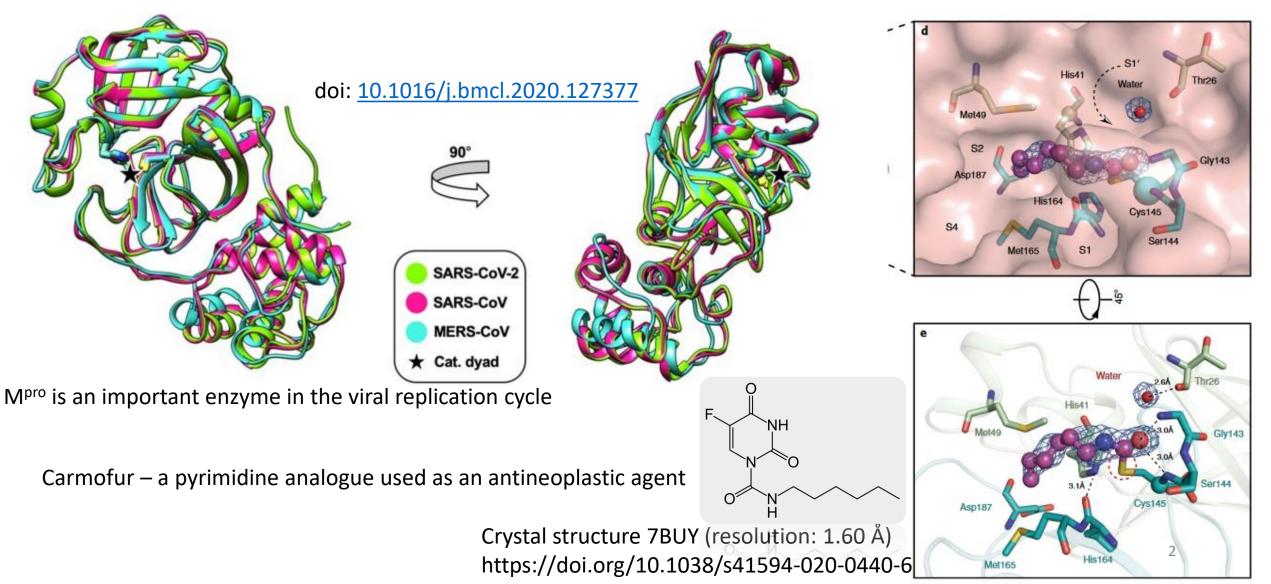
SARS-COV-2 MAIN PROTEASE INHIBITION WITH CARMOFUR: A COMPUTATIONAL STUDY

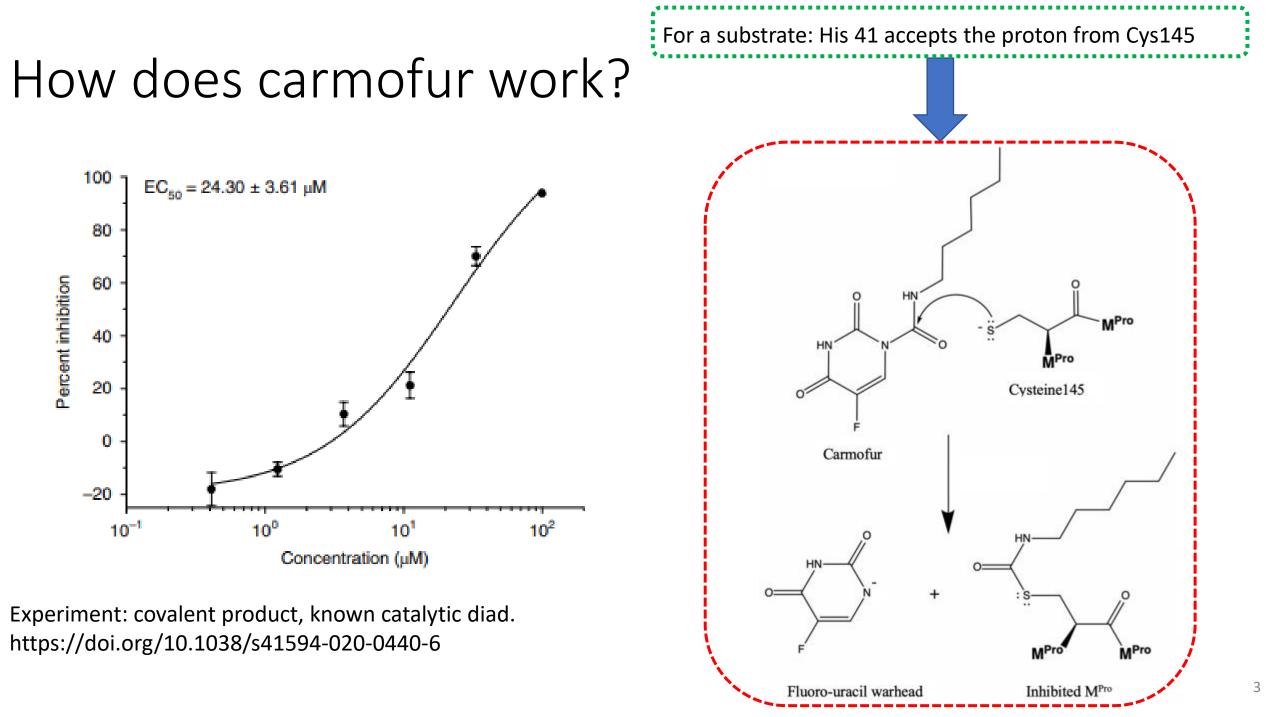
Igor Polyakov^{1,2}, B.L. Grigorenko^{1,2}, A.V. Nemukhin^{1,2}

¹Department of Chemistry, Lomonosov Moscow State University, Moscow, Russia ²Emanuel Institute of Biochemical Physics RAS, Moscow, Russia

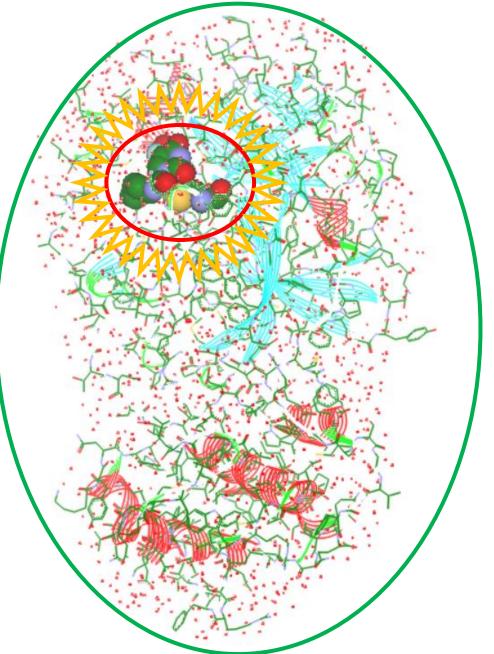
SARS-CoV-2 main protease



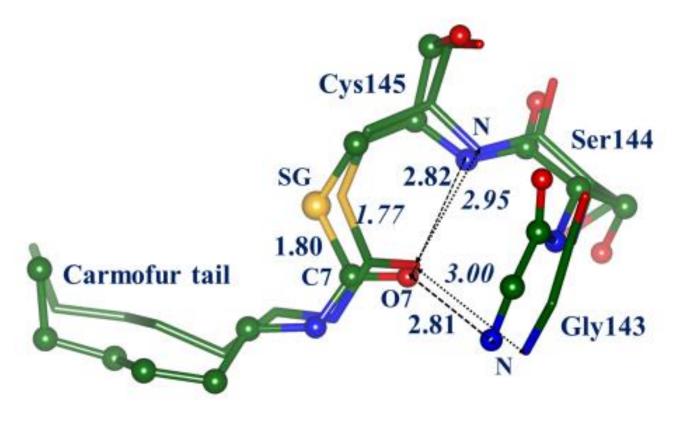
Cys145



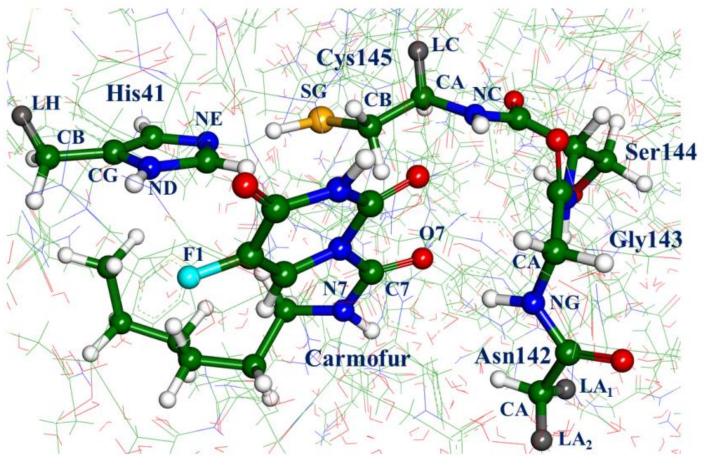
E(tot)=E(QM)+E(QM/MM)+E(MM)



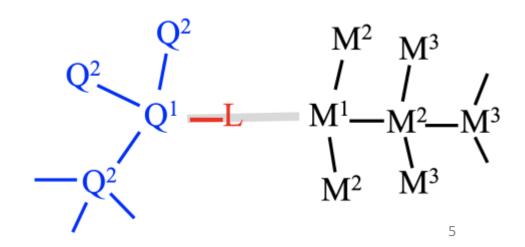
Direct comparison of QM/MM results to the experiment

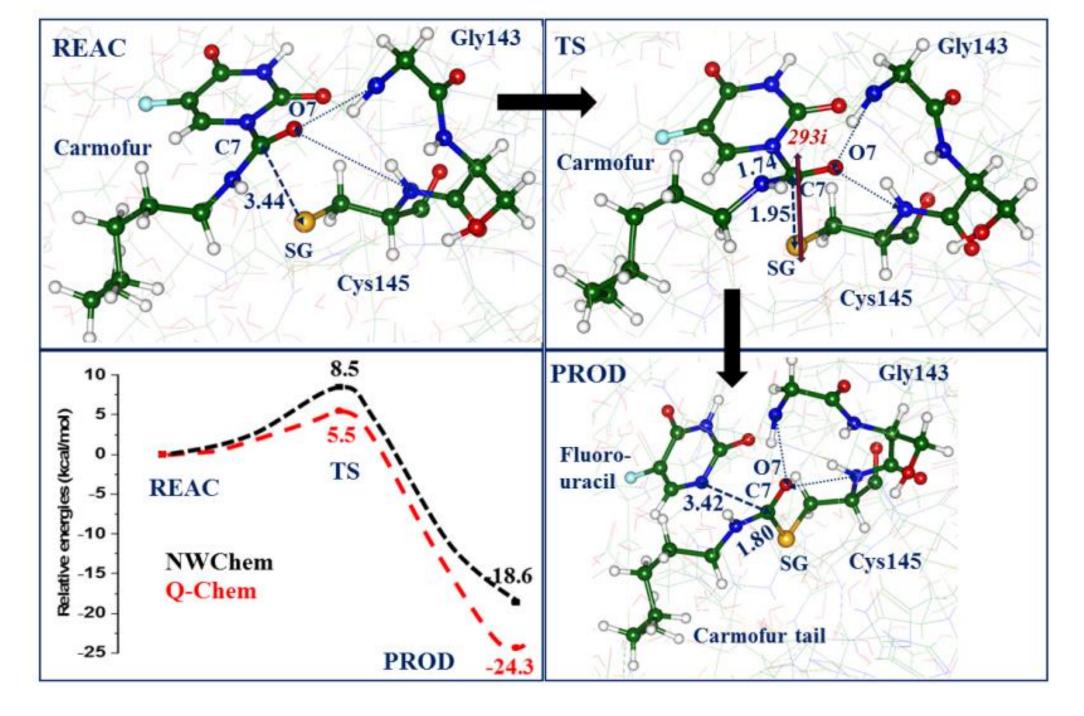


Model system description



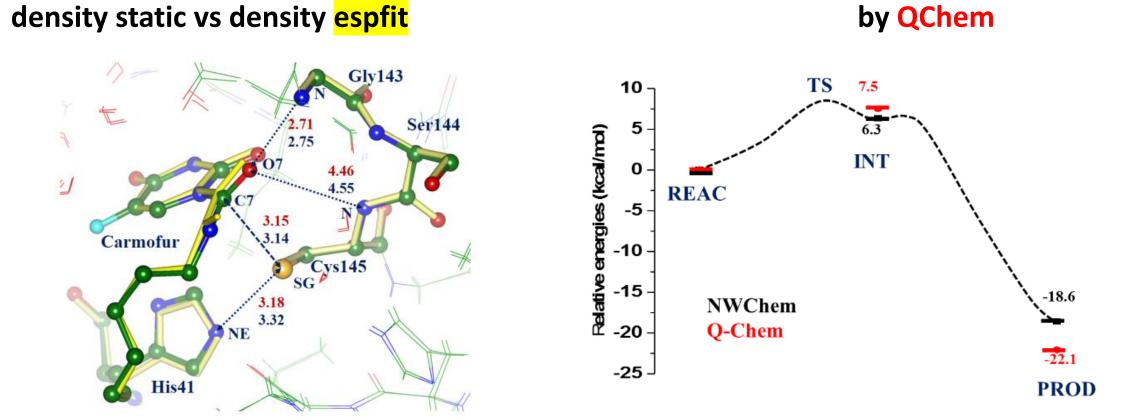
- "Electrostatic embedding"
- NWChem, QChem
- 83 atoms: carmofur, side chain/backbone atoms from His41, Asn142,Gly143, Cys145, one water molecule, and 4 hlink atoms
- PBEO-D3/6-31G**//AMBER
- No electrostatic cutoff





Energy		Energy (a.u.)	Energy relative to REAC (kcal/mol)		Single point energy with the NWChem located structures!		
contribution	Software	REAC					
			TS	PROD			
QM in	NWChem	-2474.6967	13.9	-5.4	PETI.IL		
gas phase	Q-Chem	-2474.6983	14.1	-5.2			
QM in	NWChem	-2474.5907	12.2	-5.7			
MM charges	Q-Chem	-2474.6637	12.9	-5.1			
$\mathbf{Q}\mathbf{M}$	NWChem	-2475.1349	14.9	-9.7	Explicit contributions from charges:		
+ QM/MM	Q-Chem	-2474.9139	11.5	-17.0	 charge-nuclei charge-density 		
$\mathbf{M}\mathbf{M}$	NWChem	-39.1656	-6.3	-8.9	$- Q^2 \qquad M^2 M^3 \qquad I \qquad $		
	Q-Chem	-39.2451	-5.9	-8.8	$Q^1 - L = M^1 - M^2 - M^3$		
Total energy	NWChem	-2514.3005	8.5	-18.6	\dot{M}^2 \dot{M}^3		
QM + QM/MM + MM	Q-Chem	-2514.1591	5.5	-25.8	7		

What, another profile!?



Structures optimized by NWChem

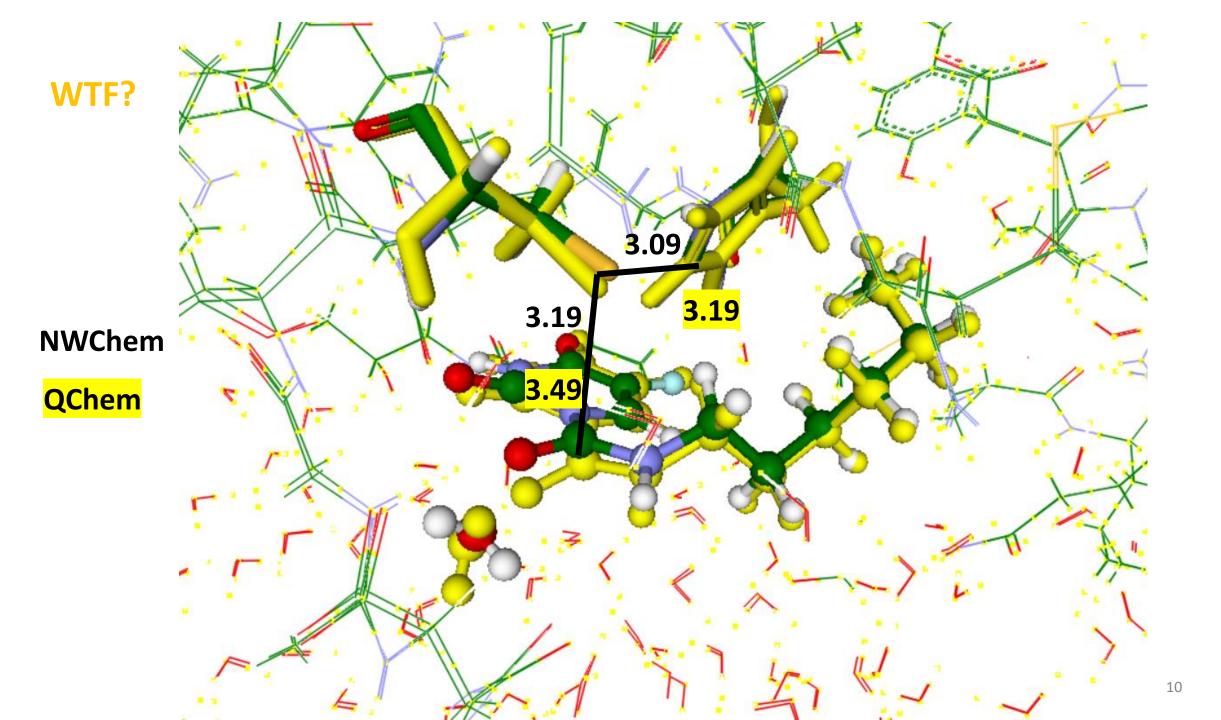
Not a huge difference for REAC, but able to locate an intermediate!

					i
Energy		Energy (a.u.)	Energy relative		
contribution	Software	REAC	to REAC (kcal/mol)		
			INT	PROD	
QM in	NWChem	-2474.5961	13.5	-3.5	
MM charges	Q-Chem	-2474.6833	10.9	-5.6	U
$\mathbf{Q}\mathbf{M}$	NWChem	-2475.1218	7.1	-16.8	
+ QM/MM	Q-Chem	-2474.9402	11.2	-16.6	
MM	NWChem	-39.1798	-0.8	-1.8	W
	Q-Chem	-39.2606	-5.8	-5.3	
Total energy	NWChem	-2514.3017	6.3	-18.6	
QM + QM/MM + MM	Q-Chem	-2514.2008	5.5	-21.9	

UGLY

WTF?

OK

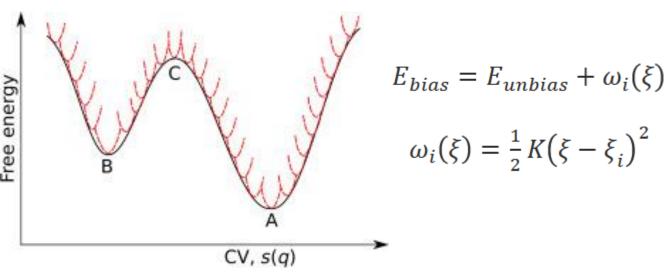


Takeaways:

- Difference in QM/MM boundary charge treatment leads to significant discrepancies in the total and relative energies
- A number of close-lying minima on the PES of an enzyme => change some options or software = end up in different minima for the same kind structure
- Qualitatively QM software "agrees" that carmofur is a potent covalent inhibitor

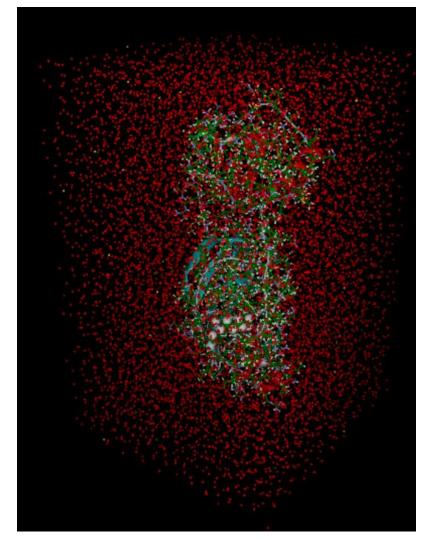
...but what about the first stage?...and free energy calculation?

Umbrella integration/WHAM



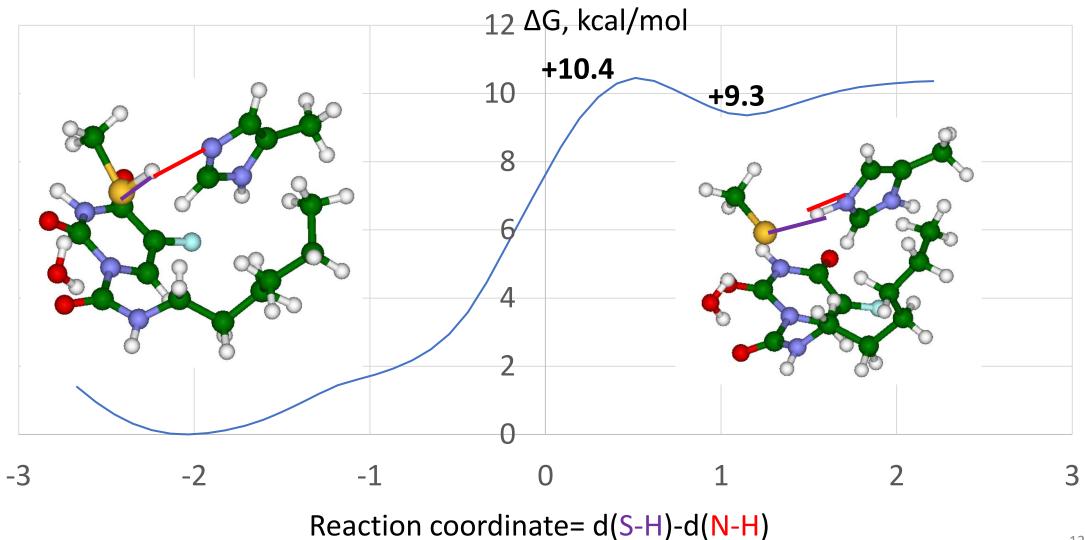
$$P_i^u(\xi) = \frac{\int \exp[-\beta E(r)] \delta[\xi^r(r) - \xi] d^{N_r}}{\int \exp[-\beta E(r)] d^{N_r}}$$
$$P_i^u(\xi) = P_i^b(\xi) \exp[\beta \omega_i(\xi)] \exp[-\beta \omega_i(\xi)]$$
$$E_{unbias} = -\left(\frac{1}{\beta}\right) \ln P_i^b(\xi) - \omega_i(\xi) + F_i$$

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33157 atoms, NPT, PME/PBC Terachem/NAMD PBE0/6-31G** /CHARMM36

For a substrate: His41 accepts the proton from Cys145



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