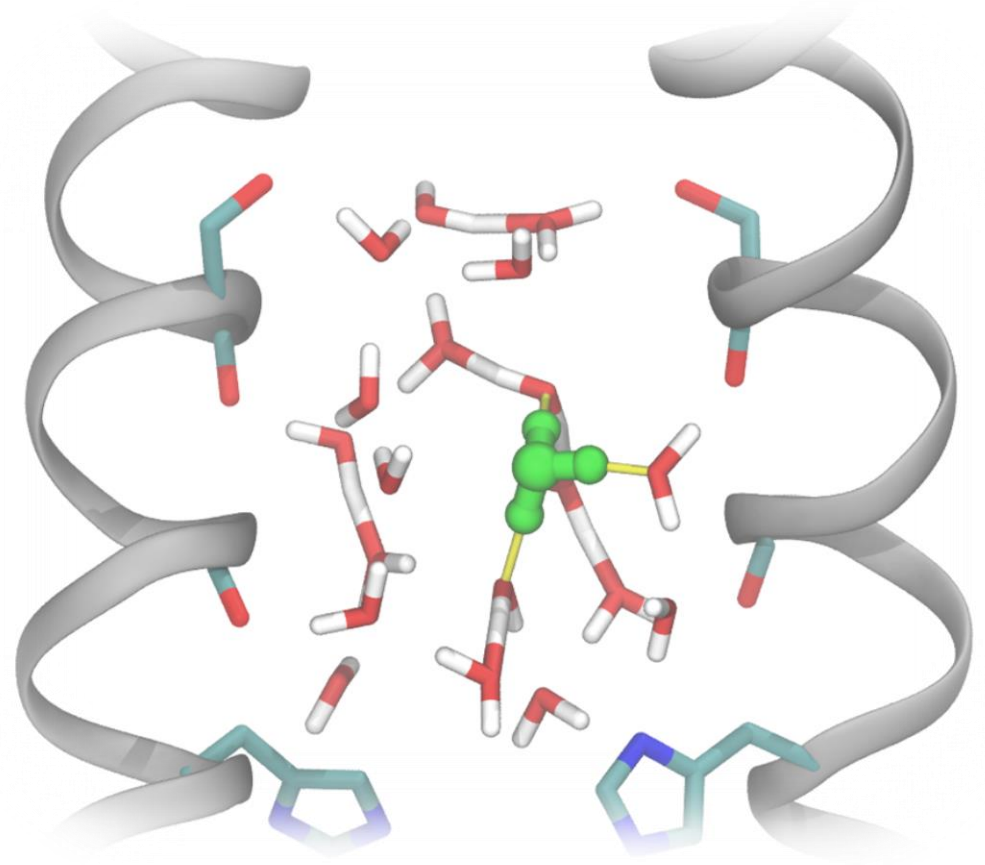


Proton Transport in Influenza A M2 Channel

Laura Watkins

DOE CSGF Virtual Program Review

July 2020

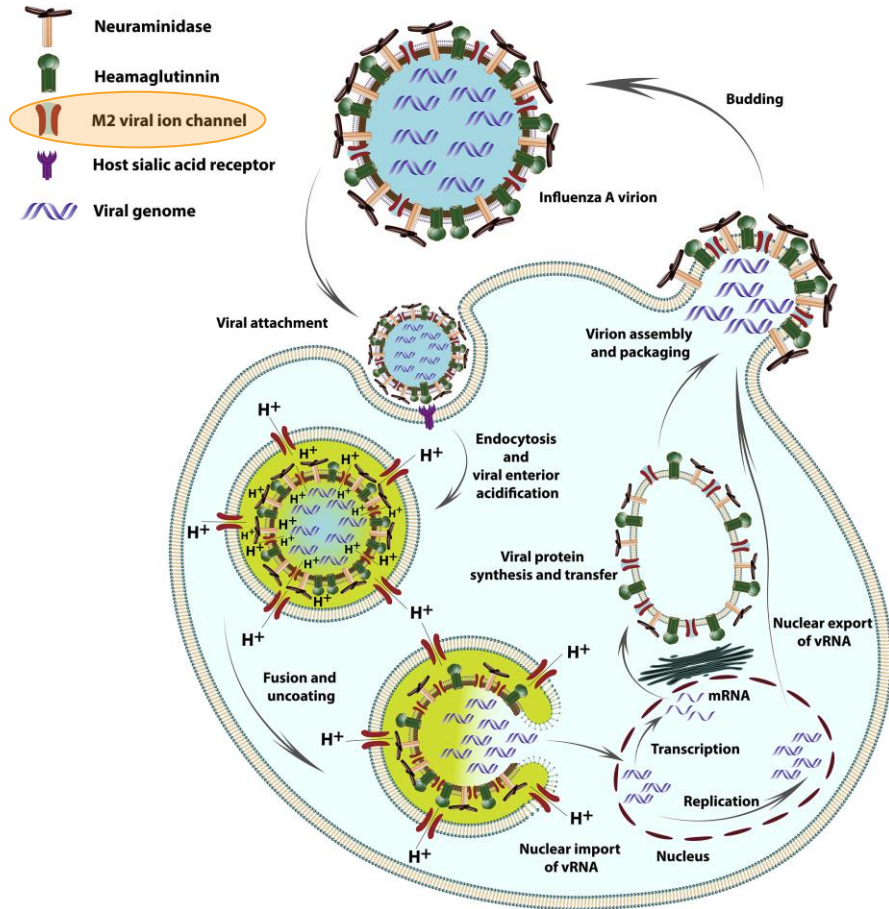


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CHICAGO

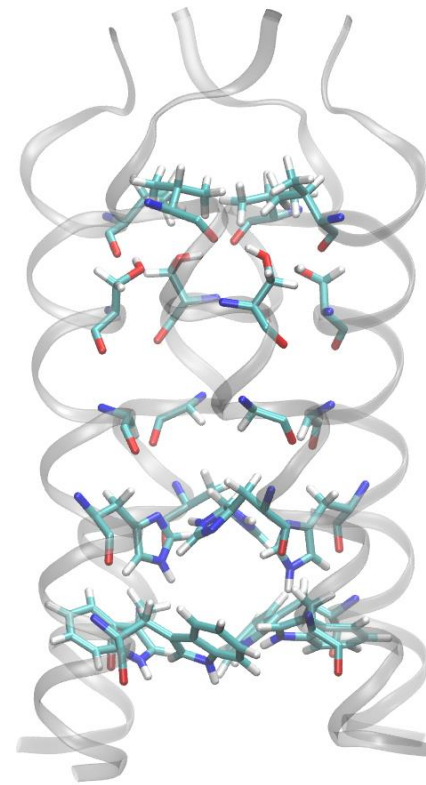


Influenza A M2: Critical Drug Target in Influenza Virus

Influenza A Lifecycle

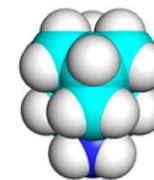


M2 Proton Channel

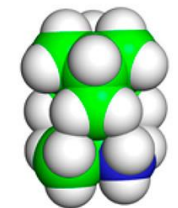
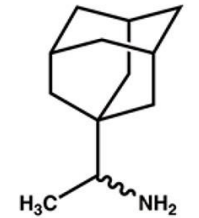


Inhibitors (now ineffective)

Amantadine

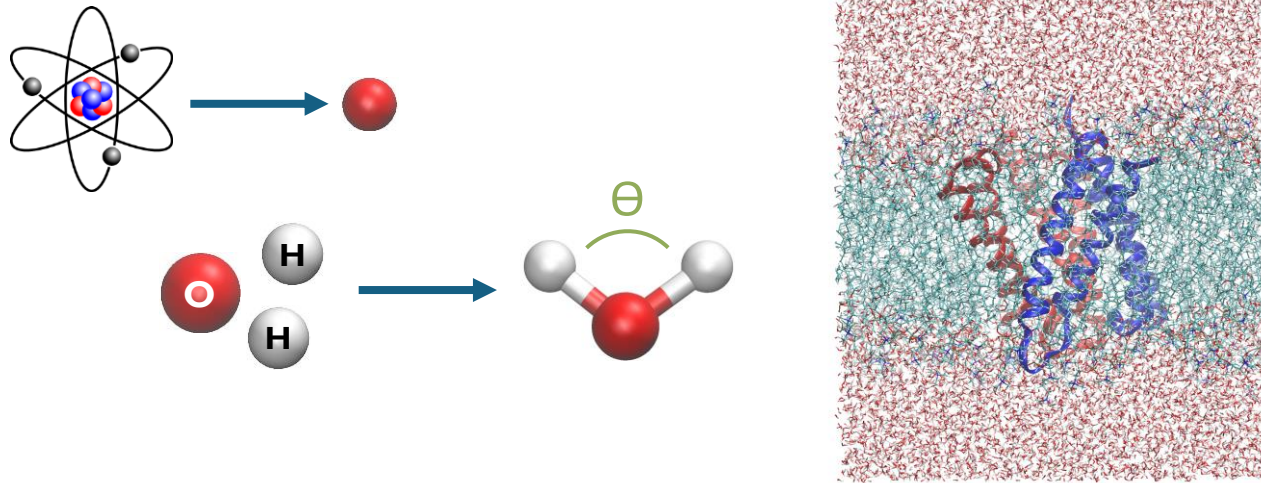


Rimantadine



Proton Transport Requires Reactive Simulation Method

Classical Molecular Dynamics

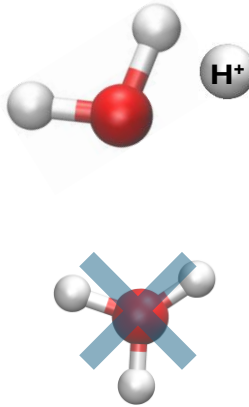
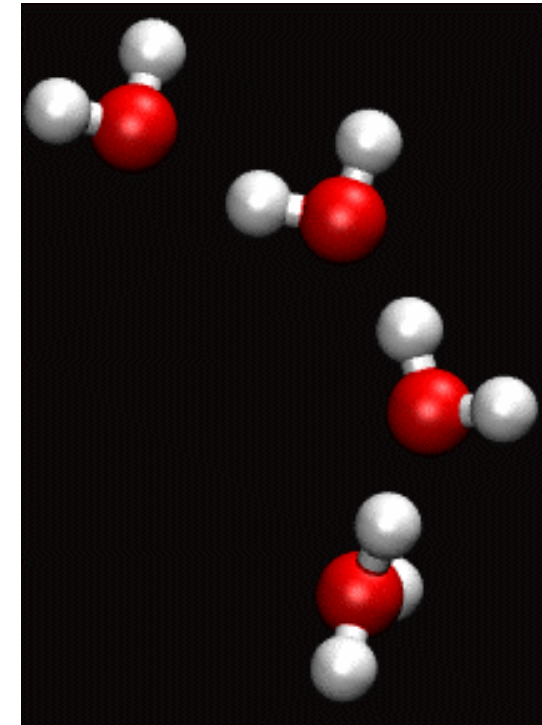
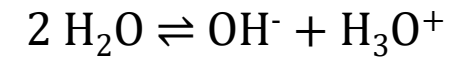


$$U(\mathbf{x}) = E_{bond} + E_{angle} + E_{dihedral} + E_{nonbonded}$$

$$\mathbf{F} = m\mathbf{a}$$

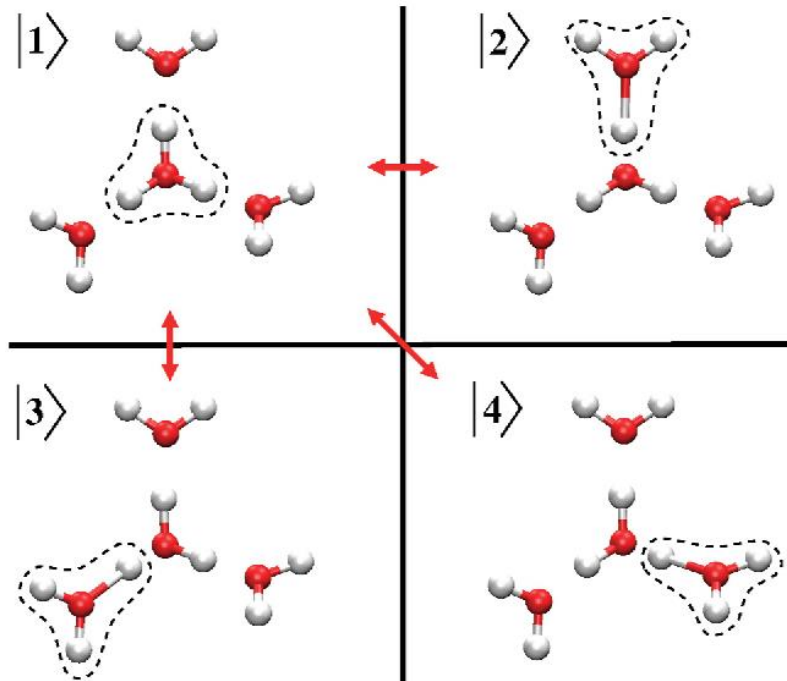
$$\mathbf{F}(\mathbf{x}) = -\nabla U(\mathbf{x})$$

Proton Hopping Mechanism



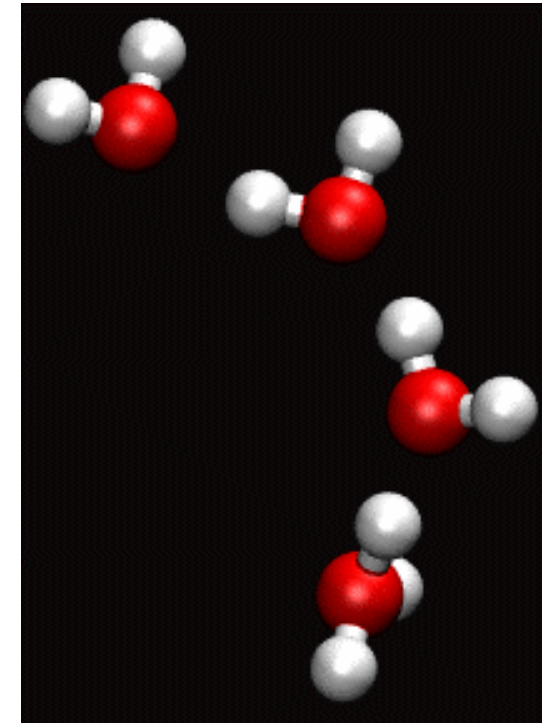
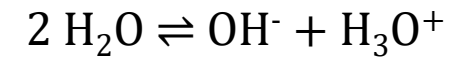
Proton Transport Requires Reactive Simulation Method

Multiscale Reactive Molecular Dynamics



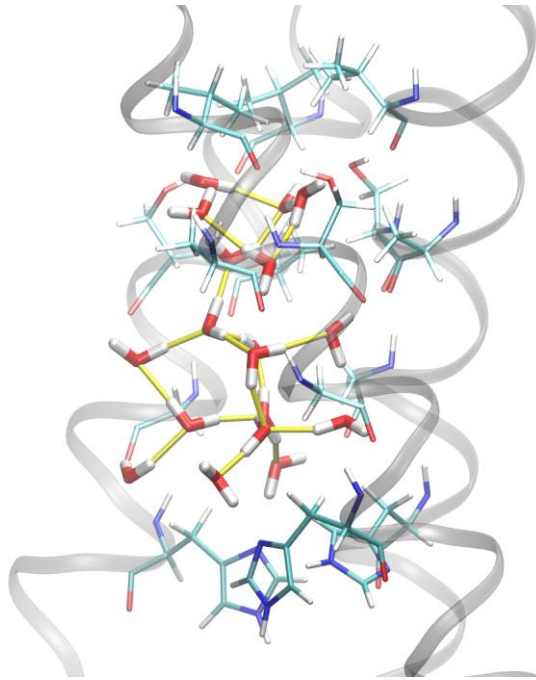
MD with an **explicit, reactive** excess proton
Allows bonds to break and form

Proton Hopping Mechanism

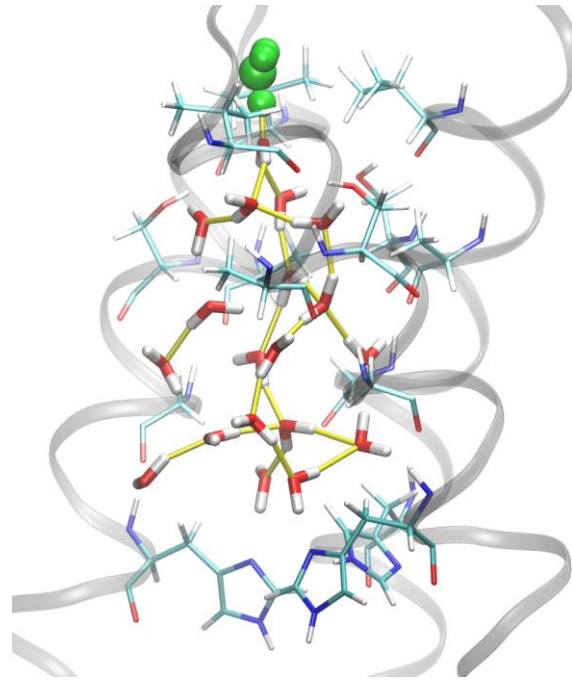


Excess Proton Reorients Hydrogen Bond Network

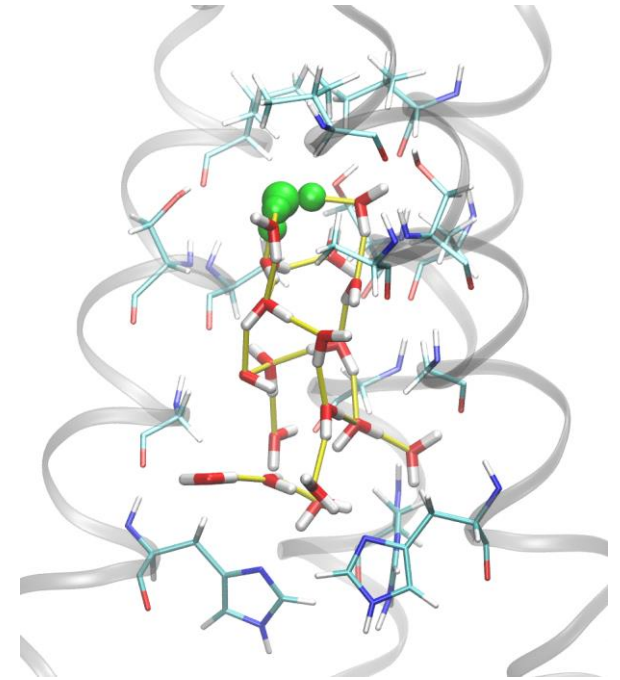
Proton outside of channel:



Proton near:



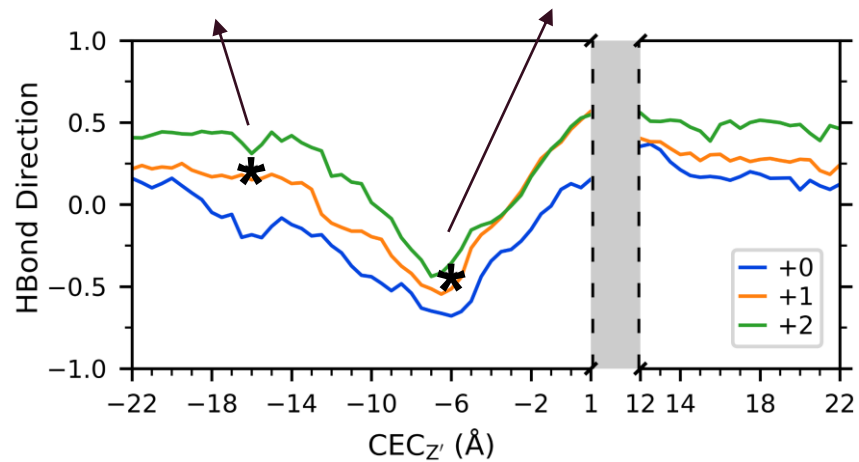
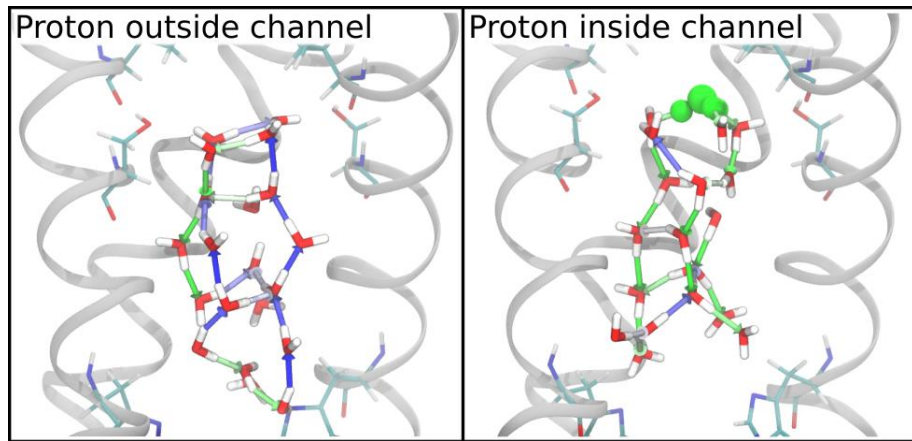
Proton directly above:



Green = most hydronium-like water
Yellow = hydrogen bonds

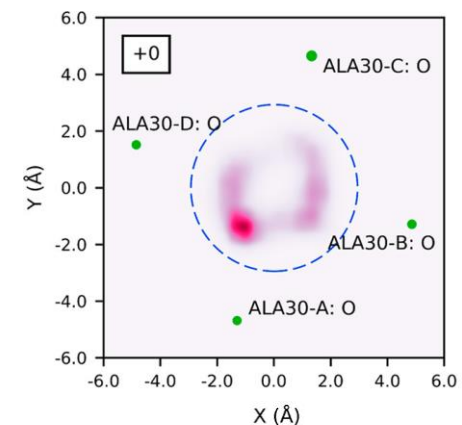
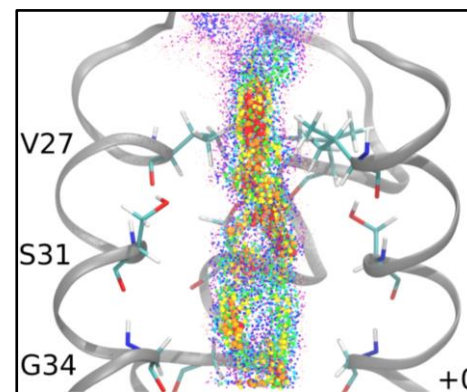
Excess Proton Interacts with Water and Channel

Proton reorients hydrogen bond network



CEC = Center of excess charge

Proton path and channel asymmetry

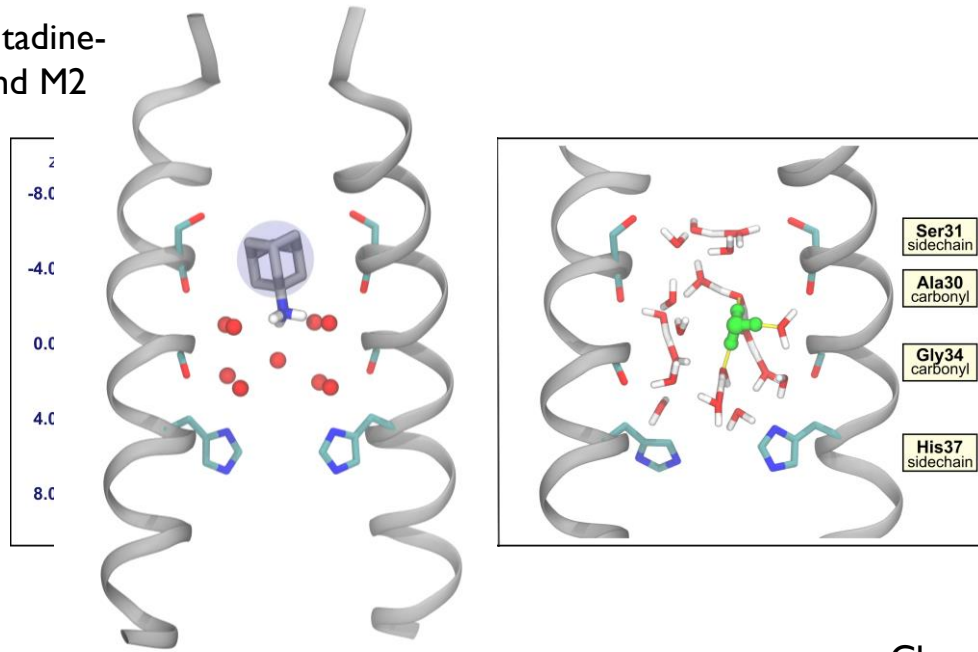


Important feature for drug design

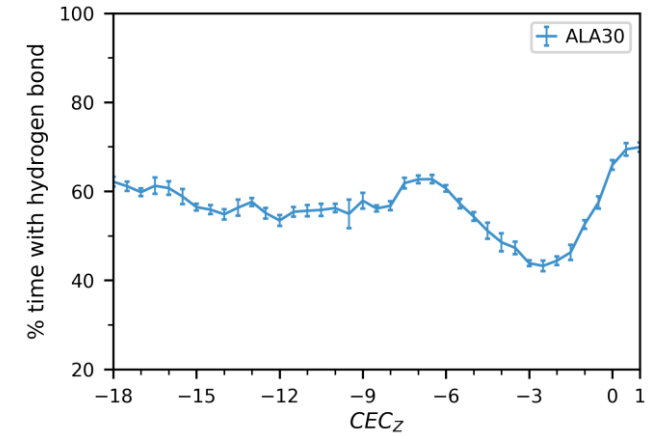
Static structures from crystallography
are not the full story

Inhibitors Take Advantage of Channel's PT Mechanism

Amantadine-bound M2

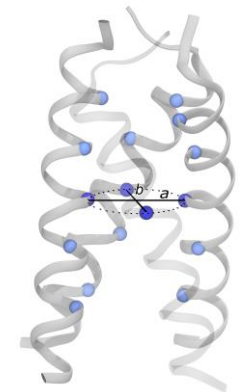
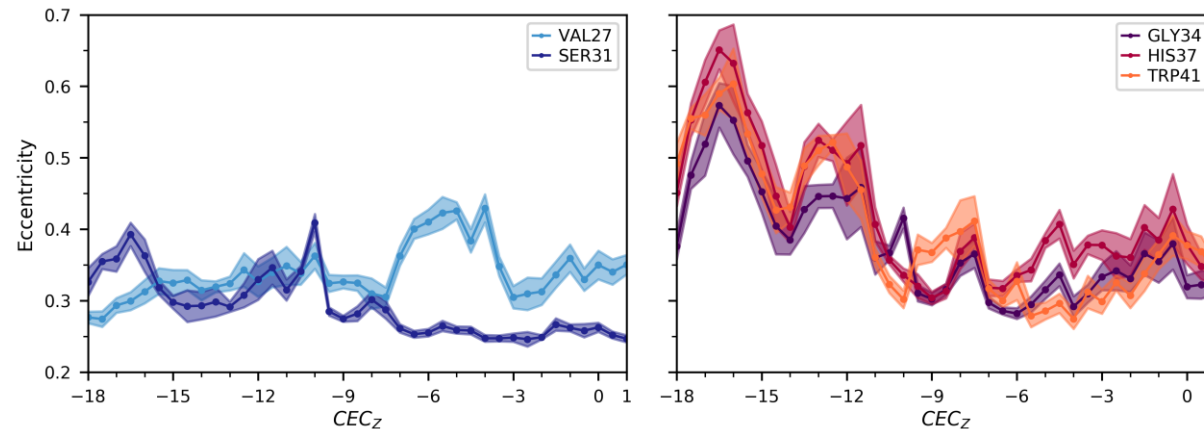


Flexible hydrogen bonds stabilize excess charge



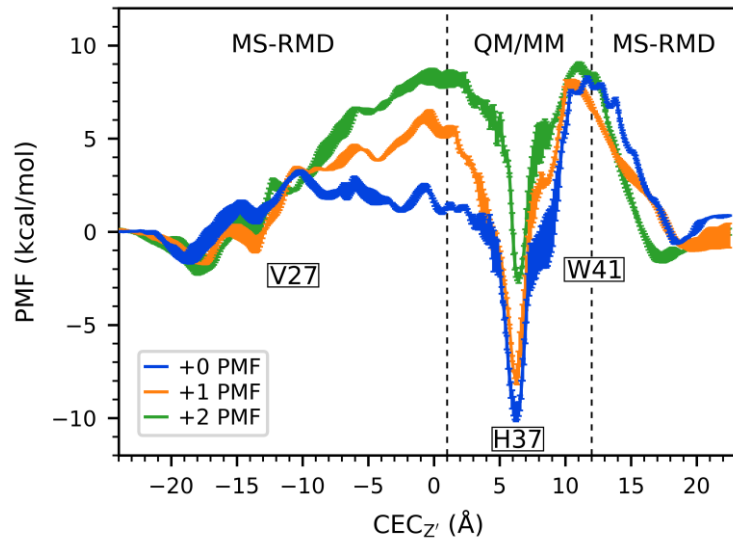
Channel is most stable and spherical where drug binds

$$e = \sqrt{1 - \frac{b^2}{a^2}}$$



M2 Conclusions and Other Results

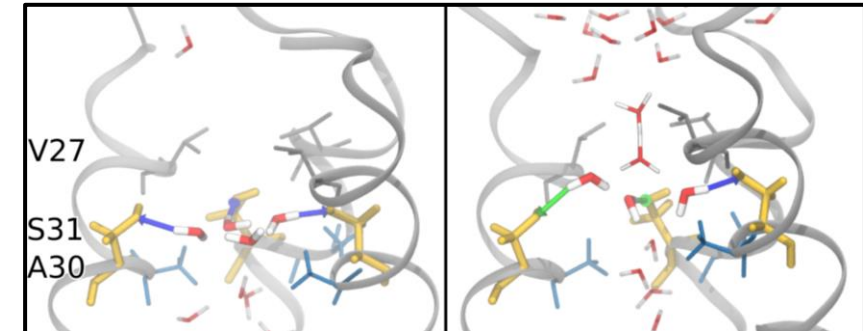
Proton Transport Mechanism in M2 Mutant



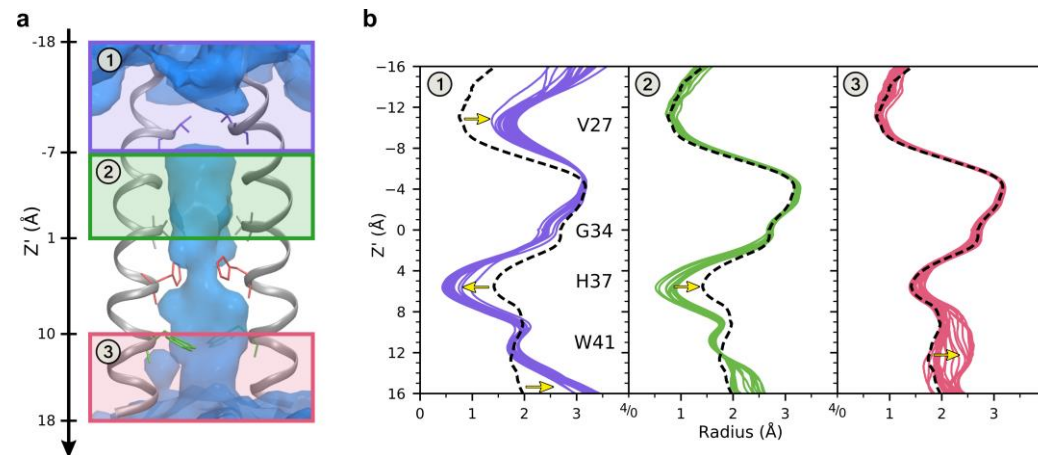
Proton transport is incredibly dynamic!

An excess proton can “pave its own path”

Protein creates scaffold for proton transport

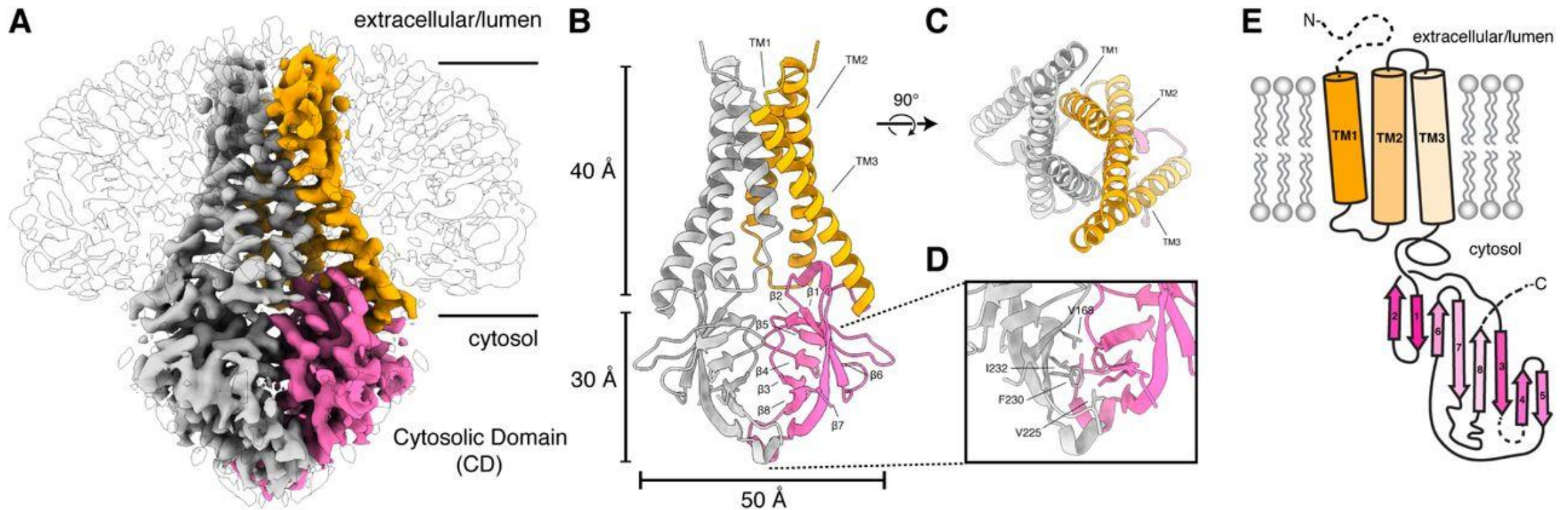


Proton Dynamically Alters Protein Structure



This looks like biology, what about COVID-19??

Just published structure of protein p3 from SARS-CoV-2



Acknowledgements

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Voth group members

DOE, Krell Institute

