

Biomedical Engineering

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In our laboratory, we develop novel methods for the analysis of nucleotide variations in the genome and apply them in the identification of genetic factors that are linked to common human diseases such as autoimmune diseases, cancers and cardiovascular diseases. We are currently investigating several DNA analysis methods based on MALDI-TOF (Matrix-Assisted Laser Desorption/Ionization Time-Of-Flight) mass spectrometry. Utilizing a molecular affinity system, these high throughput methods allow effective characterization of genetic variations such as SNPs (Single Nucleotide Polymorphisms) and various mutations.

Recent Papers:

1. Kim, S., M.E. Ulz, T. Nguyen, C. Li, B. Tycko and J. Ju (2004). Digital high-throughput multiplex genotyping in human tumors. *Genomics* 83:924-931.
2. Kim, S., H.D. Rupal, T.C. Gilliam and J. Ju (2003). Digital genotyping using molecular affinity and mass spectrometry. *Nature Review Genetics* 4:1001-1008.
3. Kim, S., S. Shi, T. Bonome, M.E. Ulz, J.R. Edwards, H. Fodstad, J.J. Russo and J. Ju (2003). Multiplex genotyping of the human beta2-adrenergic receptor gene using solid phase capturable dideoxy nucleotides and mass spectrometry. *Analytical Biochemistry* 316:251-258.



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