Good afternoon, everyone! My name is Jiaming Huang and the topic for today’s presentation is inhibition of Chitinase by allosamidin.

Chitinase is a protein which plays an important role in both agriculture and medicine. For agriculture, chitinase protects plants against parasites and pathogens. For medicine, chitinase are focused for developing treatments for various allergies and inflammatory diseases. However, the precise structure of chitinase remains unknown. To make a prediction of its structure, modelling approaches, including homology modelling and ab initio modelling, are applied. Homology modelling is a modelling technique which predict the 3D structure of the target protein sequence from the known structure of its homologous protein sequences referred as templates. In contrast, ab initio modelling is a modeling technique which predicts the 3D structure of the target protein sequence from scratch by using clustering algorithm and the principle of energy minimization. After the prediction of target’s structure, docking can be performed. In this work, we choose allosamidin as our inhibitor since it not only has high affinity and specificity but also complements the active site of chitinase.

Now let’s turn to the materials and methods part. In the left hand side, the overall workflow is demonstrated. Particularly, EasyModeller and SWISS-MODEL are utilized for homology modelling while I-TASSER is utilized for ab initio modelling. After that, SPDBV is utilized for energy minimization while SCRWL is utilized for side chain refinement. To evaluate generated models, overall quality factor is focus through UCLA SAVES website. Moving forward, PDBsum is used for secondary structure analysis and VINA is used for docking. For further docking studies including docking site visualization and docking visualization, discovery studio is applied.

Now let’s move into the results and discussion session which has been divided into two parts. Here comes part one: quality evaluation, model selection and secondary structure analysis. Table 1 demonstrated the overall quality factors for models generated from homology modelling. Table 2 demonstrated the overall quality factors for models generated from ab initio modelling. We can see from those two tables that for homology modelling, the SWISS-MODEL with one template has the highest overall quality factor, outperforming other homology modelling generated models. For ab initio modelling, Model 3 generated from I-TASEER has the highest overall quality factor, outperforming other ab initio modelling generated models.

Then, toward those two models, energy minimization and side chain refinement are conducted for which the result has been summarized in table 3. For simplicity, the process done to the model are color in green while the process not done are color in red. For SWISS-MODEL generated models, the model with highest overall quality factor are turn into be the model before energy minimization and before side chain refinement and the model after energy minimization but before side chain refinement. To select a final model for docking, the model generated from SWISS-MODEL without energy minimization and side chain refinement are selected since it has higher proportion of allowed region (which is 88.2%) than the other model with the same overall quality factor (which is 87.5%).

Towards best models in both SWISS-MODEL and I-TASSER, the topology graph and Ramachandran plot are shown in Figure 2 and Figure 3. From Figure1, we can see that both models with highest overall quality factor share similar secondary structure with 11 alpha helices, 9 beta sheets and 3 disulfide bonds. For the model from I-TASSER, it has the secondary structure with 13 alpha helices, 11 beta sheets and 3 disulfide bonds.

Now let’s move into part 2 which is the inhibition of allosamidin with Chitinase. In this part, we use allosamidin to dock the active pocket of chitinase structure (GLU176) and choose the best orientation for visualization. In Figure 3, four combined figures are demonstrated for docking visualization. The first figure shows the 3D structure of allosamidin docking into the active site. The second figure shows Ligand-Receptor interaction with interacting residues labelled. The third figure shows allosamidin docking in the pocket with hydrogen bond. To give you a more direct feeling about the interaction, 2D graph of interaction with distance is shown in the fourth figure.

In conclusion, for this work, 3D modeling of chitinase was performed using computational methods and the best model with highest overall quality factor were further selected. To inhibit the active pocket of chitinase, allosamidin was chosen. The findings underscore the potential of computational tools in protein structure-function analysis and drug discovery. However, there exists limitation that in our experiment, the docking doesn’t consider the real environment where water molecules and ions exist. For further studies, molecular dynamics simulation approaches can be employed to give a more accurate docking result.

This is the end of the presentation. Thank you for your listening! For more analysis, you can visit my github page with link below.

Good afternoon, everyone! My name is Jiaming Huang and the topic for today’s presentation is Inhibition of *Thermomyces Lanuginosus* Chitinase by Allosamidin.

Chitinase is a protein which functions critically in both agriculture and medicine. For agriculture, it protects plants against parasites and pathogens. For medicine, it is responsible for various allergies and inflammatory diseases. However, the protein structure of chitinase remains unknown. Therefore, in our work, to predict the structure, modelling techniques, including homology modelling and ab initio modelling are applied. For homology modelling, it predicts the target’s protein structure from the templates’ known structure. The templates are usually chosen from its homologous sequences. For ab initio modeling, it predicts the target’s protein structure by using the clustering algorithm and the principle of energy minimization. After prediction of chitinase’s structure, docking can be performed. In our work, allosamidin is chosen as inhibitor since it not only has high affinity and specificity but also complements the active site of chitinase.