Modeling of Serine Protease Substrate Catalysis in Synthetic Micelle Environment

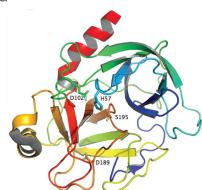
SIMCODES 2025 NSF Funded Mentors: Davit Potoyan and Xueyu Song Alisa Steele

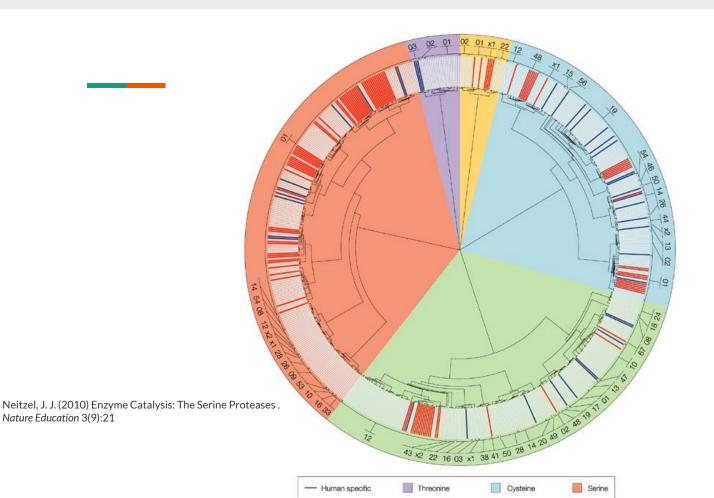
Goal of Project

 Develop a machine learning-based simulation framework to predict catalytic efficiency within micelles

Background Information - Serine Proteases

- Large family of enzymes which cleave peptide bonds in proteins by using a serine residue at the active site
- Found in almost all organisms
- Important for biological processes like programmed cell death, digestion, and immune responses
- Ex: thrombin, plasmin, trypsin





Role in Project

- Data collection and preprocessing
 - Collect a dataset or serine protease structures from Protein Data Bank
 - Represent substrate molecules through SMILES notation
 - Perform molecular docking within enzyme's active site
 - Graph data from collected datasets to search for correlation and trends
- Computational Simulations
 - Perform molecular dynamics simulations of enzyme-ligand interactions inside enzymes *
 - Investigate how enzyme environment influences binding affinity and transition state stability by modifying interactions within pocket *
 - Compare computational predictions with experimental data *

What I've Learned

- Computational research experience
- Coding
- Interpretation of data
- Poster-making and presenting

Current Progress

- Ki, Kcat, Km, and small molecule database
- All SMILES notations
- Comparative graphs
- Beginning docking

	methylimidazolidi	04-2							
1 F6541-1489	1-cyclopropyl-3- (1,2,3,4- tetrahydroisoquinolin	2097865- 50-2	1.5 256.34		0.56	2.34	23.55	550.0	O=C1C(N2CCC3=C(C=CC=C3)C2)CCN1C1CC1
2 F1739-0011	4,6-dimethyl-2- (pyrrolidin-1- yl)pyridine-3-car	693254- 24-9	1.5 201.27	solid	0.50	0.00	39.92	3548.1	CC1=CC(C)=NC(N2CCCC2)=C1C#N

MW Description FSP3 clogP TPSA

IDNUMBER

F2147-9803

F3162-0106

F3260-0021

Chemical_Name

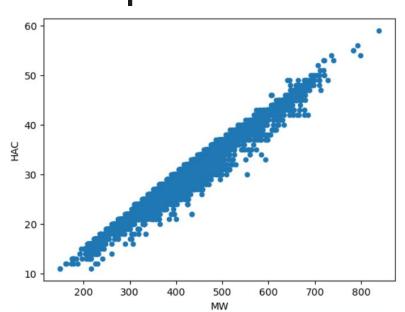
CAS PriceCoeff

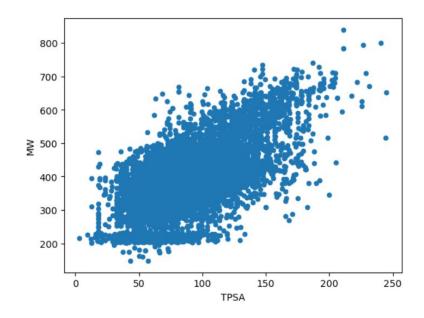
H- ... acceptors ...

Activity_value

smiles

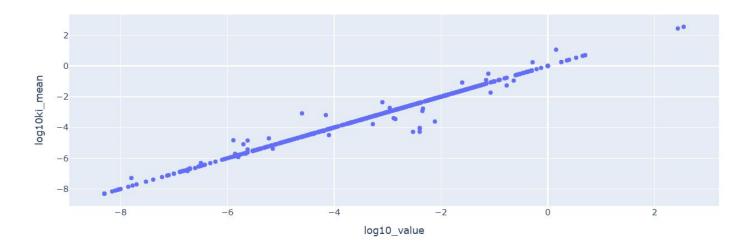
Graphs





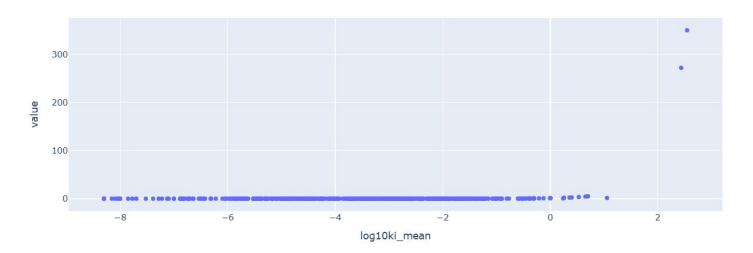
Graphs (continued)

Scatter Plot: log10ki_mean vs log10_value



Graphs (continued)

Scatter Plot: value vs log10ki_mean



Challenges

- Learning how to use Python
- Learning pace of research
- Docking

Future Goals

- Continued project goals
 - Continue docking and docking analysis
 - Begin MD simulations and trajectory analysis
 - ML model building and evaluation
- Personal goals
 - Continue learning more about coding
 - Better understand docking
 - Learn to perform MD simulations and trajectory analysis

Citations

- Di Cera E. Serine proteases. IUBMB Life. 2009 May;61(5):510-5. doi: 10.1002/iub.186. PMID: 19180666;
 PMCID: PMC2675663.
- Neitzel, J. J. (2010) Enzyme Catalysis: The Serine Proteases. Nature Education 3(9):21
- Prasanna S, Doerksen RJ. Topological polar surface area: a useful descriptor in 2D-QSAR. Curr Med Chem.
 2009;16(1):21-41. doi: 10.2174/092986709787002817. PMID: 19149561; PMCID: PMC7549127.

Acknowledgments

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