**Postdoctoral Position to Investigate Breast Cancer**

**Compromised Epigenetic Control**

*at the University of Vermont Cancer Center*

Funded by a recent National Cancer Institute Program Project grant, the research focuses on interrelationships of epigenetic control with genome organization for transcriptional competency. We are pursuing an integrated, multidisciplinary team approach to experimentally address epigenetic mechanisms that are functionally linked to transcriptional control in breast cancer. The thematic focus and working hypothesis of our Program is that genomic organization and epigenetic control of gene expression coordinately facilitate physiological regulation, including hormone responsiveness, of normal and cancer cell growth, proliferation, and cell identity. Research emphasis is on contributions of mitotic gene bookmarking, retention of transcription factors at chromosome loci to epigenetically sustain competency for gene expression during cell division.

Cancer-compromised epigenetic control of gene expression is being pursued using normal mammary epithelial, subtype-specific, and endocrine-resistant breast cancer cell models for discovery. We are validating our findings by examining potential clinical relevance using breast cancer patient tumor specimens and organoids, animal models, and public databases. We are securing valuable insight into cancer-compromised mechanisms that are associated with the epithelial to mesenchymal transition that mediate breast cancer initiation and support progression. The “degron tools” that we have developed are supporting direct investigation of contributions by the RUNX1 breast cancer tumor suppressor and the RUNX2 breast cancer tumor promotor to epigenetic control of breast tumorigenesis.

Our Program Project employs powerful new technologies for editing the genome, visualizing cells at super-resolution and in real-time, and decoding higher-order genome organization. Our capabilities include applications of single cell genomic and epigenomic analysis, multispectral confocal imaging, and CODEX/PhenoImaging of more than forty proteins as well as nucleic acids simultaneously in cells and patient tumor specimens. We are pursuing spatial transcriptomic analysis using NanoString technology. These powerful approaches are effectively supporting investigation of epigenetic control of gene expression within the three-dimensional context of cell and nuclear architecture and in relation to cancer-compromised cell and tissue organization. We are emphasizing mechanistic understanding for cancer-compromised organization and assembly of epigenetic regulatory machinery in nuclear microenvironments.

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