

## Performance of Chugai's AI-based Antibody Discovery Technology MALEXA-LI Published in Scientific Reports

- Research findings of MALEXA-LI, Chugai's artificial intelligence-based technology to support discovery of antibody therapeutics, were published in Scientific Reports by Nature Research
- MALEXA-LI proposed amino acid sequences of antibodies with greater than 1800-fold binding strength compared to existing antibodies
- Chugai continues to focus on dramatically improving the drug discovery process through AI under CHUGAI DIGITAL VISION 2030

TOKYO, March 22, 2021 -- <u>Chugai Pharmaceutical Co., Ltd.</u> (TOKYO: 4519) announced that research findings of Chugai's artificial intelligence (AI)-based technology MALEXA-LI to support discovery of antibody therapeutics were published in Scientific Reports. Scientific Reports is a comprehensive scientific journal by Nature Research known as one of the largest journals in the world by number of articles.

The final goal of Chugai's digital strategy CHUGAI DIGITAL VISION 2030 announced in 2020 is the creation of innovative new drugs using digital technologies. We aim to dramatically reform our research processes, such as the creation of new drug candidates through the use of AI and other cutting-edge technologies and the improvement of the probability of successful drug discovery.

MALEXA is an AI-technology independently constructed by Chugai to change the drug discovery process. It was named with the acronym of Machine Learning x Antibody. There are two types of MALEXA technologies, MALEXA-LI and MALEXA-LO, which are optimized for the antibody discovery process. MALEXA-LI covered in Scientific Reports this time is an AI-technology to find sequences suitable for lead antibodies, or the "species" of antibodies. The training data of this machine learning model was provided by analyzing gene sequence information that next-generation sequencers obtained from the antibody library which Chugai accumulated through many years of antibody research.

In this article, a sequence generation method based on LSTM (Long Short-Term Memory), which is one of the algorithms for deep-learning, was developed to search antibody sequences with high affinity to target antigens. As a result, MALEXA-LI proposed amino acid sequences with more than 1800-fold binding strength to target antigens compared to the existing antibody.

"Antibody design using LSTM based deep generative model from phage display library for affinity maturation"

(https://www.nature.com/articles/s41598-021-85274-7)

"The significance of digital transformation lies in what new value we can realize in the core of our business with digital technologies," said Satoko Shisai, Chugai's Vice President, Head of Digital & IT Supervisory Division. "In the case of Chugai, this means making digital technologies the driving force for generating innovative new drugs. The results demonstrated that AI and other advanced technologies greatly open up the possibilities of drug discovery. We will continue to promote DX to break the mold of conventional drug discovery research."

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