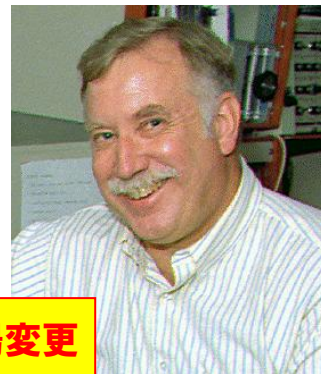


" Distinct p53 Genomic Binding Patterns in Normal and Cancer-derived Human Cells "

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日 時 : 2011 年 10 月 25 日 (火) 15:00-16:00

場 所 : 理学部 ~~本館 N-308 室~~ **2 号館 402 室に会場変更**

The p53 tumor suppressor is a tetrameric transcription factor. Genome-wide analysis of its binding sites in normal human IMR-90 fibroblasts revealed 743 high-confidence ChIP-seq peaks representing putative p53 binding sites. More than 40% were located within 2 kb of a transcription start site (TSS), a distribution similar to that documented for individually studied, functional p53 response elements. Nearly half of the peaks reside in CpG islands, in marked contrast to sites reported in cancer-derived cells. The distinct genomic features of the IMR-90 binding sites do not reflect a distinct preference for specific sequences since the *de novo* developed p53 motif based on our study is similar to those reported by genome-wide studies of cancer-derived cells. More likely, the different chromatin landscape in normal compared to cancer-derived cells influences p53 binding via modulating the availability of sites through epigenetic mechanisms. We compared the IMR-90 ChIP-seq peaks to the recently published IMR-90 methylome and demonstrate that they are enriched at hypomethylated DNA. A hypothesis for the differences in p53 binding between normal human cells and cancer-derived cell lines will be presented.

1. 本講演会および Dr. Anderson による 4 回の講義に全参加し(集中講義・別紙参照)、レポートを提出すると「先端総合化学特論 II (Modern Trends in Chemical Sciences and Engineering II)」の 1 単位が認定されます。

2. 上記とは別に、本講演会は「化学研究先端講義 (Topical Lectures in Chemical Sciences & Engineering) / 総合化学特別研究第二 (Research in Chemical Sciences & Engineering II)」の一部として認定されています。

3. 出席回数は上記 1・2 どちらかの科目でのみのカウントとなります。