June 2023 Vol. 21 No. 6
NTT Technical Review
6 2023

https://www.ntt-review.jp/archive/2023/202306.html

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Keigo Kajimura, Senior Executive Vice President, NTT Communications

▼Abstract

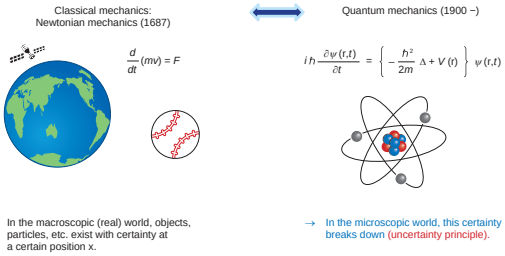
In 2022, the new DOCOMO Group was formed after a reorganization of NTT DOCOMO, NTT Communications, and NTT COMWARE. Since then, the Group has integrated the three companies' business functions and clarified their respective roles to improve the value it provides to customers and boost growth. Under its brand slogan "Changing worlds with you," the new DOCOMO Group aims to reform the structure of society/industry and create new lifestyles. We interviewed Keigo Kajimura, senior executive vice president of NTT Communications, which is responsible for the enterprise business, about the initiatives he is focusing on and his beliefs as a top executive.

Feature Articles
Toward Quantum Technology Innovation

Expectations and Prospects for Innovation in Quantum Technology

▼Abstract

NTT laboratories have been engaged in basic research on various quantum-related technologies, including quantum information, since the mid-1980s before research on quantum computers took off. The Feature Articles in this issue present the latest global trends in quantum technology and NTT's research portfolio regarding quantum technology. In addition to quantum computing, quantum sensing and quantum networks are also extensively discussed from both experimental and theoretical perspectives.



Regular Articles

Identification of Transcription Factors and the Regulatory Genes Involved in Triacylglycerol Accumulation in a Unicellular Red Alga

▼Abstract

Triacylglycerols (TAGs) generated by microalgae are a raw material for liquid biofuel production, so increasing the amount of TAGs generated will contribute to reducing the environmental impact of, for example, greenhouse gas emissions. Since transcription factors (TFs) regulate the expression of a group of genes with related functions, it is thought that TAG accumulation can be enhanced by identifying TFs involved in TAG accumulation and enhancing their functionality. In this study, my research colleagues and I used transcriptomic and phosphoproteomic data—obtained under conditions of TAG accumulation in a unicellular red alga, *Cyanidioschyzon merolae*, to identify 14 TFs that may regulate TAG accumulation. To verify the function of these TFs, we constructed functionally enhanced strains overexpressing each TF and analyzed changes in TAG accumulation. The analysis results indicate that the amount of TAGs regarding the four overexpressing strains increased 2.2 to 3.8 times compared with that regarding the control strain, so we can consider that those four TFs are involved in TAG accumulation.