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From label free mass spectrometry of nappa and snap generated proteins to qmc_d sensor of new conception

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Abstract

In order to unravel the key elements of Biological and Environmental Science we run a test in a model protein system where the known query proteins following in blinded order were successfully identified, we have recently shown that is possible to utilize label free mass spectrometry for the detection of Nucleic Acid Programmable Protein Arrays (NAPPA) slides containing Jun, p53, Cdk2 and CdkN1A genes (1). As a follow-up we aim to reduce the background in cooperation with New England Biolab and Biodesign Institute at Arizona State University (work in progress and separately in press), using an innovative cell-free expression NEB SNAP system based on bacteria recently proposed (2) in which all protein species are well defined. NAPPA (3) and SNAP (2) utilize a complex mammalian cell free expression system to produce proteins in situ. On the whole, considering the abundance of protein material different from target and query protein, the results are very encouraging, showing the potential to couple the NAPPA and SNAP technologies with the MALDI-TOF MS facility for a label free investigation of protein samples (in preparation). The chemistry and the algorithms progressively implemented prove for the first time that Mass Spectrometry can characterize proteins immobilized on Nucleic Acid Programmable Protein Arrays, pointing that with further development, this label-free procedure will be fully reduced to practice in correlation with the fluorescence NAPPA work that has already seen significant clinical applications in the last decade-
In alternative to fluorescently-labelled approaches a new label free NAPPA method emerging from the combined utilization of four independent and complementary nanotechnological approaches NAPPA find applications in analyzing protein function and protein-protein interaction in basic and applied studies ideal for Nanomedicine (4), nanogenomics (2,3), QMC_D nanogravimetry (5) , mass spectrometry (1), atomic force microscopy (6) and anodic porous alumina (6) , overcomes indeed the limits of correlated fluorescence detection plagued by the background still present after extensive washes (3). This is being accomplished in conjuction with an homogeneous and well defined human cell free expression capable to achieve the above goals making realistic the ambitious objective to quantify the regulatory protein networks in humans fundamental for Nanomedicine (4) and in the fields of Biodefense and Natural Disasters through the development of a QMC_D sensor for Health and Environment of new conception (7) which is here introduced as a prototype at the preindustrial scale.