Bong-Jin Lee, Ph.D.

Professor

Address

- E-mail: lbj@nmr.snu.ac.kr
  pharmnmr@snu.ac.kr
- Web Site :http://www.snupharm.ac.kr/lbj/
- Tel : +82-2-880-7868 ,7869
- Fax: +82-2-872-3632

Education

- Ph.D. Univ. of Osaka (1990)
- M.S. Seoul Nat'l Univ. (1985)
- B.S. Seoul Nat'l Univ. (1981)

Work Experiences

- 1990 - 1991: Protein Engineering Research Institute, Japan , Post-Doc
- 1991 - 1995: SNU Assistant Professor
- 1995 - 2001: SNU Associate Professor
- 2001 - present: SNU Professor

Selected Publications

- Functional insights into the Streptococcus pneumoniae HicBA toxin-antitoxin system based on a structural study. ***Nucleic Acids Res.*** (2018).
- Functional details of the Mycobacterium tuberculosis VapBC26 toxin-antitoxin system based on a structural study: insights into unique binding and antibiotic peptides. ***Nucleic Acids Res*** (2017)
- Two distinct mechanisms of transcriptional regulation by the redox sensor YodB, ***Proc Natl Acad Sci USA*** (2016)
- Structural and functional studies of the Mycobacterium tuberculosis VapBC30 toxin-antitoxin system, ***Nucleic Acids Res*** (2015)
- Structure-based functional identification of *Helicobacter pylori* HP0268 as a nuclease with both DNA nicking and RNase activities. ***Nucleic Acids Res*** (2015)
- Structural and biochemical characterization of HP0315 from Helicobacter pylori as a VapD protein with an endoribonuclease activity. ***Nucleic Acids Res*** (2012)

Laboratory of Structure based Drug Discovery

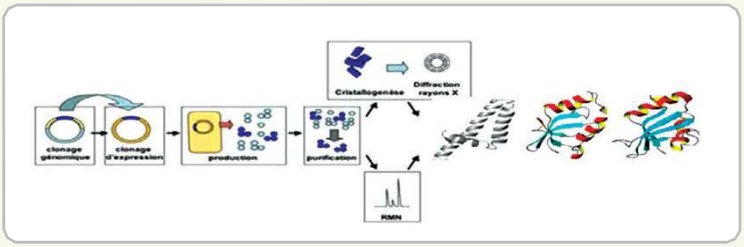
Recently , it has become possible to generate new drug candidates within a short period by utilizing the efficient and low-cost methods such as SBDD(Structure-Based Drug Discovery) and in silico screening. The importance of the protein structure after the Human or Pathogenic bacteria Genome Project has been more emphasized in developing new drugs based on disease-specificparticular proteins.

Our Research group developed antibiotic material with new mechanism of action which can overcome the antibiotics resistance. This new material could get a patentand pre-clinical study on this material was done.

3D structures of disease-related proteins

▸ *Helicobacter pylori*

Helicobacter pylori has uniqueness to survive in the extreme acidic environment in stomach. In addition, it is an important human bacterial pathogen and it can cause diverse gastric diseases such as peptic ulcers, chronic gastritis, mucosa- associated lymphoid tissue lymphoma and gastric cancer. We have determined 3-D structure of HP proteins from helicobacter pylori strain 26695



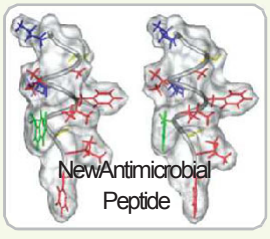
▸ Other proteins

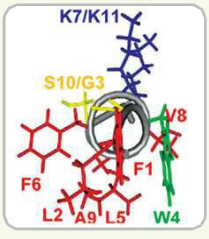
We have investigated the relationship between structure and functional mechanism of CRP and Toxin-Antitoxin system of pathogenic bacteria such as *Mycobacterium Tuberculosis* through the NMR and X-ray methods.

PEPTIDE DRUG

▸ Structure-Activity Relationship of the Peptides

Gaegurin 5 (GGN5; 24 residue) is a membrane-active antimicrobial peptide isolated from the skin of an frog, Rana rugosa. As part of an effort to search the new peptide antibiotics, we developed potent and low molecular weight antimicrobial/anticancer peptides, and determined their membrane-bound structures. Structural informations of newpeptidescanprovidetheir actionmechanism.





▸ New Antimicrobial/Anticancer Drug

Therapeutic development of new antibiotic and anticancer agents (GGN5 analogues and Model peptides) that show low-side effect and have new antibiotic/anticancer mechanism.