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**研究方向：**

生物信息学、药物基因组学和大数据分析

**主要工作：**

全面负责完成了30多种复杂疾病和几十种遗传性疾病的的全基因组研究（结果分别发表在New England Journal of Medicine、Nature Genentics,Nature Communications, PNAS, American Journal of Human Genetics，Plos genetics等杂志）等的数据分析工作，建立了近40万人份全基因组数据库。

基于大数据建立了中国人群个体化精准用药数据库和分析系统，覆盖常用药物近400种；建立了精准营养检测分析系统。

**研究成果：**

发表SCI论文 30多篇，累积影响因子超过260（包括Nature Genetics三篇，Nature Communications三篇，PNAS一篇等），共同作者发表SCI 论文100余篇（其中NEJM和Nature Genetics等10余篇）。

**获奖情况：**

获得中华医学会科技进步一等奖和安徽省自然科学一等奖。

主持和承担了国家自然科学基金、“973”和重大专项等二十多项国家级项目的数据分析工作。

**代表性成果：**

1. **Zuo X**, et al. Whole-exome SNP array identifies 15 new susceptibility loci for psoriasis. ***Nat Commun****.* 2015 Apr 9;6:6793. doi:10.1038/ncomms7793. PubMed PMID: 25854761; PubMed Central PMCID: PMC440331.
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