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### Education

1987	BS	Dept. of Chemistry, Seoul National University
1989	MS	Dept. of Chemistry, Seoul National University
1994	PhD	Dept. of Biochemistry, University of Wisconsin-Madison

### Professional Experience

1994-1997	Research Associate	Howard Hughes Medical Institute/MIT
1997-1999	Principal Investigator	Samsung Biomedical Research Institute
1999-2005	CEO and CSO	ToolGen, Inc.
2005-present	Assistant/Associate/Full Professor	Seoul National University
2014-present	Director	Institute for Basic Science (IBS)

### Research Interests

Genome engineering via programmable nucleases including the CRISPR-Cas system

- 1) Genome editing in plants, animals, and cultured human cells including iPS/ES cells
- 2) Engineered nuclease-mediated gene and cell therapy
- 3) Functional genomics using genome-scale libraries of programmable nucleases

### Publications

1. DNA-free genome editing in plants with preassembled CRISPR-Cas9 ribonucleoproteins. *Nature Biotechnol.* **33**, 1162 (2015).
2. Digenome-seq: Genome-wide profiling of CRISPR-Cas9 off-target effects. *Nature Methods* **12**, 237 (2015).
3. Functional correction of large factor VIII gene chromosomal inversions in haemophilia A patient-derived iPSCs using CRISPR-Cas9. *Cell Stem Cell* **17**, 213 (2015)
4. A guide to genome engineering with programmable nucleases. *Nat. Rev. Genetics* **15**, 321 (2014)
5. Microhomology-based choice of Cas9 nuclease target sites. *Nat. Methods* **11**, 705 (2014)
6. Highly efficient RNA-guided genome editing in human cells via delivery of purified Cas9 ribonucleoproteins. *Genome Res.* **24**, 1012 (2014)
7. A library of TAL effector nucleases spanning the human genome. *Nature Biotechnol.* **31**, 251 (2013)
8. Targeted genome engineering in human cells with the Cas9 RNA-guided endonuclease. *Nature Biotechnol.* **31**, 230 (2013) (Featured in *News and Views*, *Nature* **495**, 50; *Nat. Biotechnol.* **31**, 208)
9. Knockout mice created by TALEN-mediated gene targeting. *Nature Biotechnol.* **31**, 23 (2013)
10. TALENs and ZFNs are associated with different mutation signatures. *Nature Methods* **10**, 185 (2013)