Context-dependent design of inducedfit enzymes using deep learning generates well-expressed, thermally stable and active enzymes

Research conducted during my tenure at



Dr. Chen Brestel



Independant Al Scientist



Paper: Zimmerman et al. PNAS 2024

How to design a novel enzyme?

What are enzymes good for?

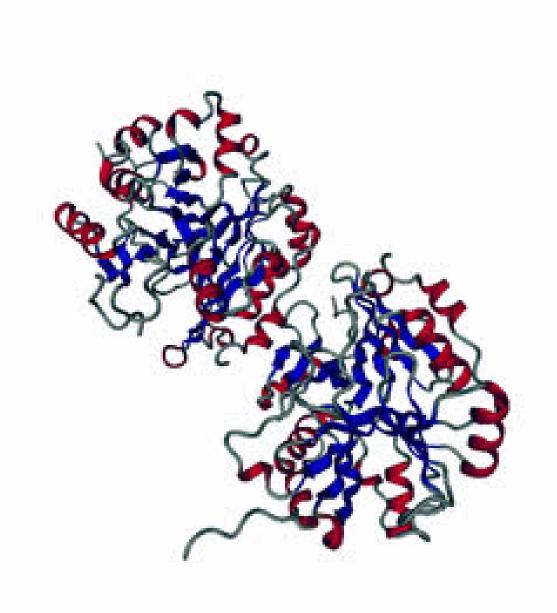
Industrial applications

- Healthcare
- Foodtech
- Energy
- Agtech
- Environment
- Militry/HLS
- etc.

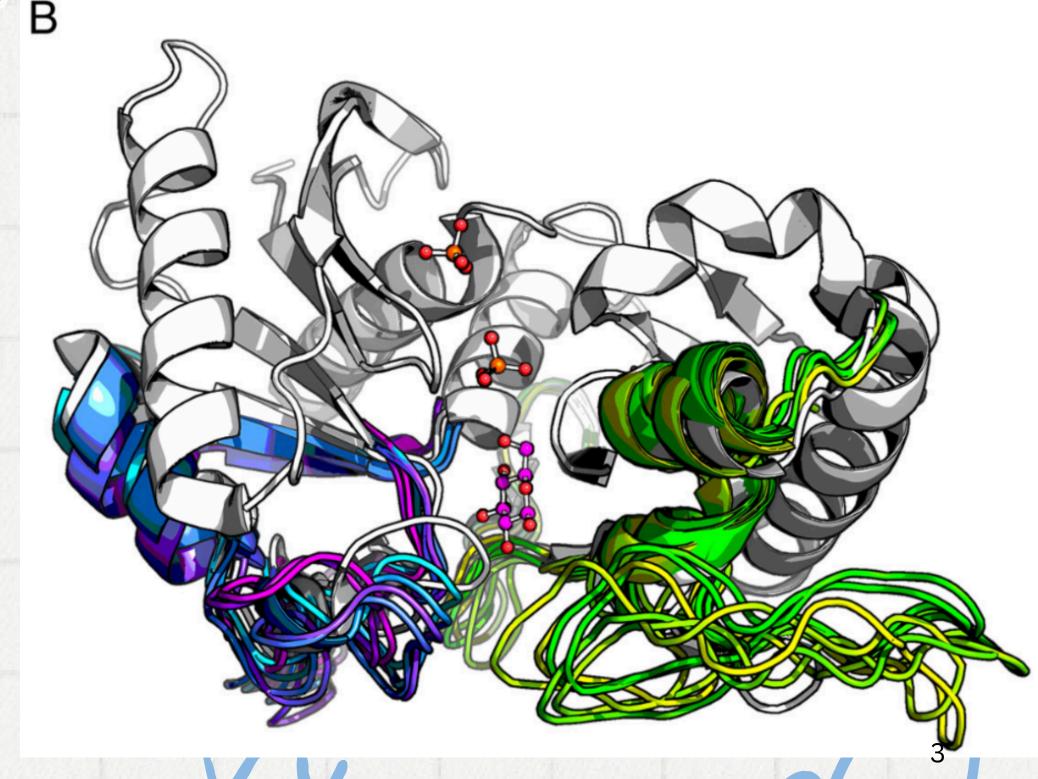
Why we need novel enzymes?

- Different substrate
- Different temprature
- Better activity
- etc.

How does enzymes look?



AndrewGNF



Current Approaches, Fields & Tools

- Fast evolution
- Protein folding
 - Rosetta
 - David Baker, Washington, Lab tools
 - AlphaFold 2 & 3 Deepmind
- Protein language models
 - ESM2, ESM3 Facebook
 - ProteinGPT
 - ProGen Salesforce & Stanford

The Nobel Prize in Chemistry 2024



Ill. Niklas Elmehed © Nobel Prize Outreach

Da∨id Baker

Prize share: 1/2



Ill. Niklas Elmehed © Nobel Prize Outreach

Demis Hassabis

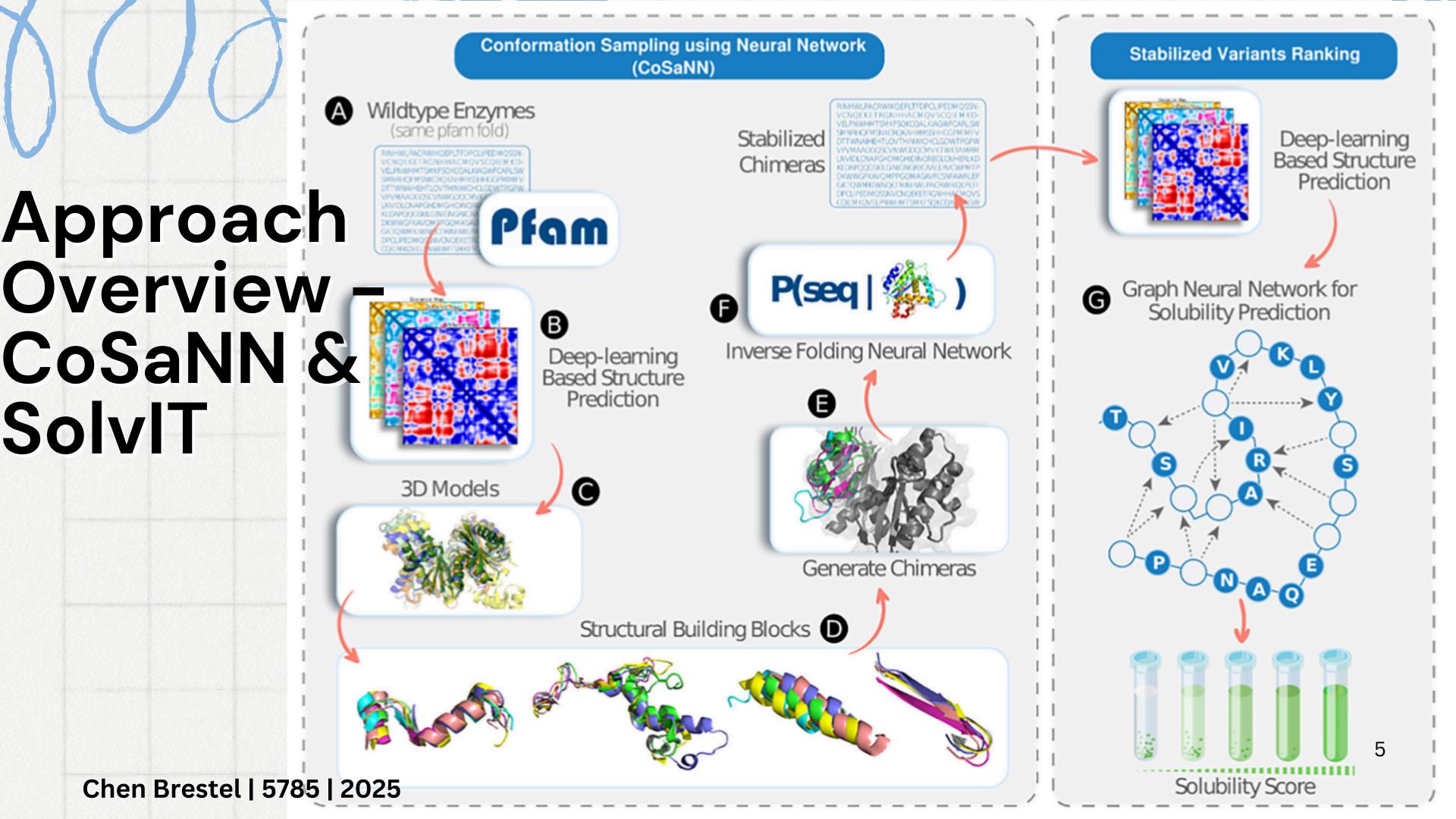
Prize share: 1/4



Ill. Niklas Elmehed © Nobel Prize Outreach

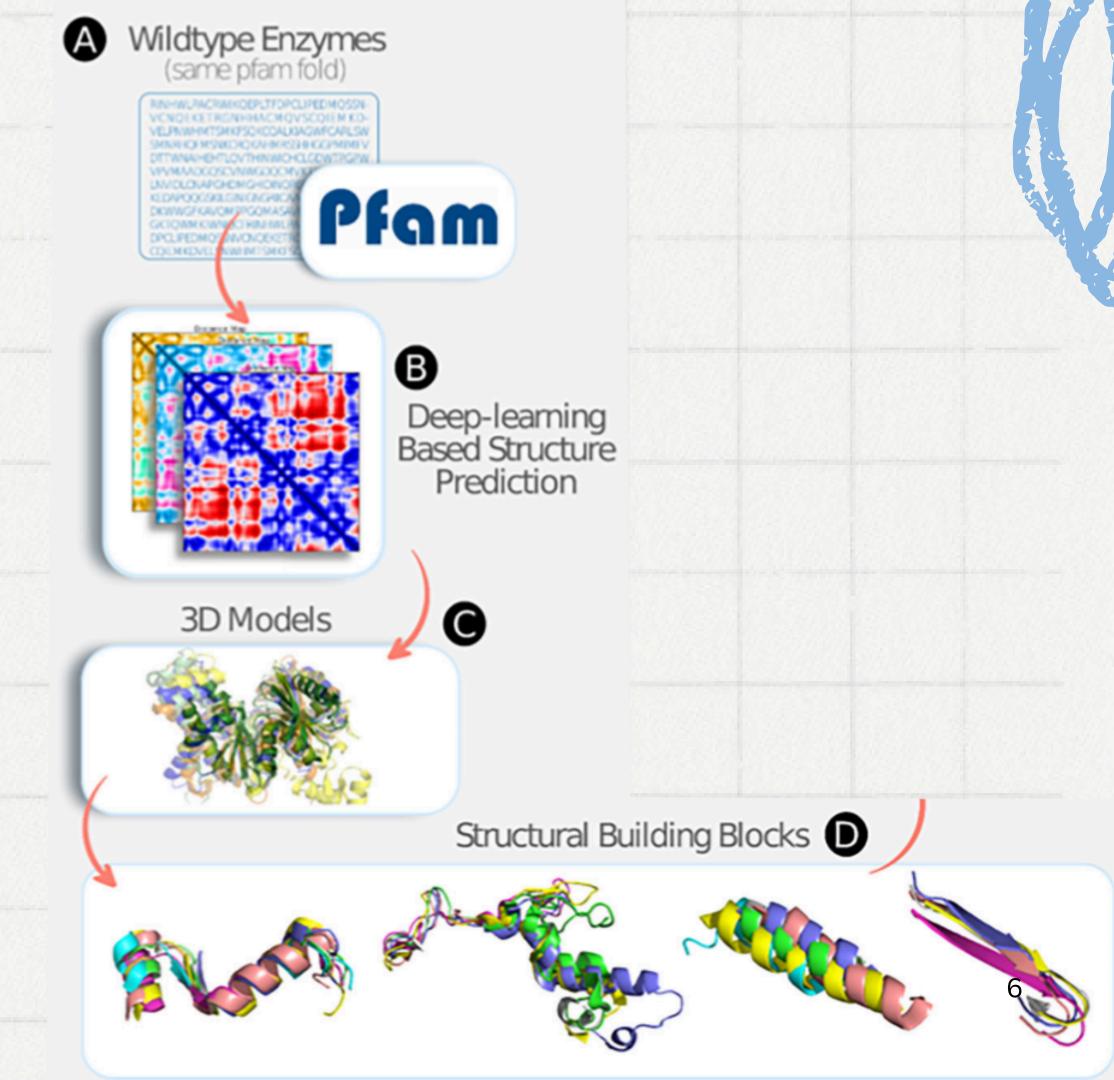
John Jumper

Prize share: 1/4



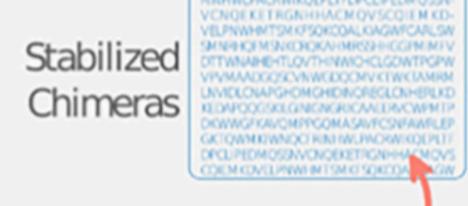
How to find structural building blocks?

Why blocks?



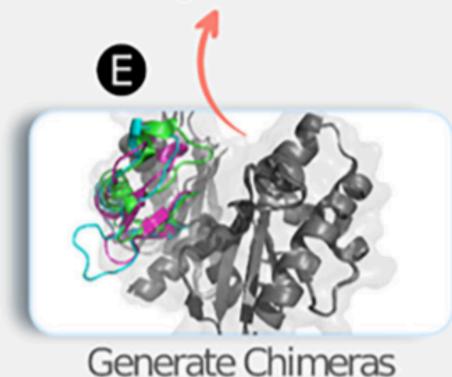
How to generate stabilized chimeras?

- What are chimeras?
- Why chimeras?
- What are satbilized chimeras?
- Why satbilized chimeras?





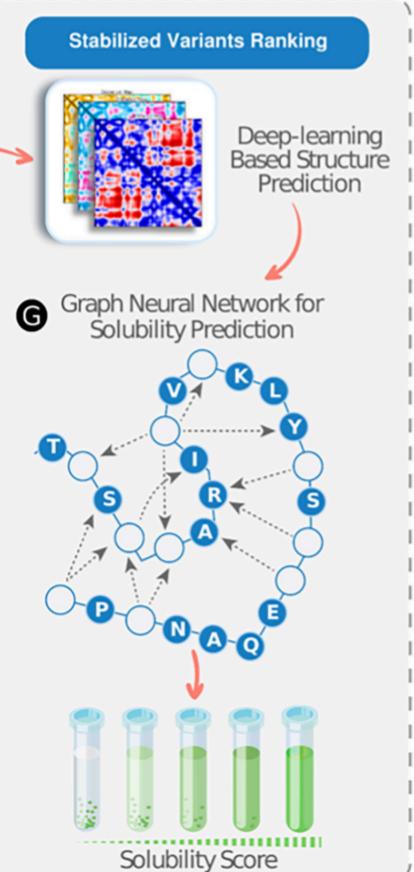
Inverse Folding Neural Network



How to get solubility-based ranking Stabilized Variants Ranking

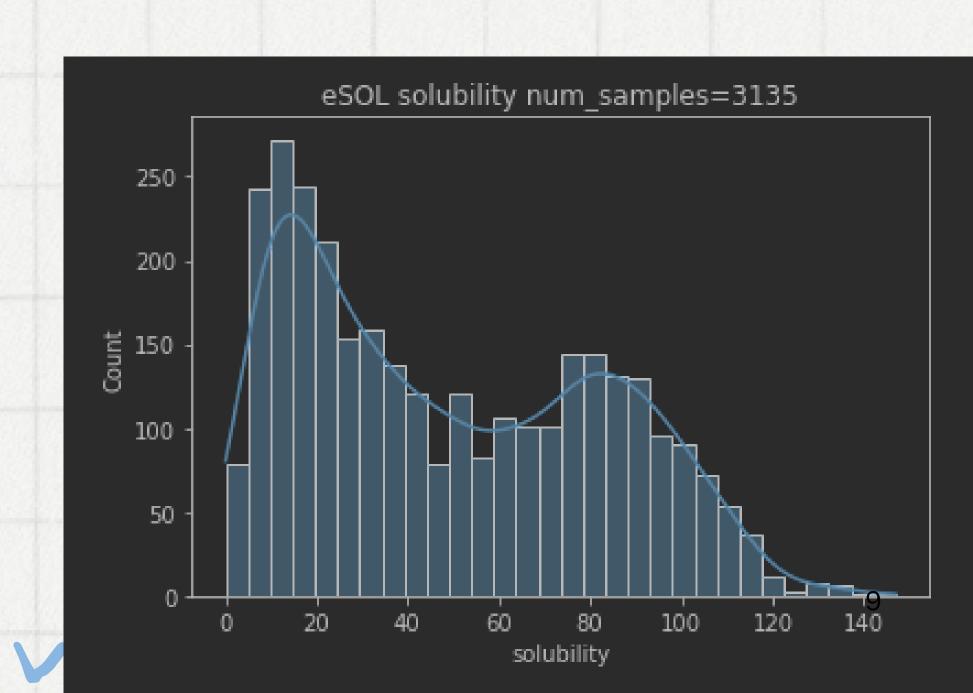
Why ranking?

What is solubility-based ranking?



What is the dataset used for training SolvIT?

- What is the target of solubility predictor?
- What is the training purpose?
- eSOL Dataset Niwa2009
- How to clean the data?
- Enzymit Dataset.
- How to ensure the prediction confidence?
- How to ensure the prediction generality?



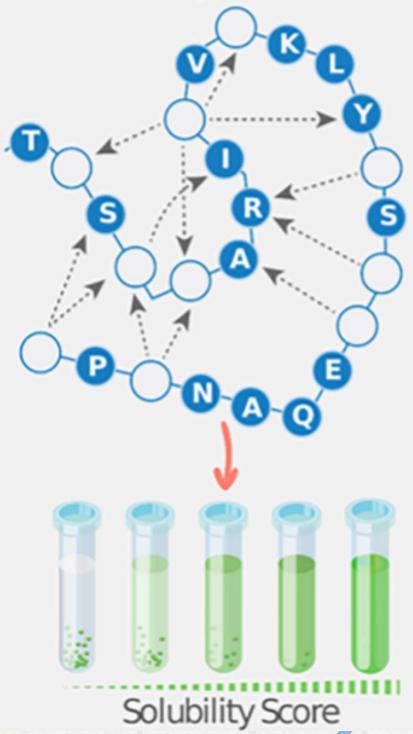
Training experiments

- Why multiple training experiments?
- What parameters were tuned?
 - Heterogeneous/homogeneous GNN
 - Type of convolution layer
 - Type of global pooling layer
 - Number of heads
 - Number of convolution layers
 - Batchnorm
 - Neighbour distance threshold for edges
 - Binary/quantized/float rosetta features
 - ESM features

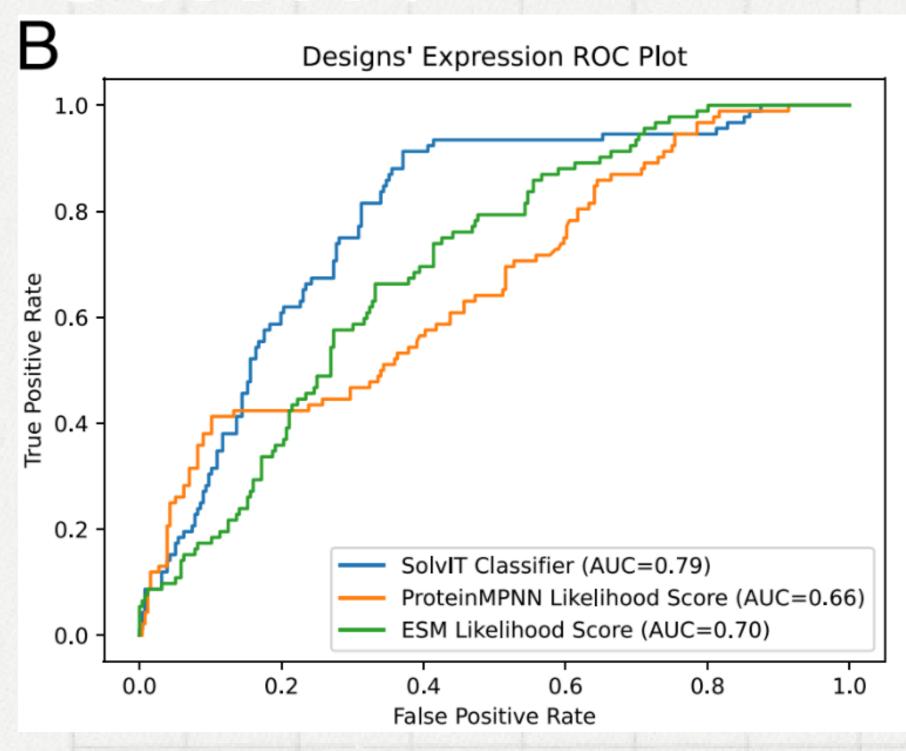
Model architecture

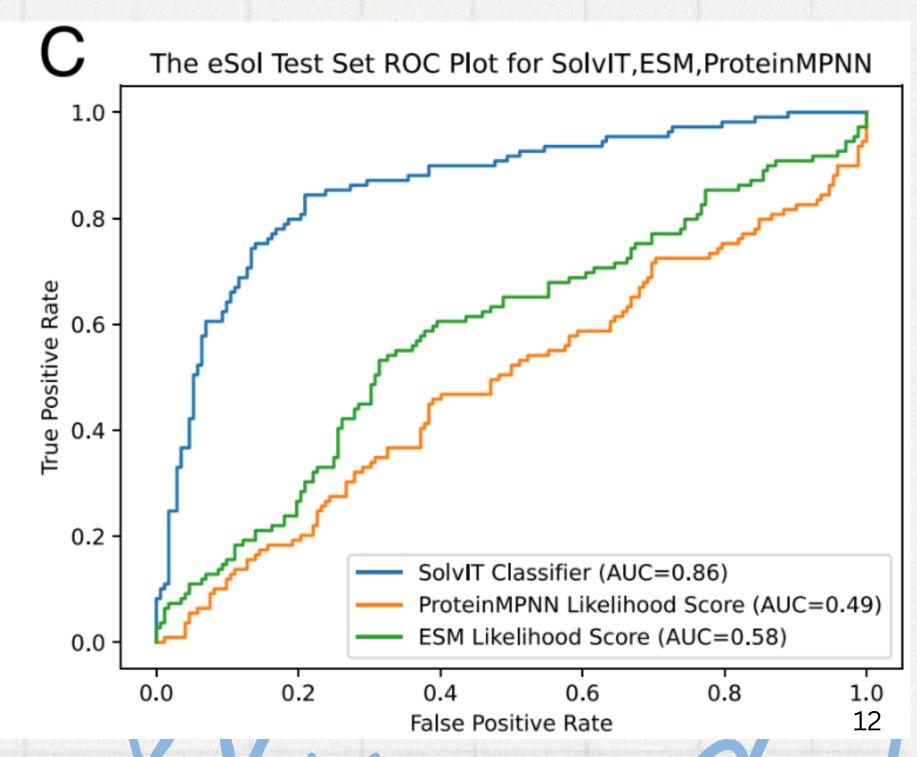
- Graph neural network (GNN)
- Convolution layer: GATv2Conv [Brody2O21]
- Global pooling layer: Global Graph Multiset Transformer pooling operator [Baek2021]
- Number of heads: 8
- Number of convolution layers: 2
- Batchnorm: Off
- Neighbour distance threshold for edges: 5 [Å]
- Amino-acid encoding: one-hot
- ESM embedding reduced size: Off
- Model target: binary

Graph Neural Network for Solubility Prediction



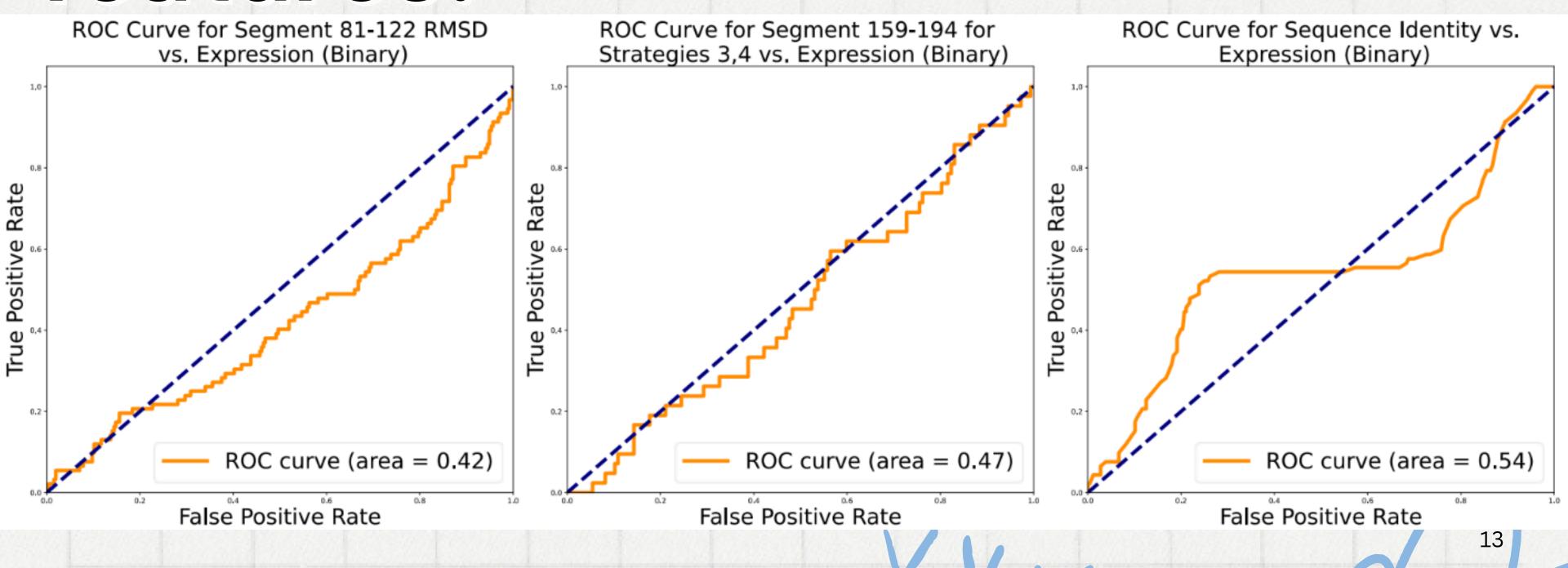
What is the performance of SolvIT?





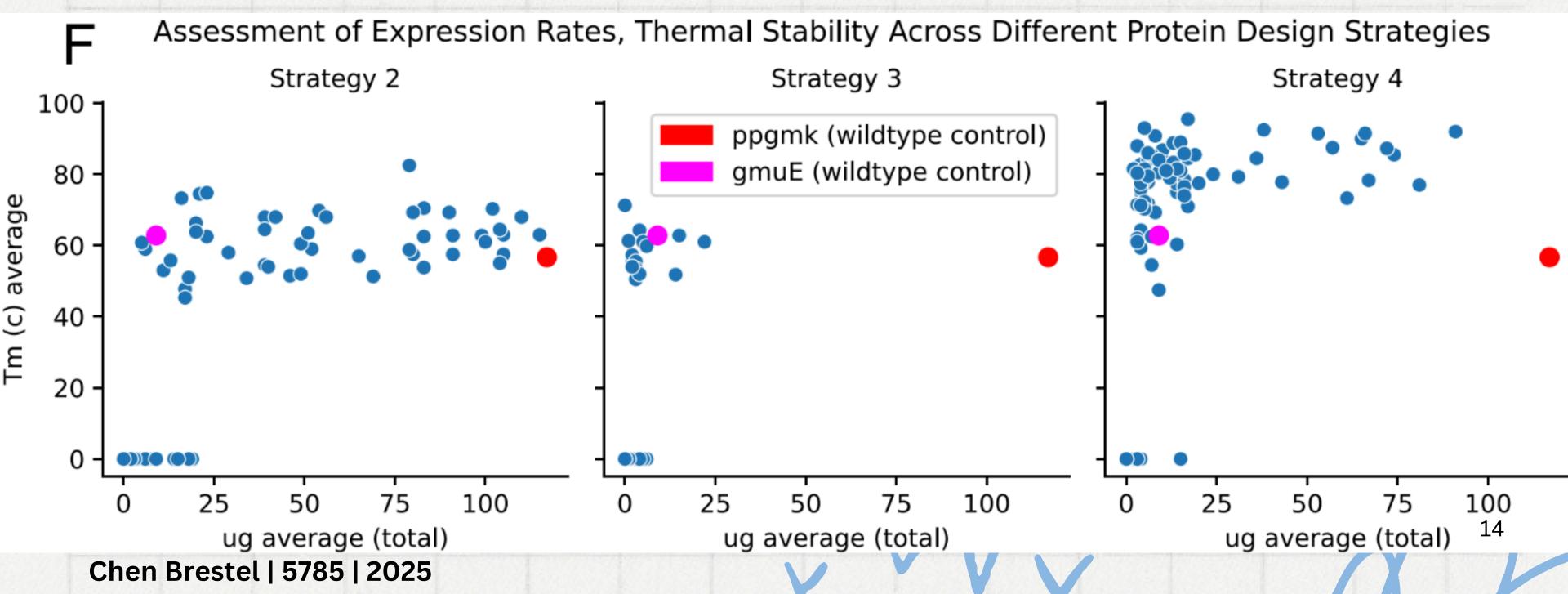
Could we achieve same performance with simpler features?

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Does the melting temperature change?

- Higher melting temperature 83% of novel designs
- Strategy 4 78% of high melting-temp. novel designs

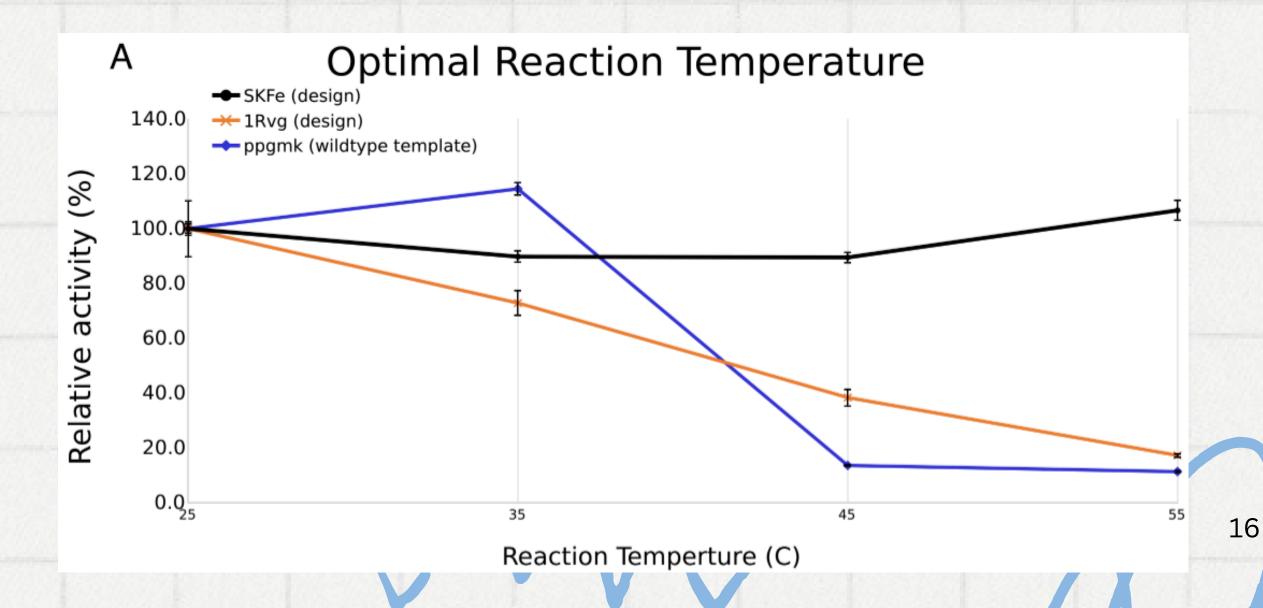


Are the enzymes activite?

- 60 designs active with either hexametaphosphate or ATP
- 8 (13%) designs showed obligatory polyphosphatedependent activity
- Template enzyme can utilize both ATP an inorganic polyphosphate
- Obligatory polyphosphate activity is not common in natural enzymes. Has been documented in a handful of cases
- Underscores the potential of our method to introduce non-natural enzymatic traits

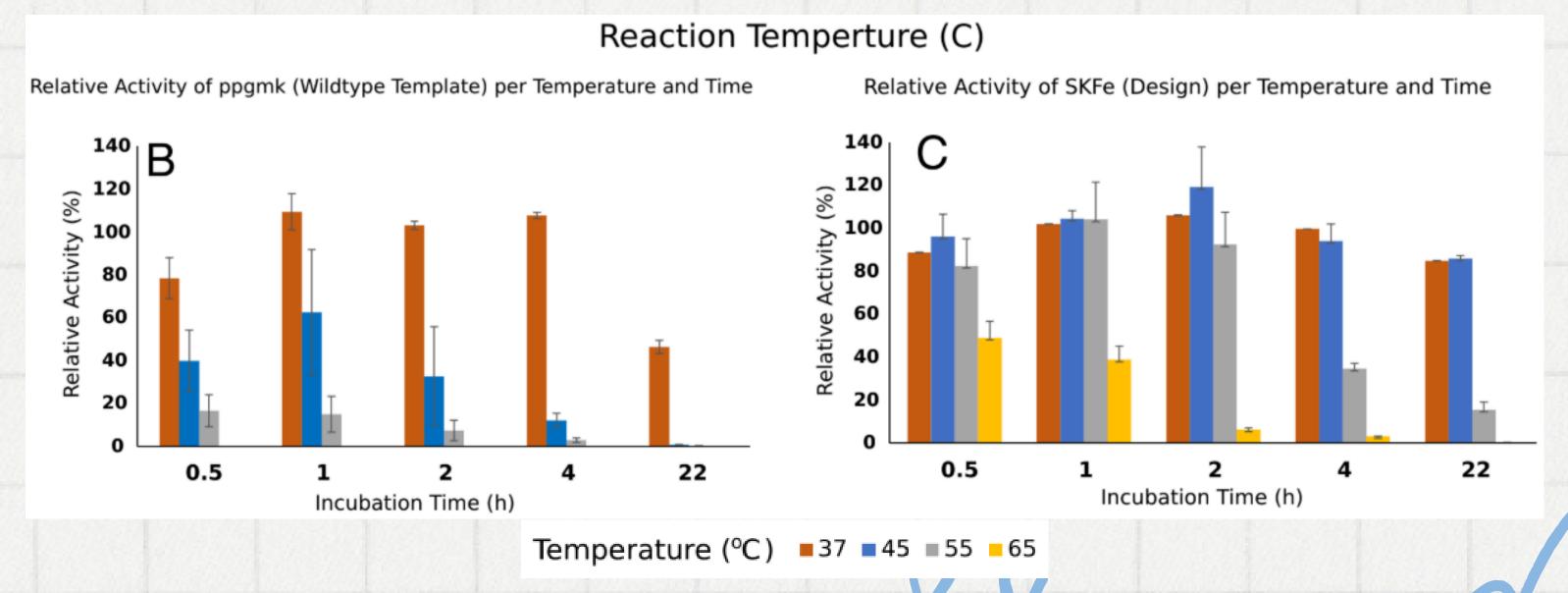
What is the activity of novel enzymes as temp. increase? Above 35C novel designs activity is higher SKFe retains 40% activity at 95C

- Wildtype has no activity at 95C



What is the activity after prolonged temperature stress? • 55C: WT non-active after 4h | SKFe 80% activity after 22h

- 65C: WT non-active after 30min | SKFe 40% activity after 30min



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Conclusion

- CoSaNN Enable rapid and robust novel enzyme designs
- SolveIT Enable high performance solubility prediction
- Tested in wet lab
- Achieve improved novel designs with
 - Higher melting temparature
 - Higher activity
 - Higher robustness to prolonged temperature stress
 - Possible non-natural enzymatic traits

Thank You

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Research conducted during my tenure at





https://chenbrestel.github.io/science/protein_engineering