

## Cancer Genomics

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*Cancer Genomics* is a special reprint of *Cytogenetics and Genomics Research* (Vol. 118, No. 2-4, 2007), dedicated to the memory of Harold P Klinger, a distinguished cancer geneticist who founded the journal. Electronic versions of the contributions are available on the journal website essentially rendering this book redundant. However, it remains pleasurable to be able scan a hard copy book and while I wouldn't recommend this finely produced edition as bedtime reading, it may serve as a useful desktop reference for cancer researchers from all fields.

The text, which contains 32 articles mostly dating from early 2007, opens with an excellent overview of head and neck cancer from Prystowsky and colleagues. Articles follow on a variety of liquid and solid tumours of both common (breast, prostate and colon) and rare (endometrial stromal sarcoma (two articles), adipocyte tumours and neuroblastoma) occurrence. Some of the articles are more technically inclined (interphase FISH), while others are

of general interest, such as discussions of the roles of telomerase or microRNAs in carcinogenesis. In some cases, articles are more suited to a cancer biology text rather than genomics; running microarray experiments coupled with rudimentary bioinformatics adds little to our knowledge about the underlying genomics. Other articles, for example a catalogue of familial cancer syndromes, are less useful than they would have been if a link to an online updatable database had been included.

An area barely touched on in this compilation is the increasingly common use of gene mutation status to drive therapeutic decision making in different common cancers (lung, breast, and colon). Another area untouched, and one that has turned this skeptical reviewer into a convert, is that of sequence analysis of tumours, the so-called cancer genome sequencing project. Although some of the more interesting papers (for example sequencing glioblastoma) have appeared in 2008, the era of the \$1000 genome is fast approaching. Perhaps a future edition of *Cancer Genomics* will be able place the methodology described in detail in this current issue in the context of common sequence abnormalities for all tumours.

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