



Principal Investigator

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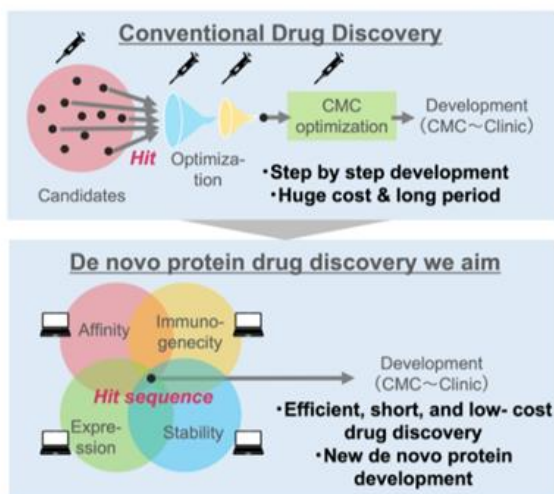
Adopted Theme

AI/data-driven platform development for de novo protein drug and vaccine

Subject of Research

AI/data-driven platform development for de novo protein drug and vaccine

Overview



We will develop a platform that can accurately predict the properties and functions of proteins required for drug discovery by AI and large-scale analysis technologies. Using deep learning and large-scale data acquisition technologies, we will construct prediction models for various functions and properties through a “design-measure-analyze-redesign” cycle. The goal is to establish a start-up that will enable rapid drug discovery by rationally optimizing the stability, productivity, and immunogenicity of vaccines and neutralizing molecules, especially for infectious diseases, and reducing the trial-and-error process that has been an issue in the conventional drug discovery process. This will significantly reduce the cost and shorten duration of drug development and enable rapid response to pandemics and emerging infectious diseases.

Business Models (when applying)

Establish a platform that will significantly reduce the cost and time frame involved in de novo protein drug discovery and vaccine development and provide the platform for existing pharmaceutical companies. In addition, we also aim to develop its own drug and/or vaccine.

Activity Planning (when applying)

We will overcome the following three Gaps

Gap 1 Development of rational design methods for binder proteins that can bind strongly to therapeutic targets

Binding to targets is one of the basic functions of proteins, and we will construct a model to predict the binding affinity and specificity with high accuracy and utilize the model for rational design of de novo proteins.

Gap2 Development of a rational design method for proteins that can be easily expressed

Protein expression is one of the most important features of a protein, yet it is still difficult to predict its expression. Therefore, we will develop a model to accurately predict the expression of proteins

Gap3, Development of a rational design method for proteins with desirable immunogenicity

We are developing a model to predict the immunogenicity because low immunogenicity for binders and high immunogenicity for antigen proteins used in vaccines are highly desirable.