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1985	M.D., Licensed physician, University of Tampere, Finland
1988	Ph.D., University of Tampere, Finland
1990	Lecturer (adjunct professor), Department of Clinical Sciences, University of Tampere, Tampere, Finland
1990-1992	Visiting Scientist, Division of Molecular Cytometry, Department of Laboratory Medicine, University of California, San Francisco, CA
1993-1995	Senior Scientist, Academy of Finland
1995-1996	Professor of Cancer Biology, Institute of Medical Technology, University of Tampere
1996-present	Investigator, Section Head, NIH, National Human Genome Research Institute, Cancer Genetics Branch

Honors

1995	Young Scientist Award, European Association for Cancer Research
1997	Anders Jahre Young Scientist Award, Oslo, Norway
1993-present	Associate editor, *Cytometry*
1997-present	Editor, *Cytogenetics Cell Genetics*
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cDNA and tissue microarray technologies for high-throughput molecular oncology research

High-throughput genome screening technologies, such as cDNA microarrays, have made it possible to survey 5,000–50,000 genes in a single experiment. The translation of functional genomics studies of cancer to improved diagnostic, prognostic and therapeutic applications requires extensive data 'mining' as well as validation and prioritization of the hundreds of possible targets that are uncovered in a typical experiment. We have developed a novel technology, tissue microarrays ('tissue chips') for 'genome-scale' translational cancer research[1]. This technology enables high-throughput, massively parallel molecular analyses of large numbers of tissue specimens or cells. Tissue microarrays are constructed by acquiring cylindrical biopsies from 500–1,000 individual tumour tissues into a tissue microarray block, which is then sliced to yield over 200 sections for probing DNA, RNA or protein targets. A single immunostaining or in situ hybridization reaction now provides information on all of the specimens on the slide, whereas subsequent sections can be probed with other probes or antibodies. Construction of multiple replicate blocks may allow up to 100,000 sections to be generated from the same series of tumour specimens. This expands the scope of microarray technologies to the rapid, very large-scale molecular analysis of thousands of tissue specimens with thousands of probes for various DNA, RNA and protein targets. For example, we have used the combination of cDNA and tissue microarray technologies to uncover genes involved in breast and prostate cancer progression. In summary, tissue microarrays provide an ideal approach for the in vivo validation and prioritization of cDNA microarray results, as well as a means to rapidly assess the clinical significance of newly discovered molecular alterations.

1. Kononen, J. et al. *Nature Med.* **4,** 844–847 (1998).