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1979	B.A. in Chemistry and Philosophy, Dartmouth College, Hanover, NH
1984	Ph.D. in Molecular Biology, California Institute of Technology
1985–1987	Helen Hay Whitney Postdoctoral Fellowship
1989	Post-doctoral, M. I. T. Cambridge, MA
1989–1996	Assistant Professor, Department of Developmental Biology, Stanford University, Stanford, CA
1996–present	Associate Professor, Department of Developmental Biology, Stanford University, Stanford, CA

Honors

1979–1984	National Research Service Award Traineeship
1988–1994	Lucille P. Markey Fellow
1990–1994	Searle Scholar

Developmental biology in the post-genome era: worms and chips

We are entering a new age in molecular genetics in which we can use expression data from microarray experiments to dissect cell, developmental and disease pathways more completely and more sensitively than ever before. *Caenorhabditis elegans* is the only animal model system with a complete genome sequence, and thus will have a key role in establishing approaches that make use of the full genome sequence. DNA microarrays could be used to identify genes that are regulated by programmed cell death pathways, specific transcription factors, specific cell-signalling pathways, expression of homologues of human disease genes in transgenic animals or addition of various pharmaceutical drugs. We have produced DNA microarrays that contain approximately 12,000 *C. elegans* genes (60% of the genome), and have nearly completed construction of full-genome microarrays containing over 19,000 genes. We have currently used the 12,000-gene microarrays in over 120 microarray experiments. In one set of experiments, we used a global approach to define 1,432 germline-enriched genes to illuminate the molecular basis for all of the germline-specific functions, including how the germ line remains totipotent and immortal.