

## Brief Curriculum Vitae



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2) Degrees

M.D., 1973  
Ph D., 1982

3) Academic Background

1973-1976 Department of Internal Medicine, University of Tokyo  
-1976-1977 Hitachi Hospital, Ibaragi Prefecture  
1977-1979 Department of Internal Medicine, University of Tokyo  
1979-1982 Scripps Research Foundation, La Jolla, California  
1982-1983 Department of Internal Medicine, University of Tokyo  
1983-2006 Institute of Rheumatology, Tokyo Women's Medical University

1996-2006 Professor, Institute of Rheumatology, Tokyo Women's Medical University  
2001-2006 Professor, Division of Genomic Medicine, Department of Advanced Biomedical Engineering and Science, Tokyo Women's Medical University  
2003-2006 Laboratory Head, Laboratory for Statistical Analysis, SRC, RIKEN  
2005-2006 Group Director, Research Group for Medical Informatics, SRC, RIKEN

#### 4) Selected Publications

1. Tsuge M, Hamamoto R, Silva FP, Ohnishi Y, Chayama K, Kamatani N, Furukawa Y, Nakamura Y. A variable number of tandem repeats polymorphism in an E2F-1 binding element in the 5' flanking region of SMYD3 is a risk factor for human cancers. *Nat Genet.* 37, 1104-1107, 2005.
2. Ito T, Inoue E, Kamatani N. Association test algorithm between a qualitative phenotype and a haplotype or haplotype set using simultaneous estimation of haplotype frequencies, diplotype configurations and diplotype-based penetrances. *Genetics.* 168, 2339-2348, 2004
3. Shibata K, Ito T, Kitamura Y, Iwasaki N, Tanaka H, Kamatani N. Simultaneous estimation of haplotype frequencies and quantitative trait parameters: applications to the test of association between phenotype and diplotype configuration. *Genetics.* 168, 525-539, 2004
4. Taniguchi A, Kamatani N. Pharmacogenetic approaches to rheumatoid arthritis. *Pharmacogenomics J.* 4, 350-353, 2004
5. Kamatani N, Sekine A, Kitamoto T, Iida A, Saito S, Kogame A, Inoue E, Kawamoto M, Harigai M, Nakamura Y. Large-scale single-nucleotide polymorphism (SNP) and haplotype analyses, using dense SNP Maps, of 199 drug-related genes in 752 subjects: the analysis of the association between uncommon SNPs within haplotype blocks and the haplotypes constructed with haplotype-tagging SNPs. *Am J Hum Genet.* 190-203, 2004.
6. Ito T, Chiku S, Inoue E, Tomita M, Morisaki T, Morisaki H, Kamatani N. Estimation of haplotype frequencies, linkage disequilibrium measures and combination of haplotype copies in each pool using pooled DNA data. *Am J Hum Genet* 72: 384-398 (2003)