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The Wilms' tumor (WT1) gene: Methods and protocols, N. Hastie, editor (Humana Press, Springer Science + Business Media, New York) 2016. 235 pages. Price: Not mentioned.

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This book has compilation of different chapters to review the Wilms' tumour (*WT1*) gene. In the first three chapters the role of Wilms' tumour has been

discussed in childhood cancer, clinical aspects of WT1 and kidney, embryonic development and normal organ homeostasis. All these chapters are informative. This is the first gene to be characterized in context to childhood kidney cancer. Wilms' tumour gene plays an important role in the normal development of the kidney on the one hand and its mutations result into the nephroblastoma on the other. WT1 is expressed throughout the nephrons and controls the reciprocal interactions and phenotypic changes essential for the normal development. The authors have considered Wt-null mouse as an animal model and it has been demonstrated that the mouse was unable to form the kidneys due to lack of functional gene. This proves the importance of this gene and shows how mutations result into renal and genitourinary tract abnormalities leading to different syndromes, *e.g.,* Denys–Drash syndrome, Frasier syndrome and WAGR (Wilms' Tumour-Aniridia-Genitourinary Anomalies-mental Retardation) syndrome.

The role of WT1 in embryonic development and normal homeostasis has been discussed in the 3rd chapter. Wilms' tumour suppressor gene 1 (*Wt1*) is involved in a number of developmental processes such as cell differentiation, epithelial/mesenchymal phenotypic control, cell proliferation and apoptosis. Interestingly, WT1 protein is involved with the transcriptional and post-transcriptional regulators in mRNA splicing and protein–protein interactions. This protein is also required in adult homeostasis. A detailed adult developmental anatomy and role of WT1 protein have been discussed. Various laboratory protocols have also been shown to assess the reporter expression.

WT1 is important to understand the mechanisms governing the spatial and temporal activation of different genes. Transcription factors can be understood by carrying out chromatin immunoprecipitation (ChIP) for the proteins of interest using appropriate antibody in the cross-linked cells. After this, sequencing can be performed using next generation sequencing (NGS) platform. In this book, the authors have simplified ChIP-seq experiments for WT1. They have provided the guidelines to carry out such experiments. These methods are helpful in understanding how WT1 regulates gene expression. Detailed protocols for the *in vitro* transcription study of WT1 function are shown.

The WT1-associated protein–protein interaction network has been illustrated. WT1 associated proteome, tumour suppressor proteins like p53, p63 and p73 interaction with *Wt1* is illustrated. Different transcription factors such as STAT3 (signal transducer and activator of transcription), ER (estrogen receptor)-alpha, SRY (sex-determining region Y) and Pax2 TATA-binding protein and TFIIB (transcription factor IIB) are shown to interact with *Wt1*. Interestingly, co-activators and co-repressors such as CBP (CREB-binding protein), WTIP (WT1 interacting protein) and Basp1 (brain abundant membrane attached signal protein 1) influence the transcriptional response. Different cell cycle regulators, splicing pathways and other interacting proteins have been shown. A detailed methodology of analyzing proteome interaction has also been discussed.

An interesting aspect of WT1-DNA interaction using a filter-binding assay is presented in this book. This assay is suitable for binding of a single protein to a variety of new DNA-binding sites or site-directed mutants of initially characterized DNA-binding sites; however, it has been suggested that medications may be carried out when required. Stepwise protocols have been mentioned which are user-friendly.

A full chapter is devoted to bioinformatic analysis useful in NGS data to identify WT1-associated genes and isoform expressions. NGS is now a known platform used for coding as well as non-coding regions. Additional information related to the expression changes of specific isoforms has also been discussed. The book also contains information related to NGS datasets on *Wt1* knockout and embryonic stem cell lines.

Development of peptide-based methods for cancer vaccine is the latest area of interest has been discussed. This is a potentially lucrative area for cancer therapy. Protocols of peptide-based methods for cancer vaccine development have been discussed in an elucidative manner. The vaccines proposed so far elicit WT1-specific cytotoxic T cells (CTLs) and have demonstrated improvement in the survival time. All these trials are however, in infancy and hence require further validation. It is shown that there is a need for a combination of immunotherapy using various tools like vaccines and antibodies which can inhibit immune checkpoints.

All the chapters provide an in-depth understanding of the recent advances in research on Wilms' tumour genetics. At the end of each chapter, an exhaustive list of references is available. Overall, the book summarizes different clinical aspects of *WT1* gene

along with methodologies showing how to analyze it. This publication will be of interest to scientists all over the world and will be helpful for various researchers working in this field. The technical aspects would help the students to carry out research in this area and explore many unexplored genes and their respective proteins.

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