

Complex responsible for protein breakdown in cells identified using Bio TEM

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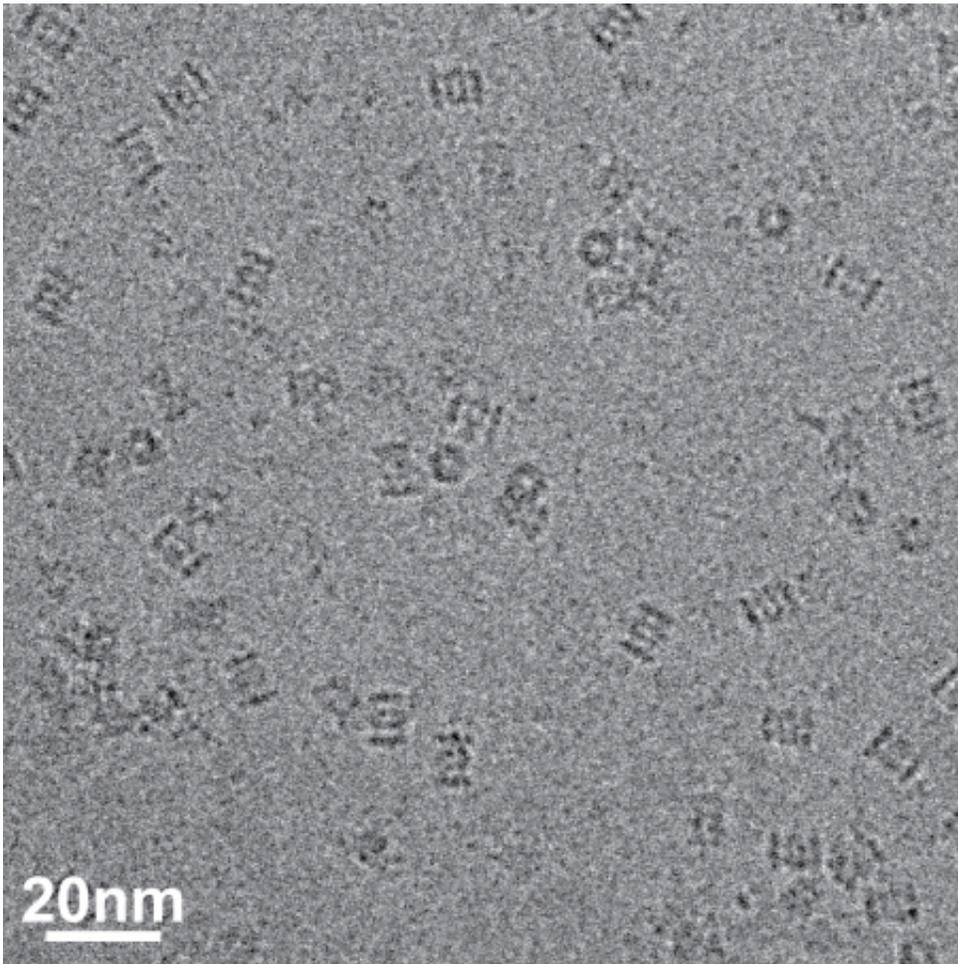


Figure 1: A picture taken by Bio TEM of open state protein sample (proteasome complex)

Using TEM to observe protein molecules and analysing its high

resolution 3D structure is now possible. KAIST Biomedical Science and Engineering Department's Professor Ho-Min Kim has identified the high resolution structure of proteasome complexes, which is responsible for protein breakdown in cells, using Bio TEM.

This research has been published on the world's most prestigious journal, *Nature*, online on May 5th. Our body controls many cellular processes through production and degradation of proteins to maintain homeostasis. A proteasome complex acts as a garbage disposal system and degrades cellular proteins when needed for regulation, which is one of the central roles of the body.

However, a mutation in proteasome complex leads to diseases such as cancer, [degenerative brain diseases](#), and autoimmune diseases.

Currently, the anticancer drug Velcade is used to decrease proteasome function to treat Multiple Myeloma, a form of blood cancer. Research concerning proteasome complexes for more effective [anticancer drugs](#) and treatments with fewer side effects has been taking place for more than 20 years. There have been many difficulties in understanding proteasome function through 3D structure analysis since a proteasome complex, consisting of around 30 different proteins, has a great size and complexity.

The research team used Bio TEM instead of conventionally used [protein crystallography](#) technique. The protein sample was inserted into Bio TEM, hundreds of photographs were taken from various angles, and then a high-performance computer was used to analyse its structure. Bio TEM requires a smaller sample and can analyse the complexes of great size of proteins.

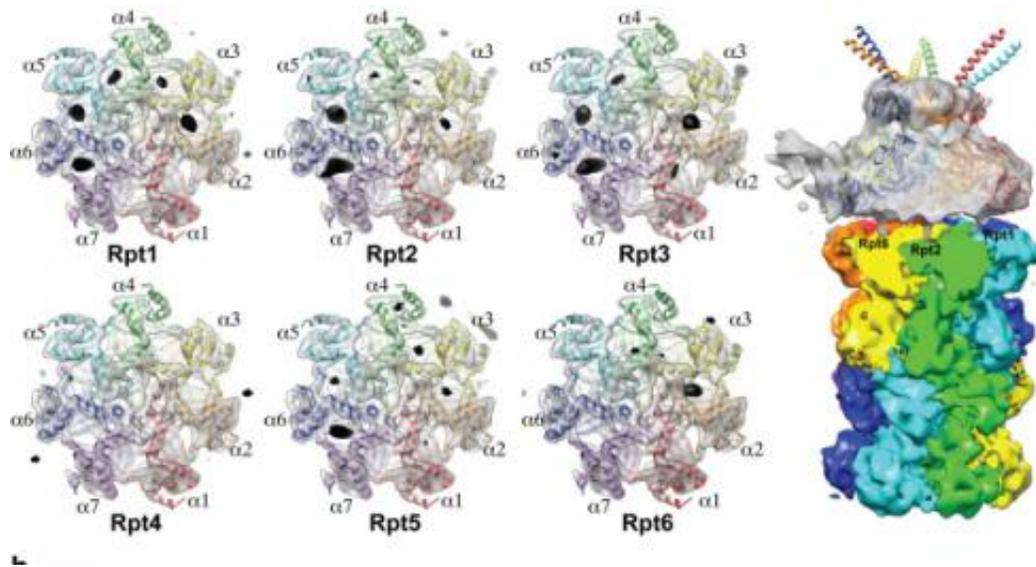


Figure 2: Bio TEM image analysis showing protein 3D structure

Professor Ho-Min Kim said, "Identifying proteasome complex assembly process and 3D structure will increase our understanding of cellular [protein degradation](#) process and hence assist in new drug development using this knowledge." He added, "High resolution protein structure analysis using Bio TEM, used for the first time in Korea, will enable us to observe structure analysis of large protein complexes that were difficult to approach using protein crystallography." Professor Kim continued, "If protein crystallography technology and Bio TEM could be used together to complement one another, it would bring a great synergetic effect to protein complex 3D structure analysis research in the future."

Professor Ho-Min Kim has conducted this research since his post-doctorate at the University of California, San Francisco, under the advice of Professor Yifan Cheng; in co-operation with Harvard University and Colorado University.

Provided by The Korea Advanced Institute of Science and Technology (KAIST)

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