**세미나초록**

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| 발표주제 | **Go hybrid : Structural Biology & Application** |
| 발표내용 | The knowledge gained from structural studies of biomolecules including protein domain, protein/protein complex, protein/DNA complex, and protein/RNA complex, has significantly advanced our understanding of biological phenomena at the molecular level and has catapulted the development of therapeutics. Since the structure of myoglobin was first determined in the 1950s by X-ray crystallography, this technique has been the most powerful tool in modern structural biology. Recently, a resolution revolution in single particle Cryo-EM has been led by technical breakthroughs, particularly direct electron detector (DED) with unprecedented speed and sensitivity, a state of the art electron microscope (Titan Krios), image processing software with better algorithms and GPG-based parallel computation. These achievements herald the beginning of a new era in the field of structural biology and has been appreciated as the Method of the Year in 2015 and the Nobel prizes in chemistry in 2017. The great advantage of Cryo-EM is that it can determine the 3D structure of macromolecular complexes in near native condition with a much smaller amount of sample and can even capture multiple dynamic states by using advanced image-processing algorithms. However, the lower molecular weight limitation is a challenge for Cryo-EM at present, mainly because the low signal-to-noise ratio (SNR) due to the small mass hampers identification and error-free alignment of such particles in low dose images. Here, I will introduce a couple of our complementary structural research (using X-ray Crystallography and Cryo-EM) from which I can reveal important biological questions. I will also introduce several cases of the structure-based protein engineering, which enabled us to translate the structural information into the development of therapeutic protein candidates |
| 발표자 | Ho Min Kim |
| 학력(학사이상) | 연도 | 내용 |
| 1995. 3 ~ 1999. 2 | B.S., KAIST, Department of Biological Science (Republic of Korea). |
| 1999. 3 ~ 2001. 2 | M.S., KAIST, Department of Biological Science (Republic of Korea). (Advisor : Ook Joon Yoo) |
| 2001. 3 ~ 2005. 8 | Ph.D., KAIST, Department of Biological Science (Republic of Korea). (Advisor : Ook Joon Yoo and Jie-oh Lee) |
| 2005. 9 ~ 2006. 11 | KAIST, Bio-medical Research Center (Republic of Korea) |
| 2006. 11 ~ 2007.11 | KAIST, Department of Chemistry (Republic of Korea) |
| 2007.12 ~ 2011.8 | University of California, San Francisco, Department of Biophysics & Biochemistry (USA).(Advisor : Yifan Cheng) |
| 주요약력 | 연도 | 내용 |
| 2011.8 ~ 2016.2 | KAIST, GSMSE, Assistant Professor |
| 2016.3 ~ Present | KAIST, GSMSE, Associate Professor |
| 2013.7 ~ Present | Korean Society for Structural Biology, Committee |