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Download with GoogleDownload with FacebookDownload with TwitterThe goal of this K02 is to help support Dr. Kristin Hill's research in order to enable her to devote more time to mentoring students and having ongoing collaborations with faculty and fellows at Yale. Dr. Hill's research program has focused on the development of novel tools for the analysis of human tissues. Current methods for analyzing gene expression in human tissues are primarily based on mRNA detection and are subject to various complications. Dr. Hill has developed a novel whole-genome approach to analyze genetic (including epigenetic) regulatory events, which has become one of her major research interests. This approach has only recently become feasible given the availability of next-generation sequencing and data analysis tools. The major issue that Dr. Hill will work on in this project is to develop next-generation sequencing technologies that can be applied to studies of human samples. The specific aims for this K02 research plan are: 1) To design new next-generation sequencing instruments, which will allow us to sequence a large region of the human genome at increased depth and accuracy. 2) To develop bioinformatics tools for accurate and detailed analyses of next-generation sequencing data. 3) To apply the developed next-generation sequencing tools and bioinformatics methods to develop a novel approach to the genome-wide analyses of gene regulatory events, including epigenetic modifications and 3D nuclear structures. Successful completion of this research plan will allow Dr. Hill to develop and validate next-generation sequencing tools for research studies, which are needed to advance both her own research program and the field of cell biology and cancer. This career development award will also improve the research environment for Dr. Hill and her mentees, so that they can become outstanding independent investigators.The *Arabidopsis* genome: uncovering genes that are required for early development. Rice and maize have long been used as model organisms to study the genetic basis of early development. This perspective examines the recent progress in the study of *Arabidopsis thaliana* and argues that the availability of the entire genome sequence makes this plant an excellent model for studying the genetic basis of early seedling development. The recent use of cloning methods to uncover many of the genes involved in early plant development is also described. The data reveal that the *Arabidopsis* genetics literature is remarkable for its rich collection of many possible contributions that are being made at the level of independent discovery.The performance of B-type natriuretic peptide (BNP) or NT-proBNP for

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