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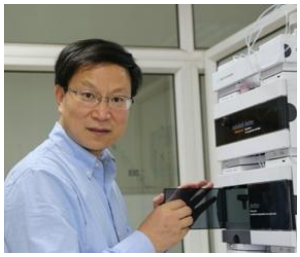

**简介：**

1990 年毕业于陕西师范大学化学系，1990-1997 年在中国科学院兰州化学物理研究所攻读分析化学硕士和博士研究生，1997 年获理学博士学位，1997-1999 年在中国科学院兰州化学物理研究所工作。1999 年 6 月至 2010 年 10 月在比利时 Leuven 大学药学院做博士后研究。2000 年 10 月至 2003 年 9 月在德国 Tubingen 有机化学研究所从事博士后研究。2003 年加入中国科学院上海有机化学研究所。2003 年 9 月至今任中国科学院上海有机化学研究所研究员，课题组长和博士生导师。2009 年至 2015 年任上海有机所分析化学研究室主任。康经武研究员从事色谱分析，生物化学分析和药物分析方面的研究。至今已在 Anal. Chem.和 J. Chromatogr. A 等期刊上发表论文 100 多篇，参加编写论著 4 本，获得中国发明专利授权 5 项，美国，欧洲和日本发明专利各 1 项。担任中国化学会色谱专业委员会委员，《色谱》责任副主编，《有机化学》，《分析实验室》和《仪器分析与技术》编委。

**研究领域：**

**药物筛选与靶标鉴定：**

我们发展了基于液相色谱、毛细管电泳以及高效液相色谱-质谱联用技术的药物筛选新技术。与传统的药物筛选技术不同，我们的方法集成了高效分离与高灵敏度检测的优势，可以直接从天然产物粗提物或者利用组合化学合成的化合物库中筛选具有重要临床治疗价值的小分子化合物。我们还进行靶标鉴定和药物作用机理的研究，在细胞层面全面评价药物的作用效果，鉴定作用靶标和脱靶效应，预测可能出现的毒副作用。

**生物大分子间的相互作用：**

生命过程离不开蛋白-蛋白，蛋白-DNA 以及蛋白-糖链之间的相互作用。研究特定蛋白质在细胞中的相互作用不仅能够阐明蛋白质的功能，揭示疾病的发病机理，还有助于发现新的治疗疾病的靶标。我们发展各种亲和色谱纯化技术结合定量蛋白组学，研究生命过程中的蛋白质相互作用和生物大分子的动态修饰。通过提高亲和纯化的效率，降低了细胞样品的复杂程度，提高了质谱数据的质量和质谱检测低丰度蛋白的灵敏度，实现无偏差的蛋白-蛋白相互作用网络的研究。我们发展的方法可以成为研究细胞生物学和生物化学的新的研究工具。

**蛋白糖链的结构与功能：**

蛋白糖基化在细胞过程中发挥重要的作用。但是蛋白糖链的结构分析一直是分析化学中的一项挑战。我们发展了毛细管电泳和亲水相互作用色谱以及与高分辨质谱的联用技术，研究蛋白糖链的结构、连接序列以及生化功能，用于生物制药中多糖的糖型分析和精细结构分析。我们在治疗型糖链的结构分析，特别是肝素和低分子量肝素的精细结构研究方面积累了丰富的经验和成果。研究成果已经被杭州九源基因工程有限公司作为企业标准，获得了中国，美国，欧洲等国家的专利授权，且获得 2019 年中国发明专利优秀奖。

**复杂体系的色谱分离方法：**

复杂体系，包括生物样品和药物杂质分析（包括手性分离）需要发展多维分离和多维检测技术。我们发展的二维液相色谱与串级质谱联用技术（2D-HPLC-MS/MS），用于药物相关杂质的分析和结构鉴定，为很多家制药公司解决了药物质量控制方面的问题。

**获奖及荣誉：**

1. 2017 年中国分析测试协会科学技术一等奖
2. 2019 年第 21 届中国发明专利优秀奖

**代表性论文：**

[1] G. Liu, T. Fu, Y. Han, S. Hu, X. Zhang, M. Zheng, P. Hao, L. Pan, J. Kang, probing protein–protein interactions with label-free mass spectrometry quantification in combination with affinity purification by spin-tip affinity column, Anal Chem 92(2020)3913-3922.

[2] F. Xu, Y. Xu, G. Liu, M. Zhang, S. Qiang, J. Kang, separation of twelve posaconazole related stereoisomers by multiple heart-cutting chiral-chiral two-dimensional liquid chromatography, J Chromatogr A (2020) 460845.

[3] Y. Zhang, C. Lou, Y. Xu, J. Li, S. Qian, F. Li, J. Kang, screening of inhibitors against histone demethylation jumonji domain-containing protein 3 by capillary electrophoresis, J Chromatogr A (2019) 460625.

[4] M. Xu, Y. Xu, Y. Shen, C. Lou, M. Zheng, J. Kang, determining the affinity of anti-mitotic compounds binding to colchicine binding site of tubulin by affinity probe capillary electrophoresis, J Chromatogr B 1121 (2019) 66-71.

[5] M. Xu, M. Zheng, G. Liu, M. Zhang, J. Kang, screening of break point cluster region abelson tyrosine kinase inhibitors by capillary electrophoresis, J Chromatogr A, 1537 (2018) 128-134.

[6] M. Xu, C. Liu, M. Zhou, Q. Li, R. Wang, J. Kang, screening of small-molecule inhibitors of protein–protein interaction with capillary electrophoresis frontal analysis, Anal Chem, 88 (2016) 8050-8057.

[7] F. Li, Y. Zhang, D. Qiu, J. Kang, screening of epidermal growth factor receptor inhibitors in natural products by capillary electrophoresis combined with high performance liquid chromatography–tandem mass spectrometry, J Chromatogr A, 1400 (2015) 117-123.
[8] Y. Zhang, F. Li, M. Li, J. Kang, screening of mammalian target of rapamycin inhibitors in natural product extracts by capillary electrophoresis in combination with high performance liquid chromatography–tandem mass spectrometry, J Chromatogr A, 1388 (2015) 267-273.
[9] X. Zhang, T. Wang, H. Zhang, B. Han, L. Wang, J. kang, profiling of drug binding proteins by monolithic affinity chromatography in combination with liquid chromatography–tandem mass spectrometry, J Chromatogr A, 1359 (2014) 84-90.
[10] Q. Zhang, X. Chen, Z. Zhu, X. Zhan, Y. Wu, L. Song, J. Kang, structural analysis of low molecular weight heparin by ultraperformance size exclusion chromatography/time of flight mass spectrometry and capillary zone electrophoresis, Anal Chem, 85 (2013) 1819-1827.
[11] J. Kang, D. Bischoff, Z. Jiang, B. Bister, R.D. Suessmuth, V. Schurig, A Mechanistic study of enantiomeric separation with vancomycin and balhimycin as chiral selectors by capillary electrophoresis. dimerization and enantioselectivity, Anal Chem, 76 (2004) 2387-2392.
[12] J.W. Kang, G. De Reymaeker, A. Van Schepdael, E. Roets, J. Hoogmartens, Analysis of bacitracin by micellar electrokinetic capillary chromatography with mixed micelle in acidic solution, Electrophoresis, 22 (2001) 1356-1362.
[13] J. Kang, D. Wistuba, V. Schurig, A silica monolithic column prepared by the sol-gel process for enantiomeric separation by capillary electrochromatography, Electrophoresis, 23 (2002) 1116-1120.
[14] J.W. Kang, Y.T. Yang, J.M. You, Q.Y. Ou, Fast chiral separation of amino acid derivatives and acidic drugs by co-electroosmotic flow capillary electrophoresis with vancomycin as chiral selector, J Chromatogr A, 825 (1998) 81-87.

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Dr. Kang graduated from the Department of Chemistry of Shaanxi Normal University in 1990 and studied as a master and Ph.D. student in analytical chemistry atthe Institute of Lanzhou Chemical Physics, the Chinese Academy of Sciences from 1990 to 1997. He received his Ph.D. in 1997. From June 1999 to October 2010, he worked as a post-doctoral research at the school of pharmacy, University of Leuven, Belgium. From October 2000 to September 2013, he did post-doctoral research at the Institute of Organic Chemistry, University of Tubingen, Germany. In 2003, he return to China to jointheInstitute Organic Chemistry, Chinese Academy of Sciences. Since September 2003, he has been a researcher, team leader and doctoral supervisor of the Shanghai Institute of Organic Chemistry. The Research ofDr. Kang is mainly engaged in the developing new analytical methods and technologies for proteomics, drug screening and drug target identification, chiral separation, and drug analysis. So far, he has published more than 100 papers in journals such as Anal. Chem. and J. Chromatogr. A, and participated in the editing of 4 books. He is serving as the deputy editor-in-chief ofChin.J Chromatography, the editorial board of Organic Chemistry, Analytical Laboratory, and Instrumental Analysis and Technology.

**Research：**

**Drug screening and target identification**:

We have developed new drug screening technologies based on liquid chromatography, capillary electrophoresis, and high-performance liquid chromatography-mass spectrometryhyphenatedtechnology. Different from traditional drug screening technology, our technologies integrate the advantages of high-efficiency separation and high-sensitivity detection. Thus, we can directly find active small molecule compounds with important clinical therapeutic value from crude extracts of natural products or compound libraries synthesized by combination chemistry. We also perform target identification and drug mechanism studies by using proteomics technology. Comprehensively evaluate the activity of the hit compounds at the cellular level, identify the targets and off-target effects so as to anticipate the possible side effect.

**Probing interactions between biological macromolecules:**

The life process is inseparable from protein-protein, protein-DNA and protein-sugar chain interactions. Studying the interaction of specific proteins in cells can not only clarify the function of proteins, reveal the pathogenesis of diseases, but also help to find new targets for treating diseases. We develop a variety of affinity chromatography purification techniques combined with quantitative proteomics to study protein interactions and dynamic modification of biological macromolecules during life. By increasing the efficiency of affinity purification, the complexity of cell samples is reduced, the quality of mass spectrometry data and the sensitivity of mass spectrometry to detect low-abundance proteins are

improved. Our developed method can become a new research tool for studying cell biology andbiochemistry.

**Structure and function of proteoglycan chains:**

Protein glycosylation plays an important role in cell processes. But structural analysis of proteoglycan chains has always been a challenge in analytical chemistry. We develop technologies and methods with the separation technologies, such as capillary electrophoresis and hydrophilic interaction chromatography, the hyphenated techniques with high-resolution mass spectrometry to study the structure, linking sequence, and biochemical functions of proteoglycan chains. We also work with biopharmaceuticals for analysis of glycoforms and fine structures of polysaccharides. We have accumulated rich experience and results in the structural analysis of therapeutic sugar chains, especially the fine structure research of heparin and low molecular weight heparin. The research results have been adopted by Hangzhou Jiuyuan Genetic Engineering Co., Ltd. as corporate standards, and have obtained patent authorization from China, the United States, Europe and other countries. It also won the Chinese Invention Patent Excellence Award 2019.

**Chromatographic separation methods for complex systems:**

The analysis of complex systems, including biological samples and drug impurities (including chiral separations) requires the development of multidimensional separation and multidimensional detection techniques. The two-dimensional liquid chromatography and tandem mass spectrometry technology we developed (2D-HPLC-MS / MS) is used for the analysis and structural identification of drug-related impurities, and has solved the problems of drug quality control for many pharmaceutical companies.

**Awards and honors:**

1. 2017 China Analytical Testing Association Science and Technology First Prize
2. The 21st China Invention Patent Excellence Award 2019

**Selected publications:**

[1] G. Liu, T. Fu, Y. Han, S. Hu, X. Zhang, M. Zheng, P. Hao, L. Pan, J. Kang, probing protein–protein interactions with label-free mass spectrometry quantification in combination with affinity purification by spin-tip affinity column, Anal Chem 92 (2020)3913-3922.

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[10] Q. Zhang, X. Chen, Z. Zhu, X. Zhan, Y. Wu, L. Song, J. Kang, structural analysis of low molecular weight heparin by ultraperformance size exclusion chromatography/time of flight mass spectrometry and capillary zone electrophoresis, Anal Chem, 85 (2013) 1819-1827.
[11] J. Kang, D. Bischoff, Z. Jiang, B. Bister, R.D. Suessmuth, V. Schurig, A Mechanistic study of enantiomeric separation with vancomycin and balhimycin as chiral selectors by capillary electrophoresis. dimerization and enantioselectivity, Anal Chem, 76 (2004) 2387-2392.
[12] J.W. Kang, G. De Reymaeker, A. Van Schepdael, E. Roets, J. Hoogmartens, Analysis of bacitracin by micellar electrokinetic capillary chromatography with mixed micelle in acidic solution, Electrophoresis, 22 (2001) 1356-1362.
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[14] J.W. Kang, Y.T. Yang, J.M. You, Q.Y. Ou, Fast chiral separation of amino acid derivatives and acidic drugs by co-electroosmotic flow capillary electrophoresis with vancomycin as chiral selector, J Chromatogr A, 825 (1998) 81-87.