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**Identifying translational regulated genes activated by insulin-like growth factor signaling**

**Investigator(s):** Douglas Yee, M.D.

**Lead Organization:** University of Minnesota, Masonic Cancer Center

**Grant Mechanism:** KS  
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**Public Abstract:**
Effective use of new breast cancer therapies requires development of robust biomarkers to predict response to these new therapies. Our laboratory has shown that the insulin-like growth factor (IGF) system has an important role in regulating breast cancer behavior, yet the clinical trials employing anti-IGF therapies have not been effective. We hypothesize that identifying the genes actively translated by IGF signaling will identify tumors that are driven by the IGF receptor. Furthermore, these genes can be used to predict benefit from anti-IGF receptor therapy. Finally, we can disrupt the first key signaling step in IGF receptor activation to further validate the signature. When successfully completed, we hope to show that disrupting IGF signaling is an effective anti-breast cancer therapy and that specific gene signatures can be used to select patients for this therapy.