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Titel des Beitrags: Targeted therapies in cancer - challenges and chances offered by newly developed techniques for protein analysis in clinical tissues.

Abstract: In recent years, new anticancer therapies have accompanied the classical approaches of surgery and radio- and chemotherapy. These new forms of treatment aim to inhibit specific molecular targets namely altered or deregulated proteins, which offer the possibility of individualized therapies. The specificity and efficiency of these new approaches, however, bring about a number of challenges. First of all, it is essential to specifically identify and quantify protein targets in tumor tissues for the reasonable use of such targeted therapies. Additionally, it has become even more obvious in recent years that the presence of a target protein is not always sufficient to predict the outcome of targeted therapies. The deregulation of downstream signaling molecules might also play an important role in the success of such therapeutic approaches. For these reasons, the analysis of tumor-specific protein expression profiles prior to therapy has been suggested as the most effective way to predict possible therapeutic results. To further elucidate signaling networks underlying cancer development and to identify new targets, it is necessary to implement tools that allow the rapid, precise, inexpensive and simultaneous analysis of many network components while requiring only a small amount of clinical material. Reverse phase protein microarray (RPPA) is a promising technology that meets these
requirements while enabling the quantitative measurement of proteins. Together with recently
developed protocols for the extraction of proteins from formalin-fixed, paraffin-embedded (FFPE)
tissues, RPPA may provide the means to quantify therapeutic targets and diagnostic markers in the
near future and reliably screen for new protein targets. With the possibility to quantitatively analyze
DNA, RNA and protein from a single FFPE tissue sample, the methods are available for integrated
patient profiling at all levels of gene expression, thus allowing optimal patient stratification for
individualized therapies.