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Dr. Fuchu He

- China State Key Laboratory of Proteomics
- Beijing Proteome Research Center

- Fuchu He PhD, Member of the Chinese Academy of Sciences, Member of the Academy of Sciences for the Developing World, founded Beijing Proteome Research Center and China State Key Laboratory of Proteomics and is currently their president and director. He was among the first group of people who founded the Human Proteome Organization (HUPO) in 2001 and the first Chinese scientist who led an international consortium to undertake a large scale project to decipher the human liver proteome as the inaugural chair of Human Liver Proteome Project (HLPP), the first proteome project for human organs. He founded the Chinese arm of HUPO (CNHUPO) and is currently the president of Asia Oceania HUPO (AOHUPO). Now he is propelling the campaign of the National Core Facility for Protein Sciences-PHOENIX (Pilot Hub Of ENcyclopediac proteomIX) in China.
- He received his B.S. degree in Genetics from Fudan University, Shanghai in 1982. Then he earned his M.S. degree in Biochemistry and Ph.D. in Cell Biology from Beijing Institute of Radiation Medicine. As corresponding author, he has published more than 240 papers in international peer-reviewed journals, including Nature Genetics, Nature Cell Biology, Nature Biotechnology, Nature Methods, Nature Medicine, Nature Communications, and the Proceedings of the National Academy of Sciences etc.

Dr. Fuchu He Biography

- Dr. Fuchu He's major fields of research are Proteomics, Genomics, Bioinformatics and Systems biology, especially for human liver.

Dr. Fuchu He
Research Interests

- LSECtin expressed on melanoma cells promotes tumor progression by inhibiting antitumor T cell responses. **Cancer Res.** 2014, 74(13):3418-28.
- Discovery of Novel Genes and Gene Isoforms by Integrating Transcriptomic and Proteomic Profiling from Mouse Liver. **J Proteome Res.** 2014, 13(5):2409-19.
- CKIP-1 regulates macrophage proliferation by inhibiting TRAF6-mediated Akt activation. **Cell Research.** 2014, 24:742-61.
- CKIP-1 suppresses the adipogenesis of mesenchymal stem cells by enhancing HDAC1-associated repression of C/EBP α . **J Mol Cell Biol.** Epub 2014 Sep 19.
- The covalent modifier Nedd8 is critical for the activation of Smurf1 ubiquitin ligase in tumorigenesis. **Nature Communications.** 2014, 5: 3733.
- GIT2 protects against colitis by negatively regulating Toll-like receptor signaling. **Proc Natl Acad Sci USA.** 2014, 111(24):8883-8.

Recent Publications Authored By Dr. Fuchu He

- What is Proteomics?
- Current Methods in Proteomics

What is Proteomics?

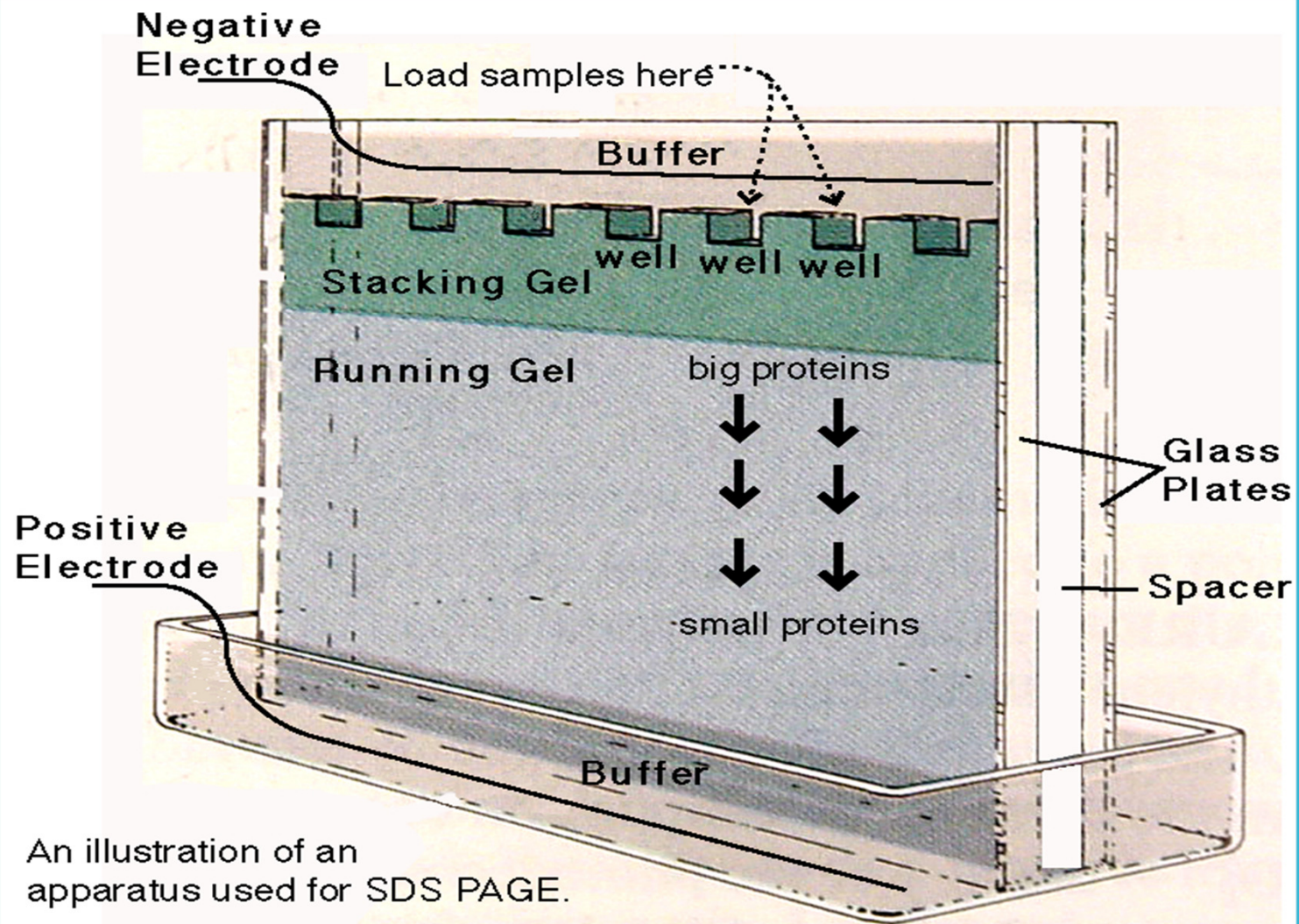
- The ever booming field of science now is proteomics, which deals with the identification of proteins, its structure, function and characterization.
- with the study of proteins have added advantage in the field of biology to understand the disease, its way to treat and to understand the cellular processes

Current Methods in Proteomics

- SDS-PAGE
- Mass Spectrometry
- Microarray
- Protein Sequencing

SDS-PAGE

- Sodium dodecyl sulfate polyacrylamide gel electrophoresis (**SDS-PAGE**) is used to separate proteins based on their ability to move within an electrical current, based on their polypeptide chains or of their molecular weight.
- SDS is a detergent used in this technique to remove secondary and tertiary protein structures thus maintaining the proteins as polypeptide chains
- SDS forms a coats of proteins, proportional to the molecular weight, and thus confers the same negative electrical charge across all proteins in the sample

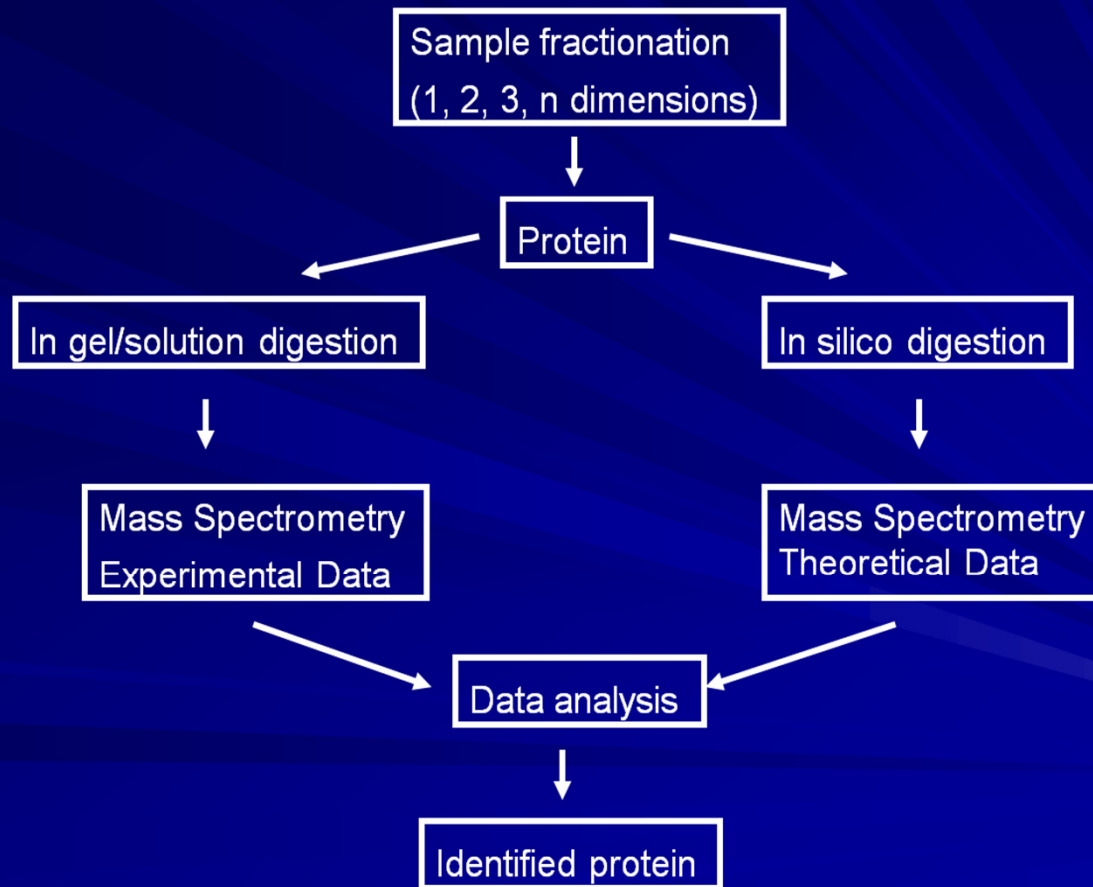


An illustration of an apparatus used for SDS PAGE.

Mass Spectrometry

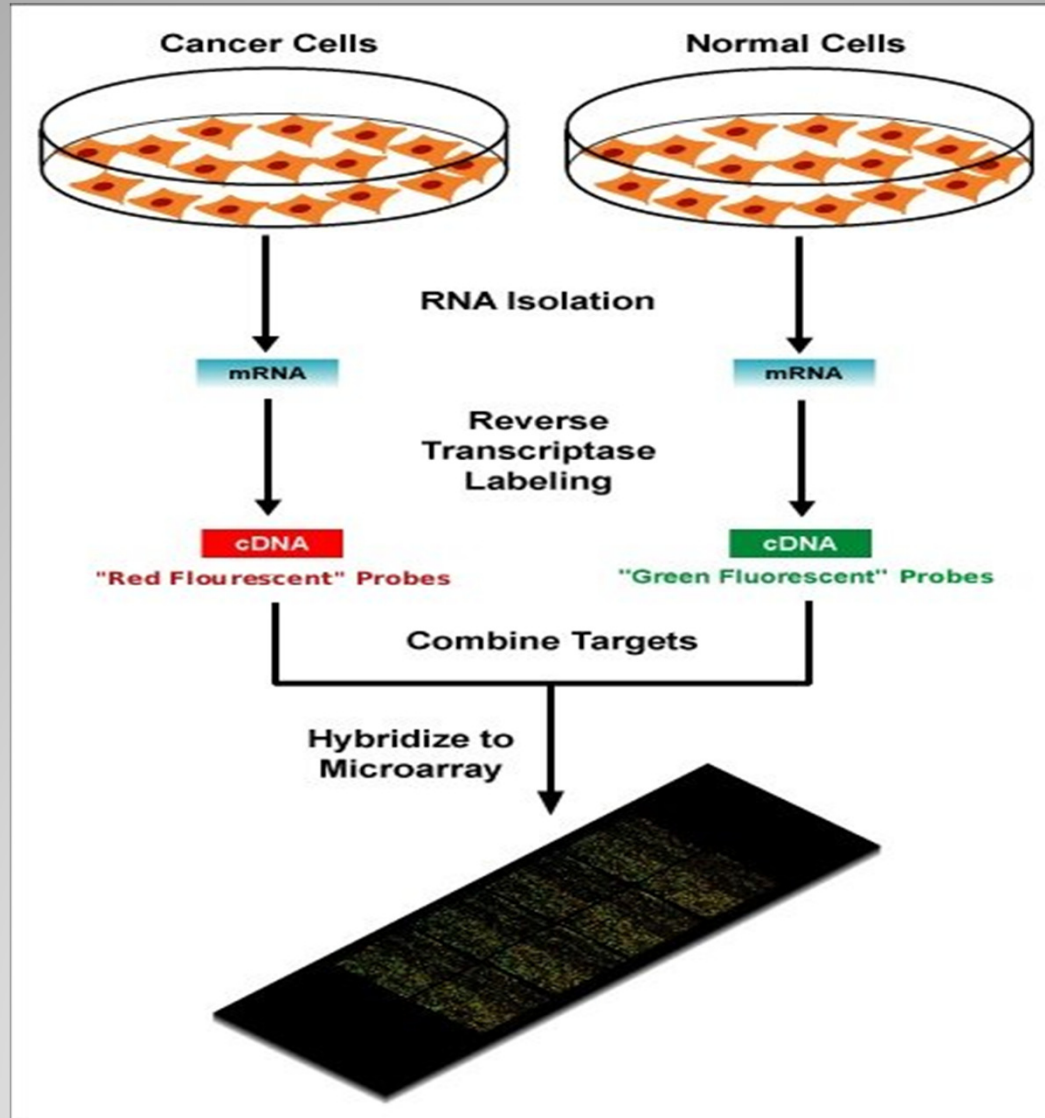
- Mass Spectrometry (MS) is an analytical technique used for determining the elemental composition of samples, quantifying the mass of particles and molecules, and elucidating the chemical structure of molecules.
- Various types of mass spectrometry with high specificity, such as Liquid Chromatography (LC-MS), Gas Chromatography (GC-MS), and Matrix-Assisted Laser Desorption/Ionization/Time-Of-Flight (MALDI-TOF MS), are being increasingly valued and utilized as tools in clinical laboratories

Mass Spectrometry and Proteomics



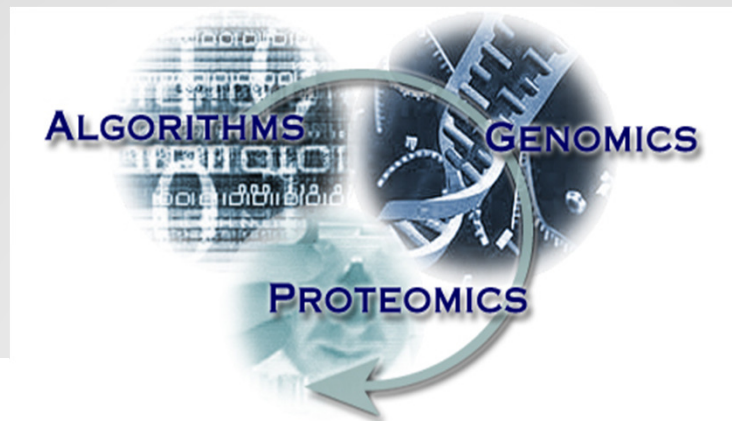
Microarray

- Is a technique in which the entire DNA sequences of an organism or particular sequence of a gene are arranged in a grid pattern and attached to a solid support,
- To determine the sequence of the entire genome or the specific gene to detect variations in the gene sequence or to map a gene.
- Major application of this technique is gene expression analysis and genetic variation analysis, thus helping scientist to analyze the defective gene in a genetic disorder.



Journal of Proteomics & Bioinformatics Related Journals

- Transcriptomics: Open Access
- Journal of Pharmacogenomics & Pharmacoproteomics
- Journal of Data Mining in Genomics & Proteomics



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