SiLAD：一种蛋白质组学动态分析的新技术

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摘　要：随着蛋白质组学的产生和发展，对蛋白质组表达水平的差异和变化进行体内的和动态的分析已势所必然地成为蛋白质组学研究的发展趋势。但是传统差异蛋白质组学方法只能提供细胞或组织内各种蛋白累积总量的信息，而不是真正意义上的蛋白质差异表达分析。 SiLAD（35S in vivo Labeling Analysis for Dynamic Proteomics）技术正是基于这种需求而在本实验室创立的。SiLAD技术由于其在差异检出的灵敏度和时间分辨率方面的明显优势，以及除提供蛋白质组表达动态以外，可以提供蛋白质代谢等相关动态变化的更多信息，所以可适用于对多种生物过程进行的动态蛋白质组学研究。本文对SiLAD技术的原理及特点进行简要综述。

关键词：SiLAD技术,差异表达蛋白,动态蛋白质组学

SiLAD: A new technology for dynamic proteomics

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Abstract: Dynamic proteomics that traces the changes in expression level of different proteins has become the new frontier of proteome research. However, most of conventional technologies are measuring the accumulated amount of different proteins instead of “differentially expressed proteins”. A novel technique, SiLAD(35S in vivo Labeling Analysis for Dynamic Proteomics), was developed in our laboratory to meet this need. This new technique provides higher temporary resolution and higher sensitivity in detection of differential expressed proteins and yet, when the resulted 35S 2-D gel phosphor-image is analyzed in combination with CBB stained image, it can provide additional information about protein turn over dynamics. This technique could be widely used in the studies of most progressive biological processions. The major principle and characteristics of SiLAD technique were briefly introduced and discussed in this review.

Key words: Dynamic proteomics,Differential expressed proteins,SiLAD