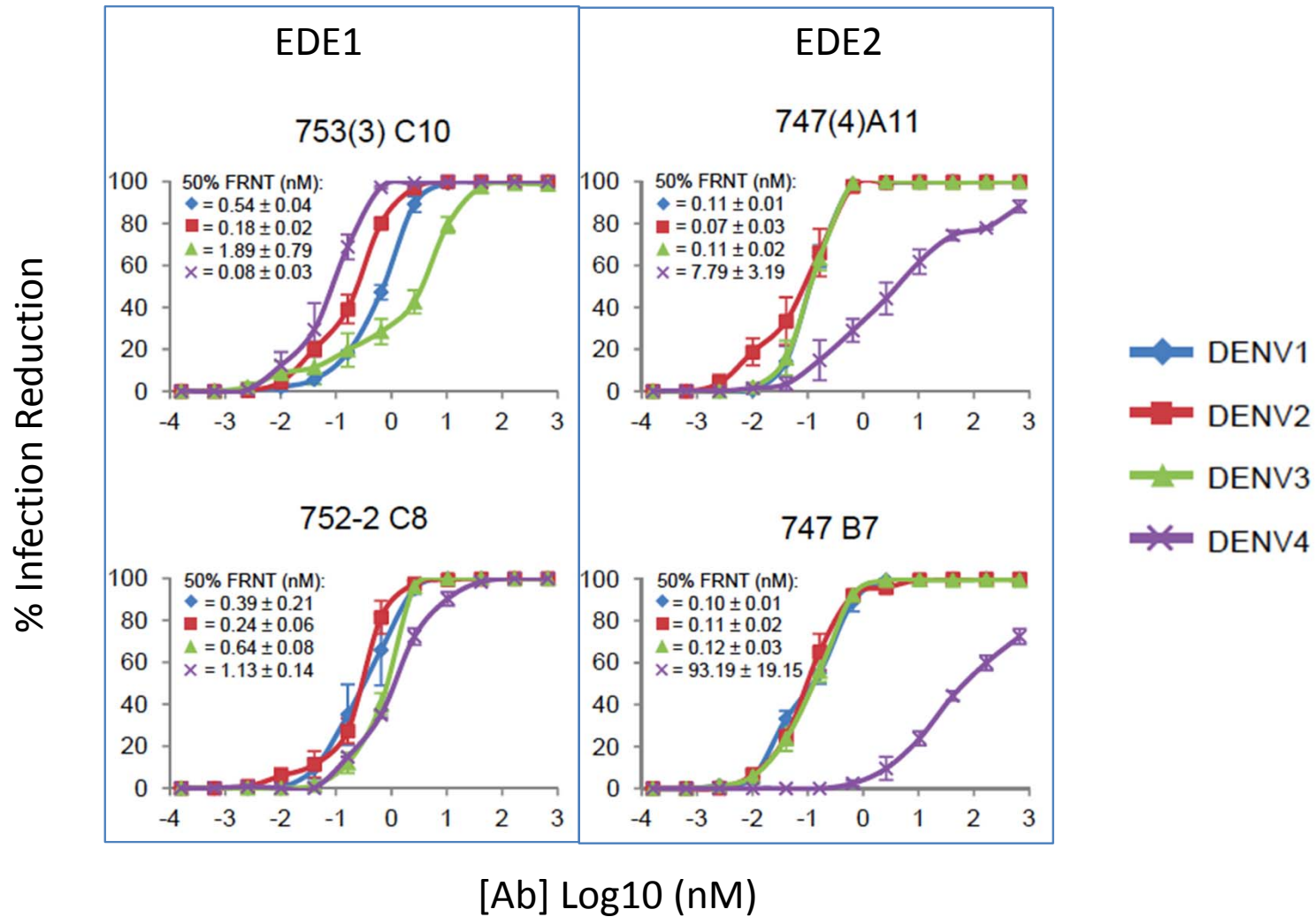
Conformational  
Linear

# Mapping epitopes by Ala scanning mutagenesis on VLPs



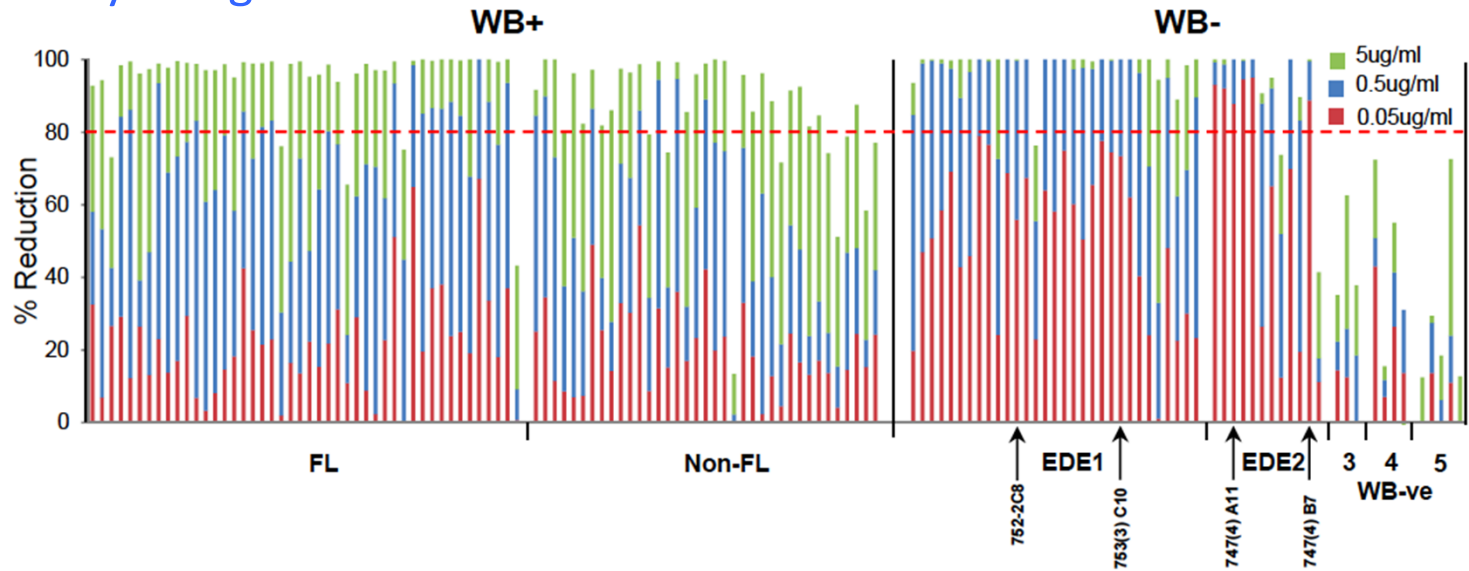


# Infection reduction by select Abs assayed on all four serotypes

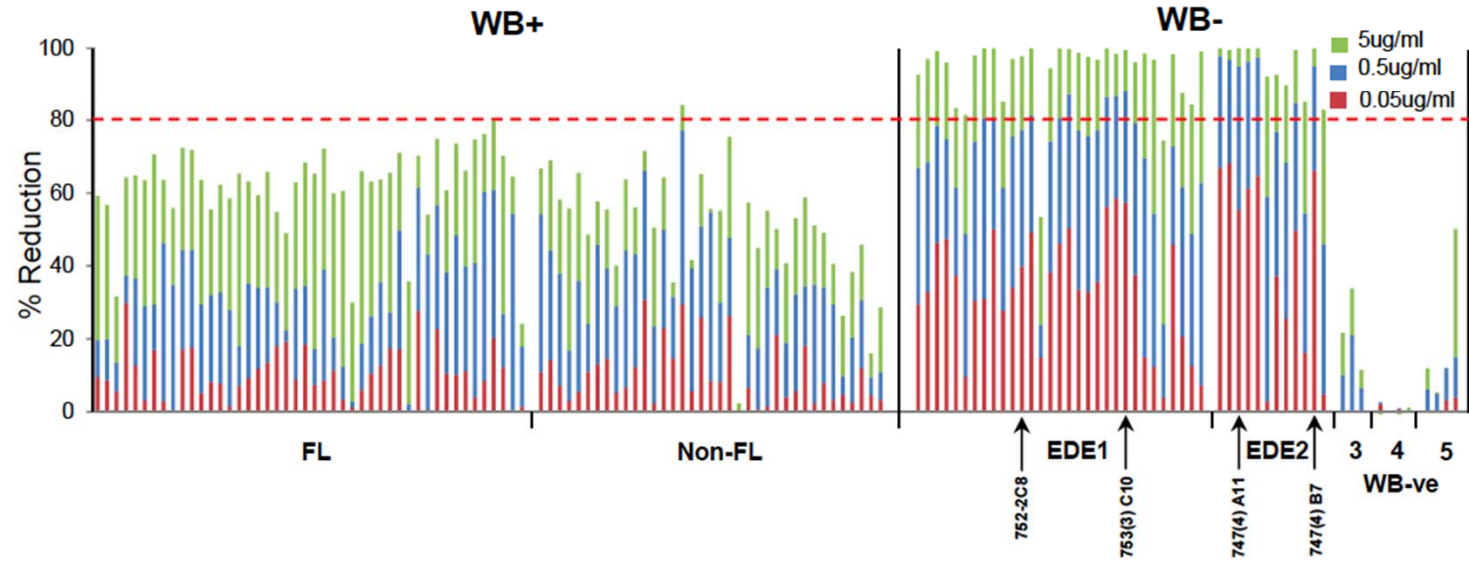


# Infection reduction assayed by focus-forming assay using DENV2

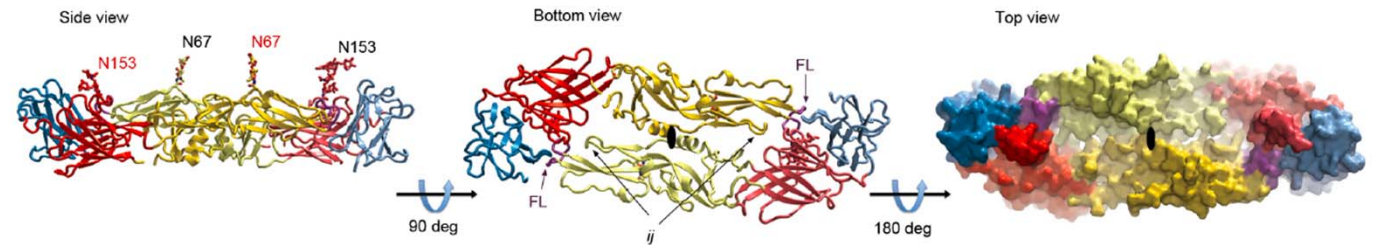
## C6/36-DENV



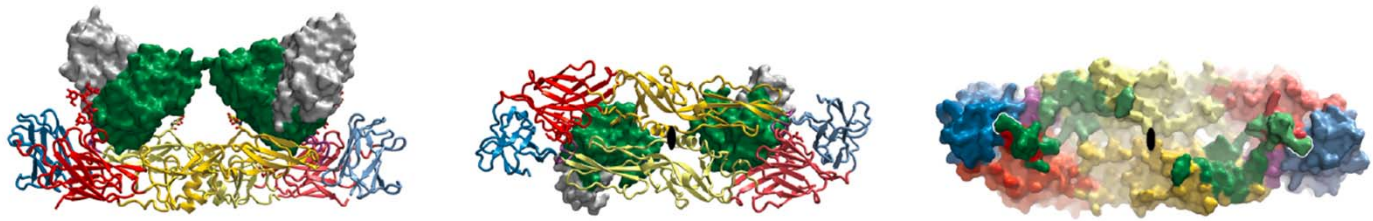
## DC-DENV



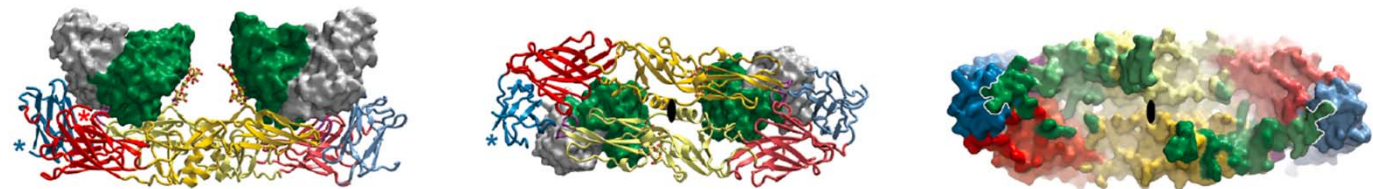
**a - DENV-2 sE**



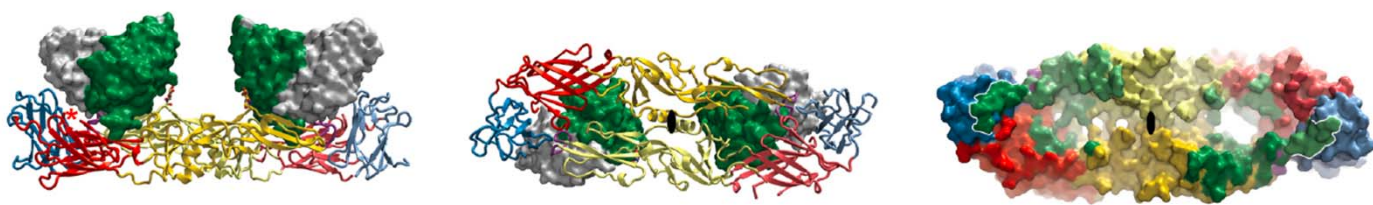
**b - DENV-2 sE / EDE2 B7**



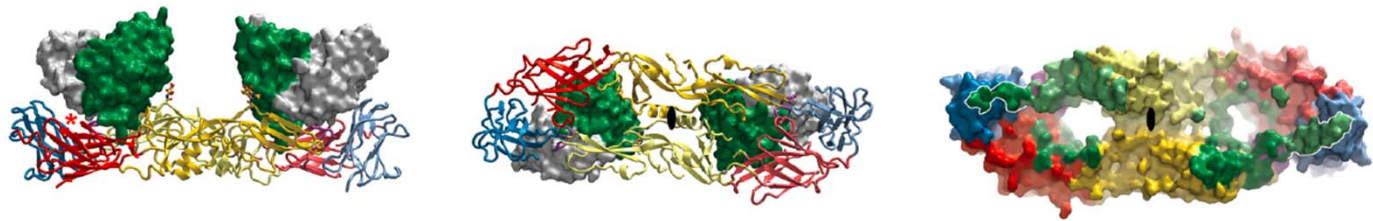
**c - DENV-2 sE / EDE1 C8**



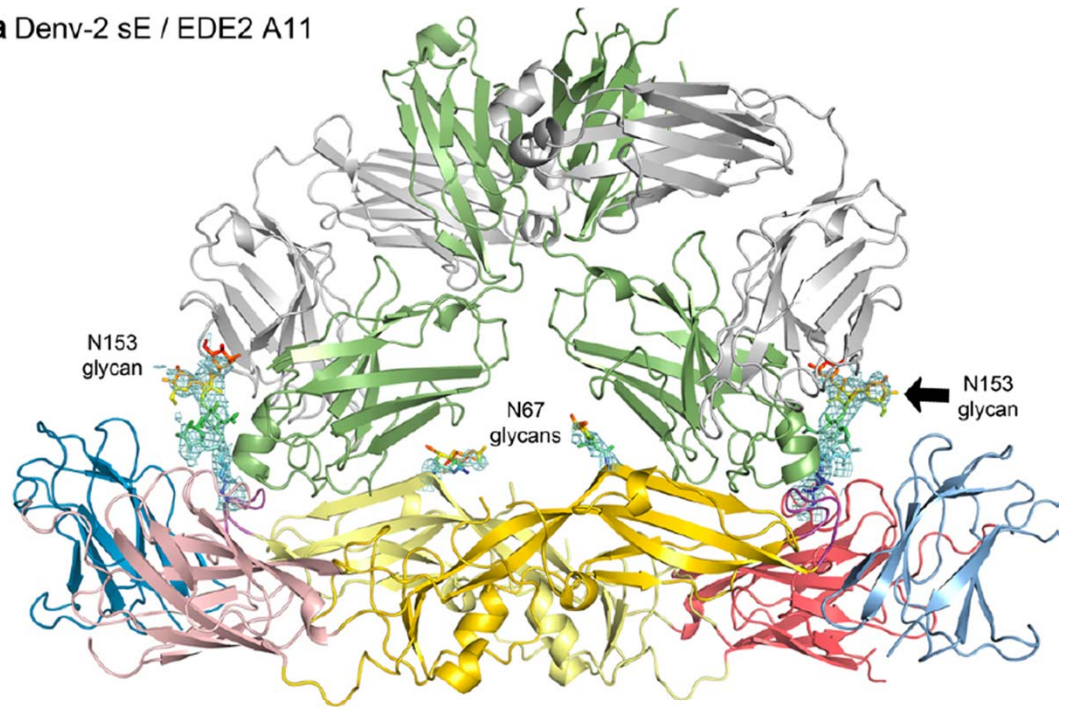
**d - DENV-2 sE / EDE1 C10**



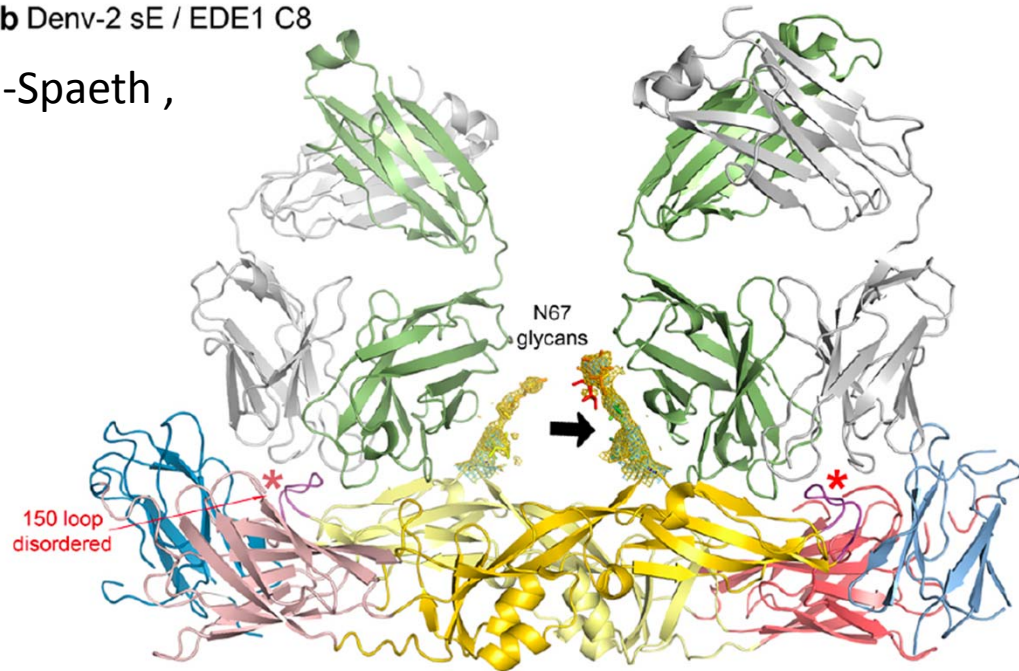
**e - DENV-4 sE / EDE1 C10**



**a** Denv-2 sE / EDE2 A11



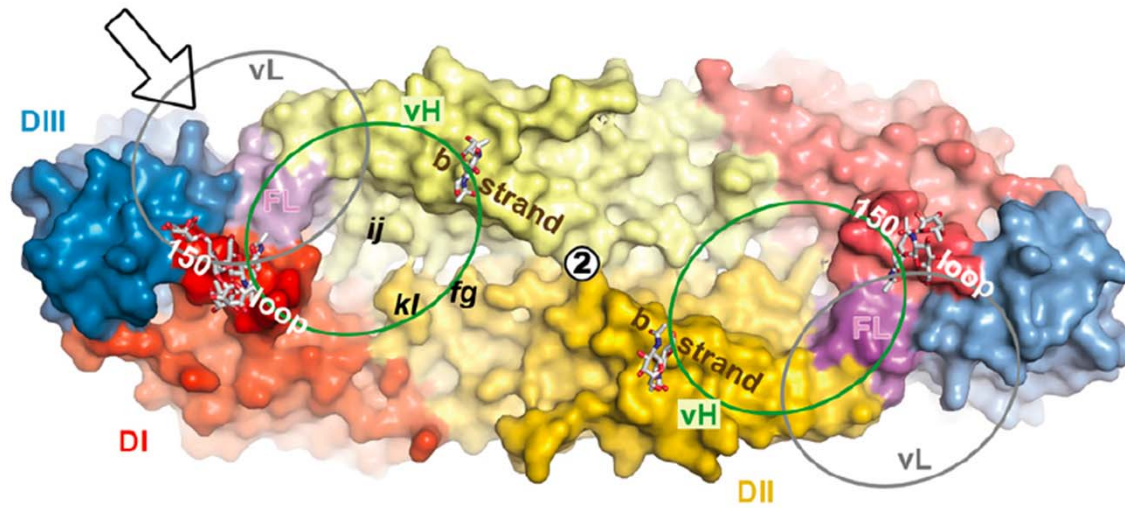
**b** Denv-2 sE / EDE1 C8



Rouvinski, Guardado-Calvo, Barba-Spaeth ,  
et al.  
Nature 2015

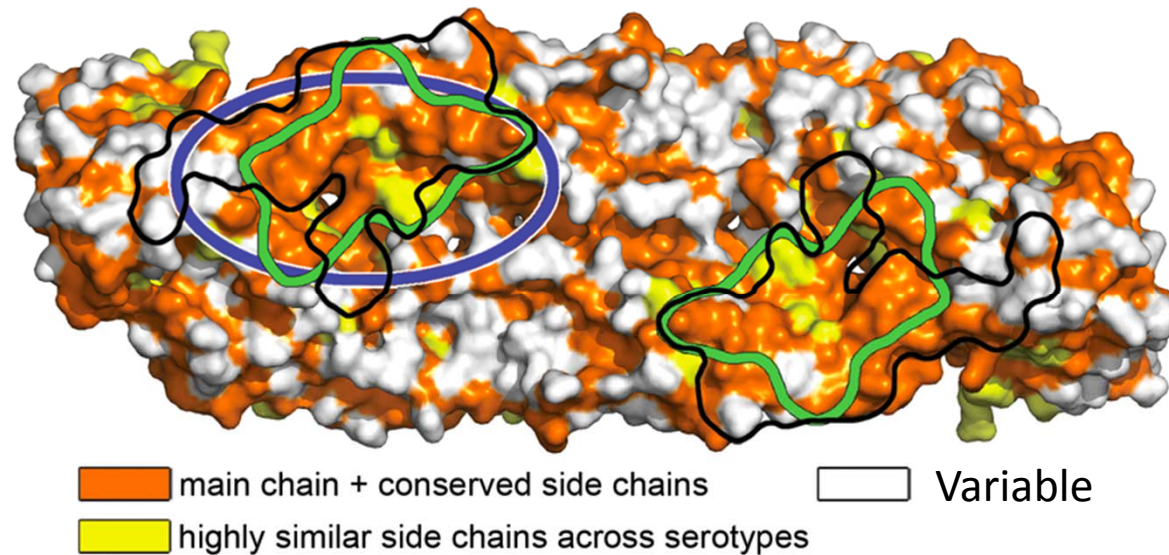
The heavy chain spans the distance between the two glycans across the dimer interface:

**b** DENV-2 sE (top view)

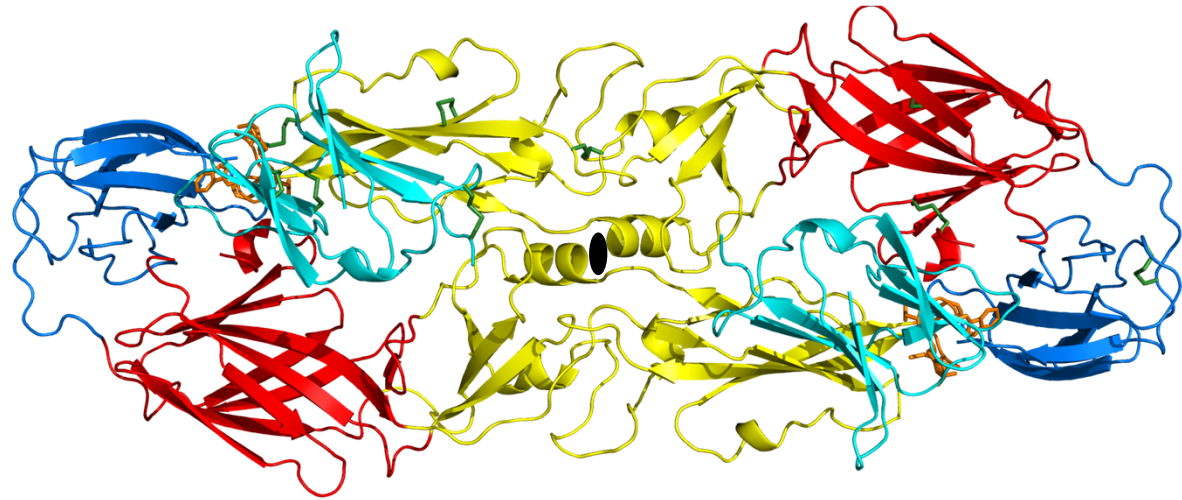
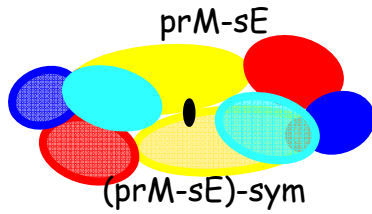


Rouvinski, Guardado-Calvo, Barba-Spaeth ,  
et al.  
Nature 2015

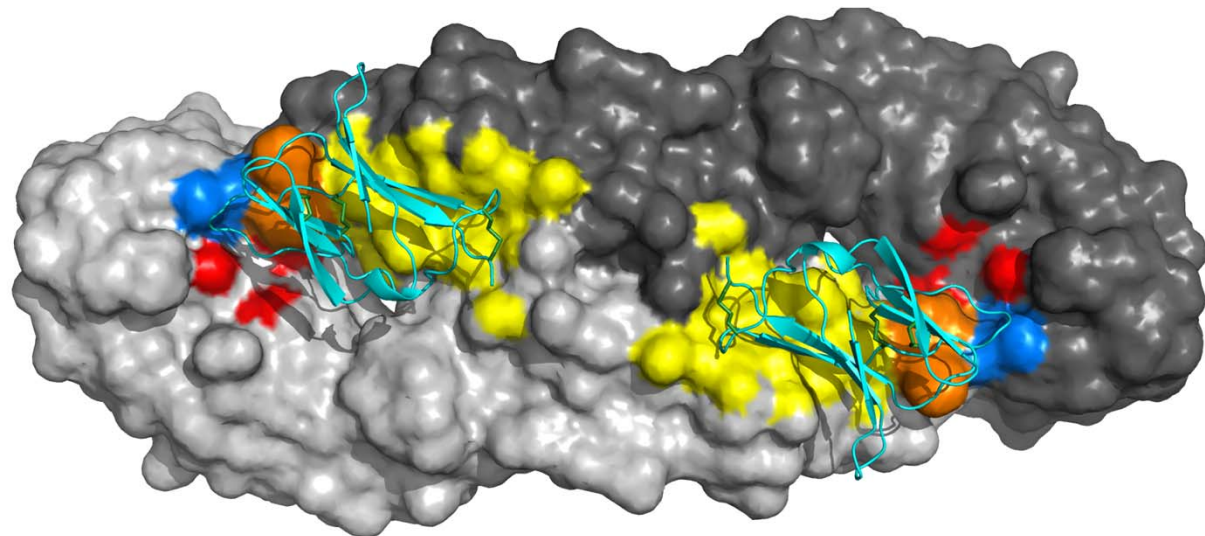
The sE surface patch corresponding to the epitope is highly conserved across serotypes:

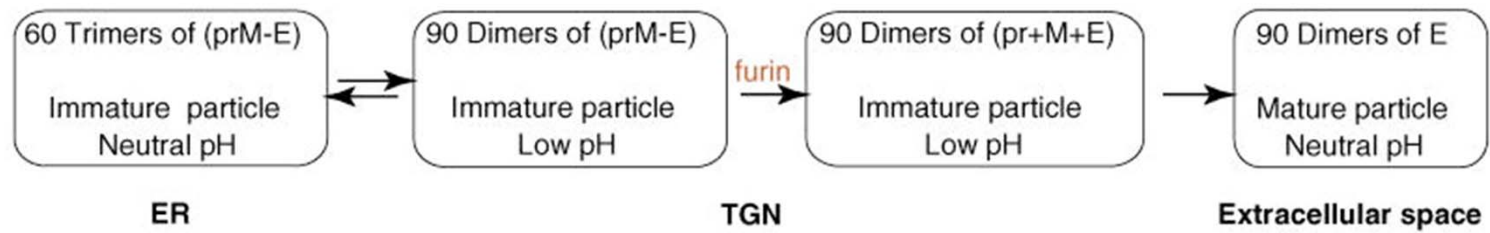
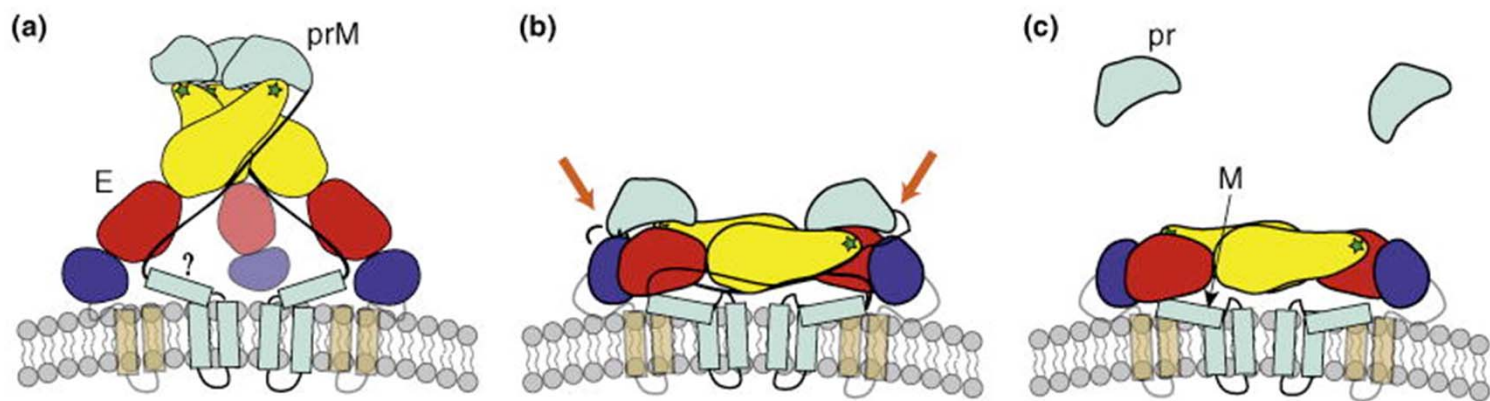


# Crystal structure of the TBEV E dimer in complex with pr:



Marie-Christine Vaney



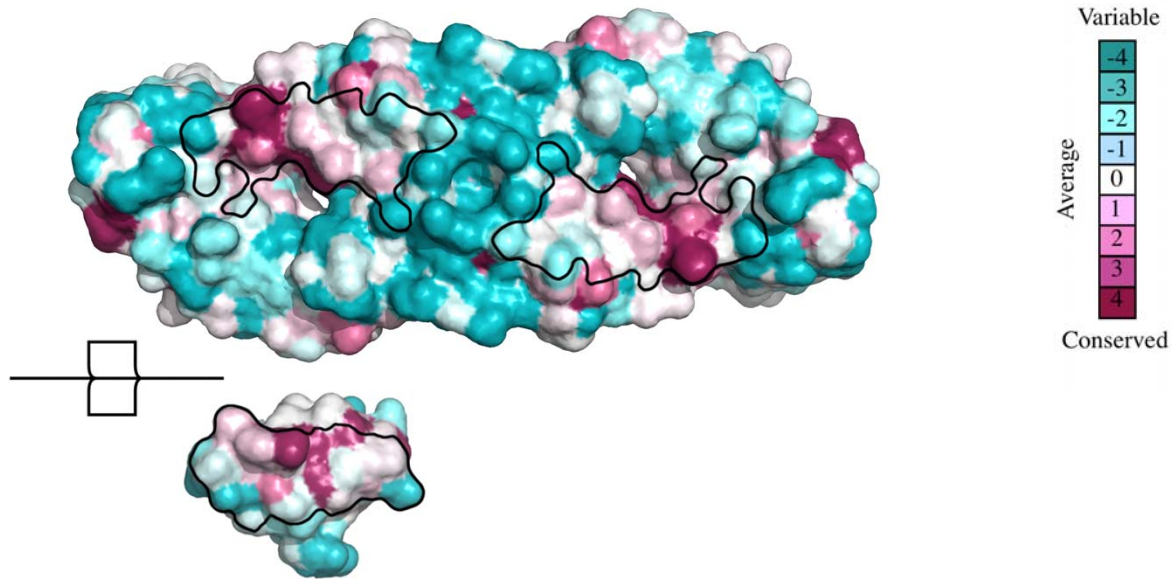




# Amino acid conservation among the flaviviruses

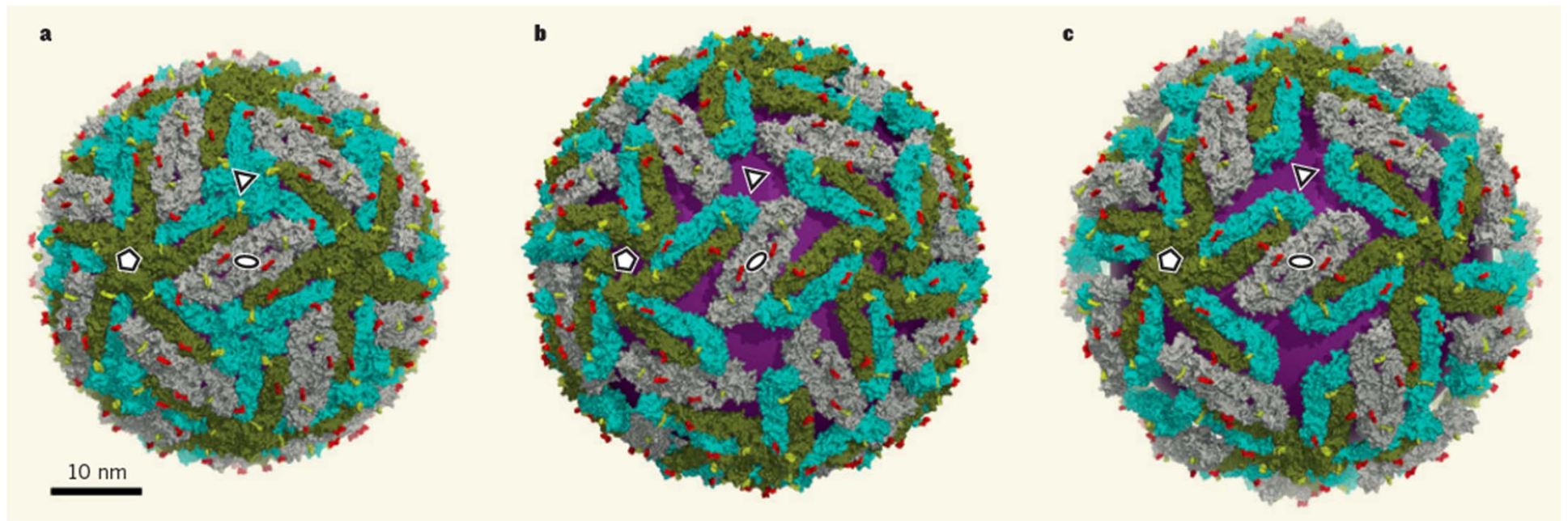
Database with 1732 prME full-length and non redundant sequences  
Sequence information (identity, deviation, ...) obtained was applied on surfaces of pr and E

Mariano Delarolle



The dengue virus particle expands at 37°C:

F Rey, Nature N&V 2013

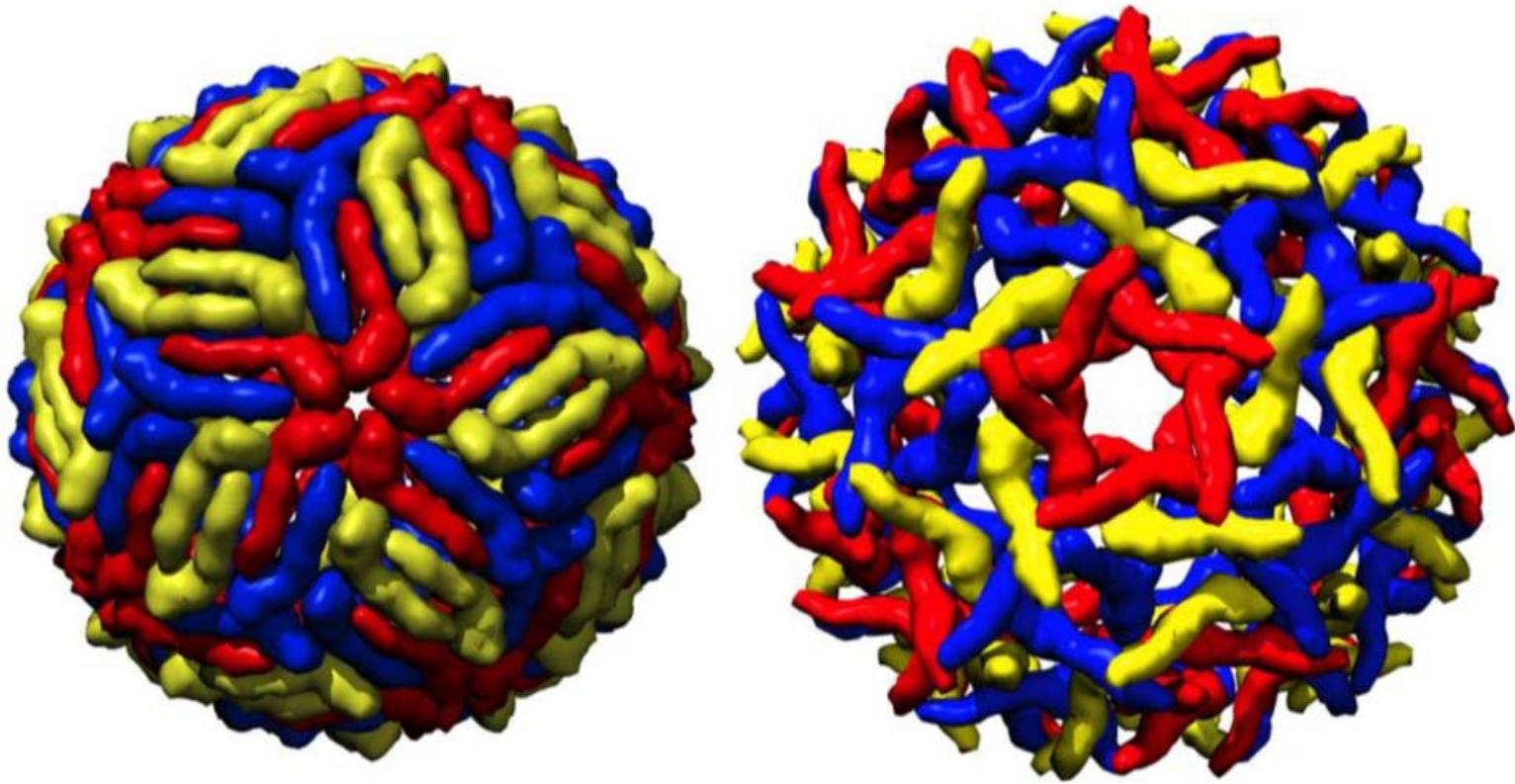


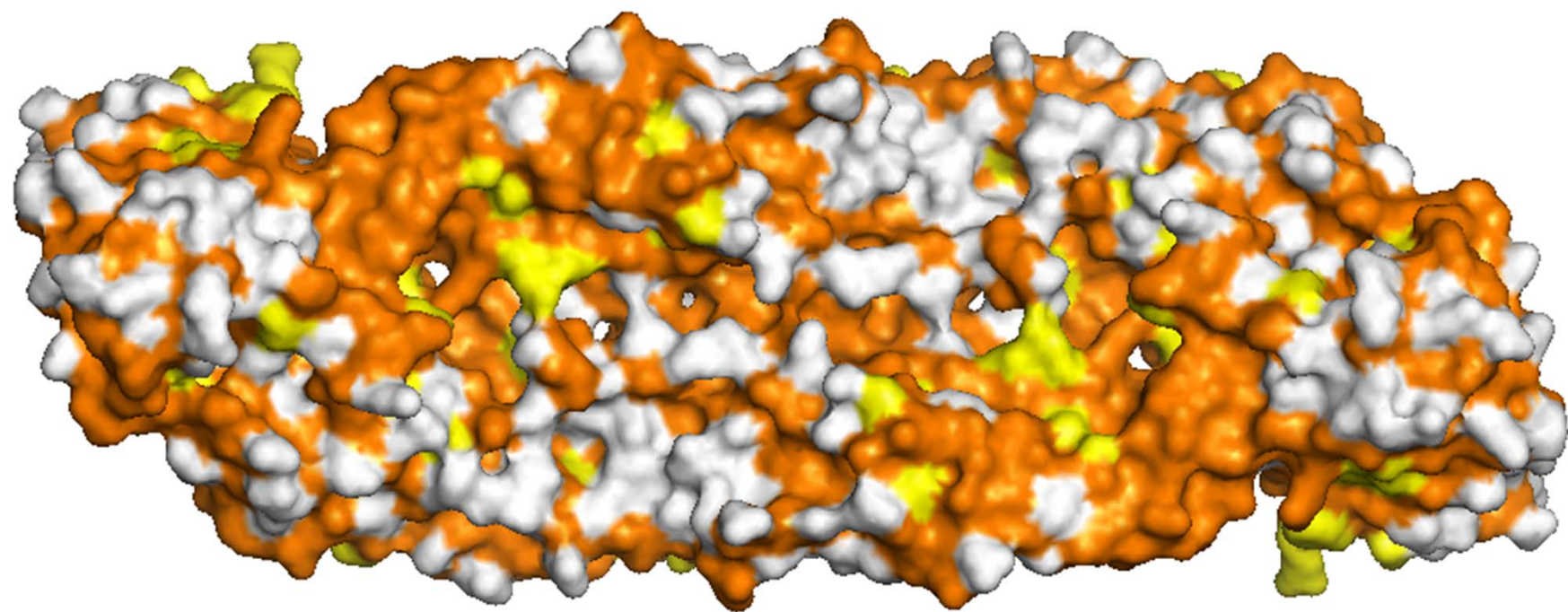
Zhang, X. *et al.* and Rossmann, M.  
Dengue structure differs at the temperatures of its human and mosquito hosts. *Proc Natl Acad Sci U S A* **110**, 6795-6799 (2013)

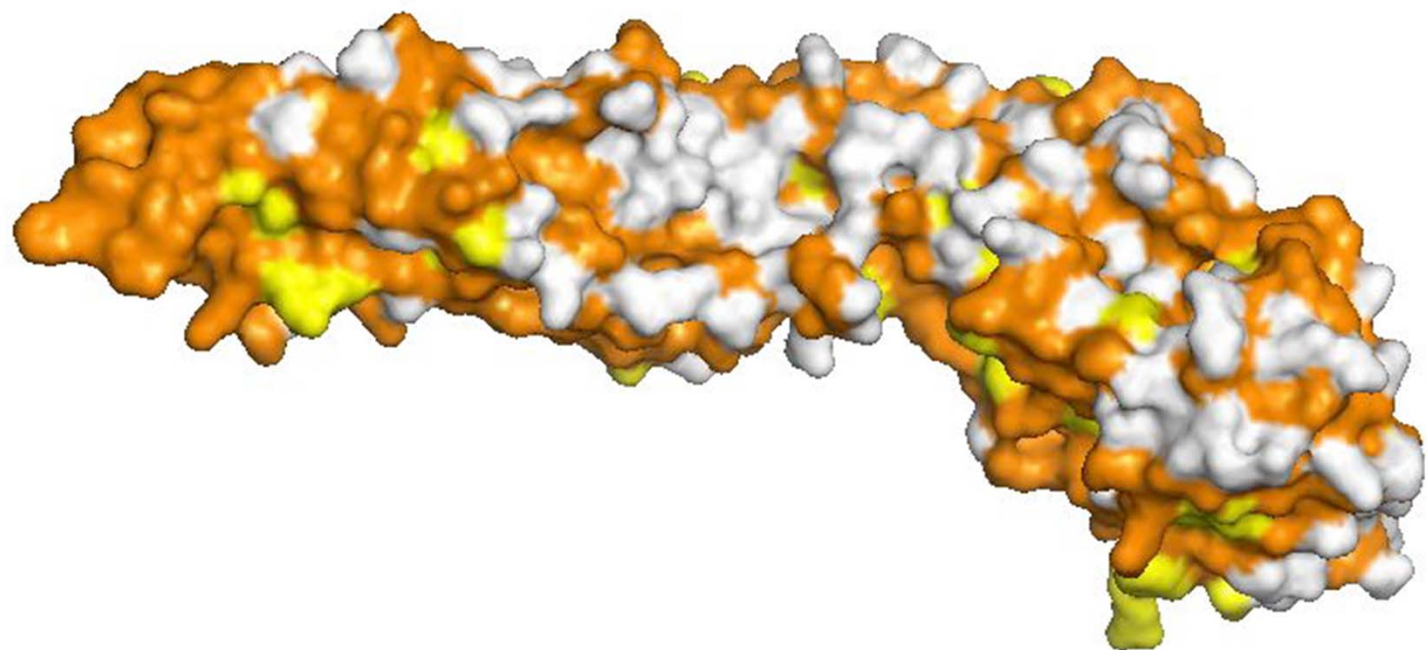
Fibriansah, G. *et al.* and Lok, S.M.  
Structural changes of dengue virus when exposed to 37°C.  
*J Virol*, doi:10.1128/JVI.00757-13 (2013).

(N153 glycan in red,  
and N67 in yellow)

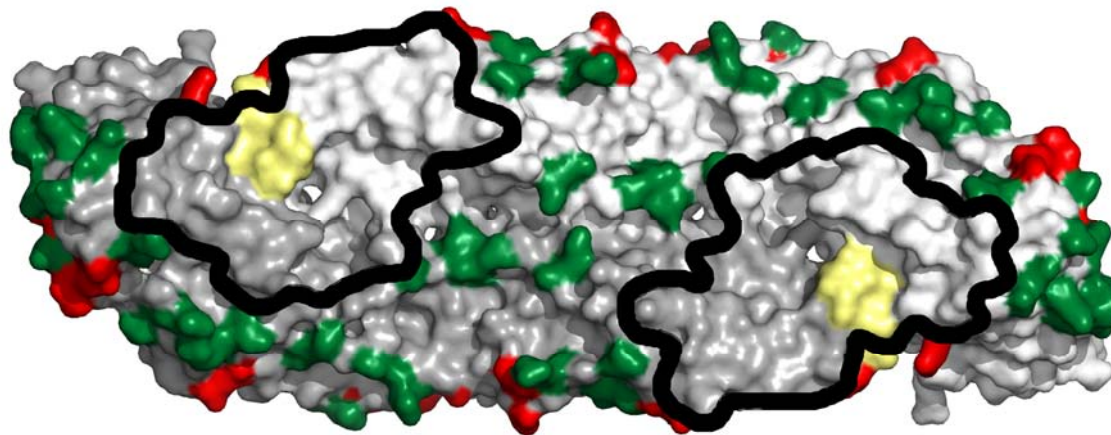
Dengue virus particle “breathing”:





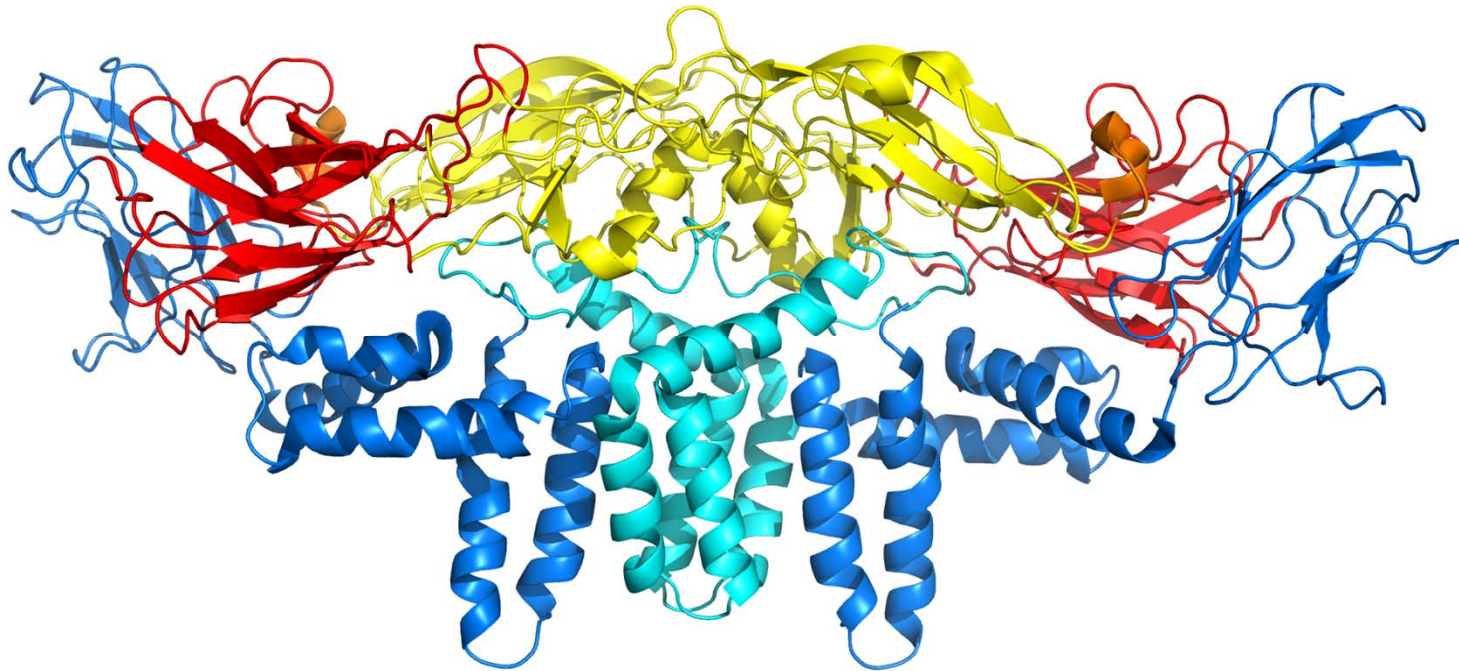


# Dimer stabilization and resurfacing



The E dimer is shown in surface representation one subunit in white and the other in grey, with the fusion loop region in yellow. The outline of the EDE is in black. Candidate residues for resurfacing are displayed in bright colors: green and red for serotype variable and conserved residues, respectively.

mature DENV-2 M-E dimer  
(3J2P)



cryo-EM structure at 3.6 Å resolution  
(Zhang *et al*, NSMB, 2012)

# Conclusions

- First thorough characterization of broadly neutralizing human antibodies against dengue virus
- These antibodies apparently point to the “Achilles heel” of the virus for neutralization escape
- The structure suggests that a single immunogen, in the form of a stabilized E dimer, should be used for subunit vaccine development





Alex  
ROUVINSKI



Pablo  
GUARDADO CALVO



Giovanna  
BARBA-SPAETH



Marie-Christine  
VANEY



Stéphane  
DUQUERROY

*UNITÉ DE VIROLOGIE STRUCTURALE, INSTITUT PASTEUR, PARIS*



Gavin Sreaton



Juthathip Mongkolsapaya

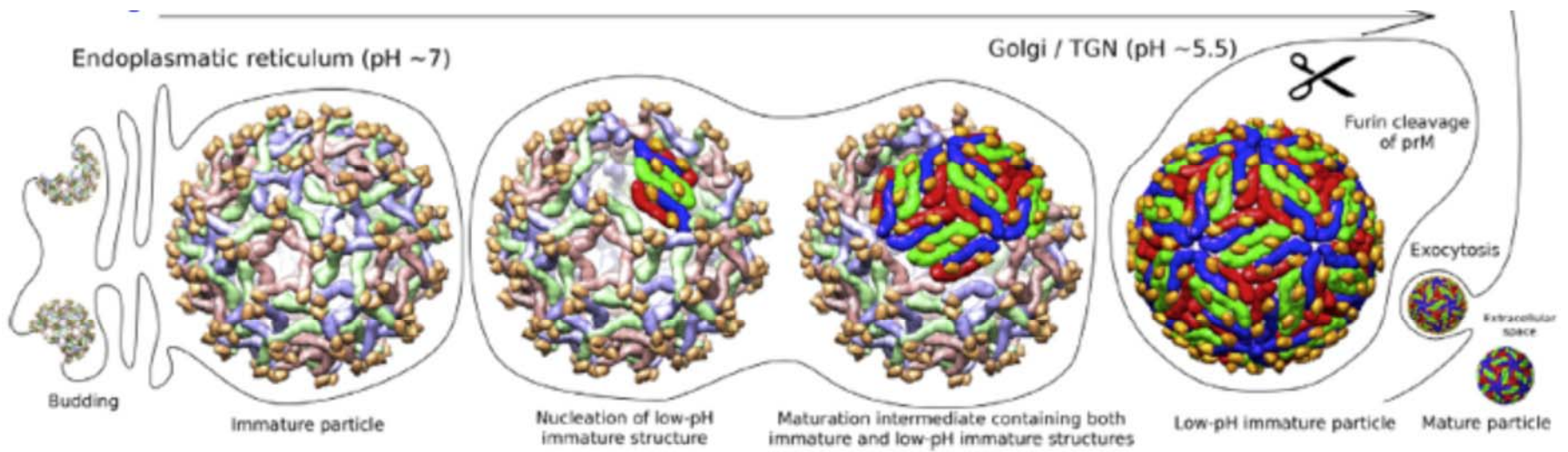
*IMPERIAL COLLEGE, LONDON*



Xiaokang Zhang

Z. Hong Zhou  
UCLA

Nui Dejnirattisai  
Hua Wongwiwat



Plevka et al, JSB 2014