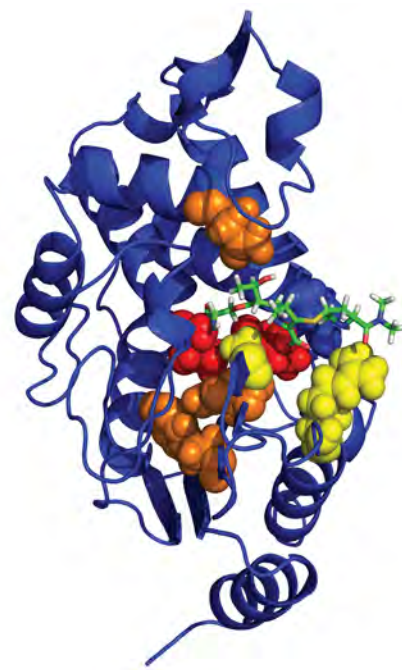
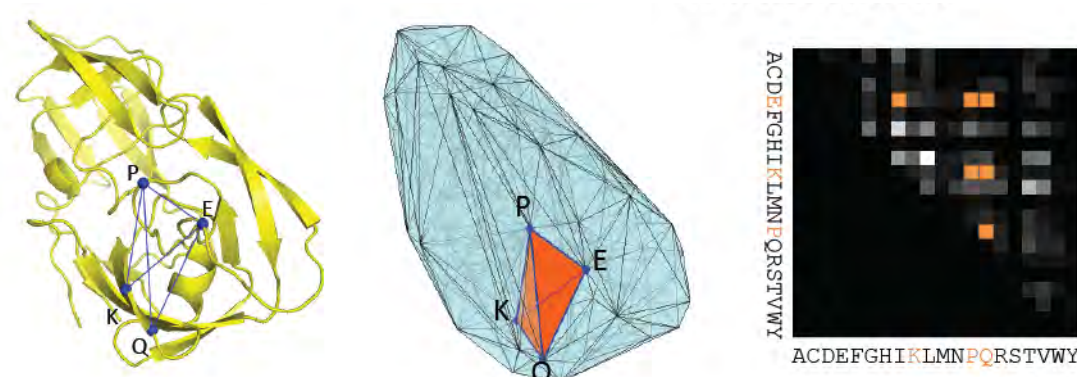


1. Predicting sequence changes altering drug resistance or target recognition.
Large-scale MD simulation
Statistical learning
Experimental testing

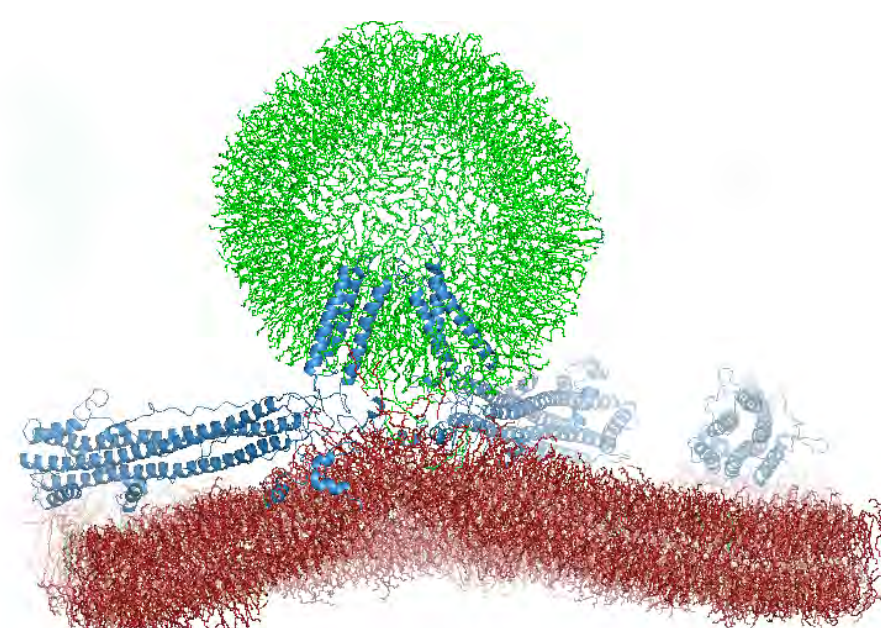


2. Predicting difficult genotype-phenotype relationships in infectious disease, leveraging: sequence structure dynamics



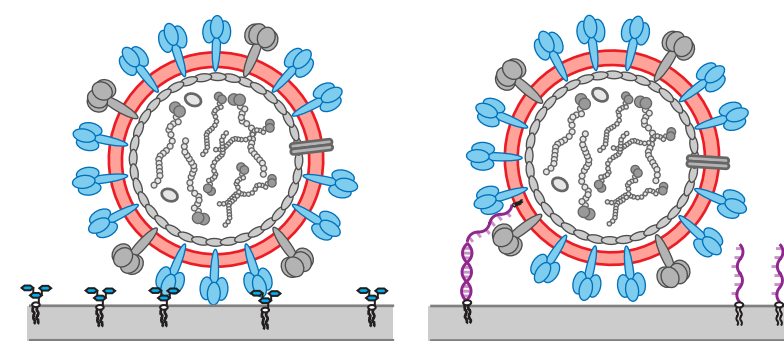
3. Tools to measure viral entry and screen for antivirals when host receptor is unknown

*Active work on:
Influenza, Zika,
drug-resistant gram-negatives*

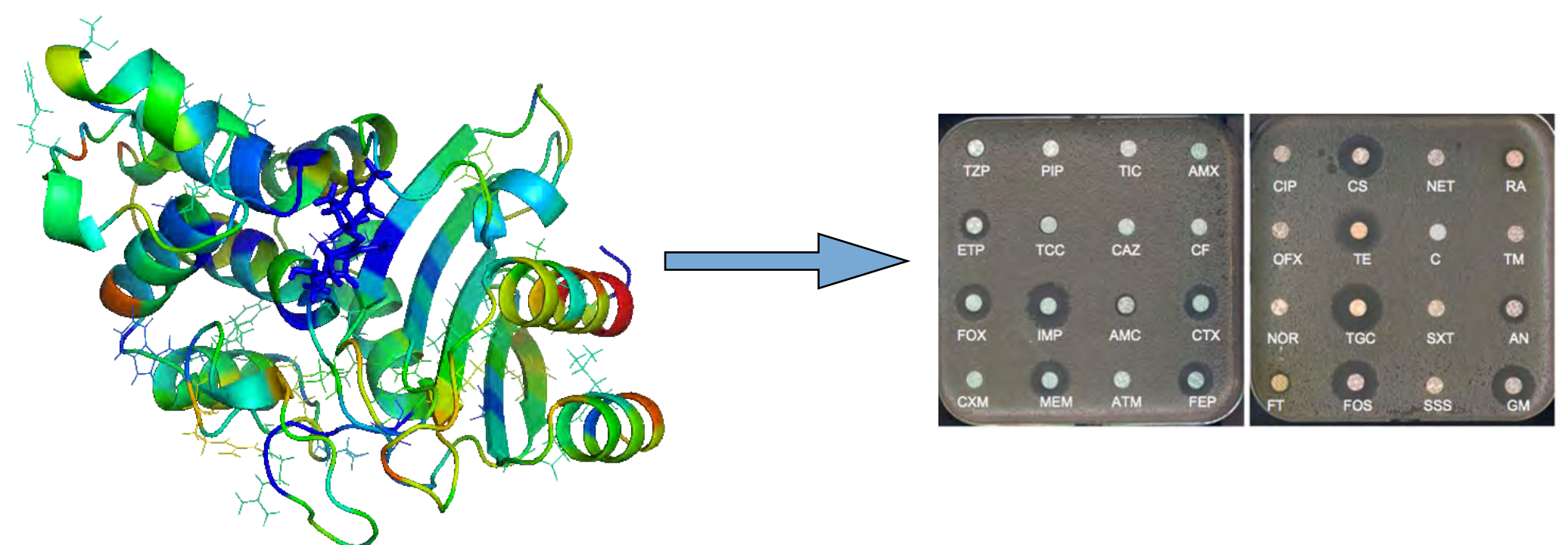


Prediction and mechanism in infectious disease: enveloped viral entry and drug-resistant bacteria

How do enveloped viruses infect cells and how can we predict virulence and design new antivirals?



What is necessary and sufficient for extreme drug resistance in bacteria?



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