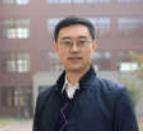
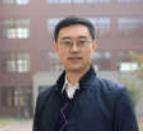
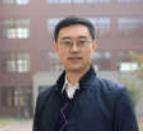


<p>师资队伍</p> <p>仪器科学与技术</p> <p>电气工程</p> <p>控制科学与工程</p> <p>兵器科学与技术</p> <p>生物医学工程</p> <p>083100生物医学工程</p>	<p>您的当前位置：首页 师资队伍 生物医学工程 083100生物医学工程 睿导</p> <p style="text-align: center;">姜伟</p> <p style="text-align: center;">文/ 访问量: 64 发布时间: 2018-09-06</p> <table border="1" style="width: 100%; border-collapse: collapse; text-align: center;"> <tr> <td rowspan="2" style="width: 15%;"></td> <td>姓名:</td> <td>姜伟</td> <td>性别:</td> <td>男</td> <td>职务:</td> <td></td> </tr> <tr> <td>职称:</td> <td>教授</td> <td>导师类别:</td> <td>硕士生导师</td> <td>办公室:</td> <td>自动化学院2号楼404-1室</td> </tr> </table> <table border="1" style="width: 100%; border-collapse: collapse; text-align: left;"> <tr> <td rowspan="2" style="width: 15%;">研究领域:</td> <td>1. 非编码RNA靶向药物预测;</td> </tr> <tr> <td>2. 肿瘤耐药性分子机制研究;</td> </tr> </table> <table border="1" style="width: 100%; border-collapse: collapse; text-align: left;"> <tr> <td rowspan="2" style="width: 15%;">电话:</td> <td></td> <td>Email:</td> <td>bioccjw@126.com</td> </tr> </table> <p>个人简介</p> <p>姜伟，博士，教授。主要从事生物信息学和计算系统生物学研究。发表学术论文78篇，其中SCI收录66篇，H因子21。主持国家自然科学基金等各类项目12项，参与973、863项目各1项。获软件著作权5项。主编、参编中英文教材、专著6部。目前担任：中国生物工程学会青年工作委员会副主任委员、中国生物工程学会计算生物学与生物信息学专业委员会委员、中国人工智能学会生物信息学与人工生命专业委员会委员、中国计算机学会生物信息学专业组委员、江苏省生物医学工程学会生物信息学专业委员会委员。</p> <p>学术成果</p> <ol style="list-style-type: none"> 1. Dai, Enyu(#); Yang, Feng(#); Wang, Jing; Zhou, Xu; Song, Qian; An, Weiwei; Wang, Lihong(*); Jiang, Wei(*), ncDR: a comprehensive resource of non-coding RNAs involved in drug resistance, <i>Bioinformatics</i>, 2017.12.15, 33(24): 4010~4011. 2. Dai, Enyu(#); Wang, Jing; Yang, Feng; Zhou, Xu; Song, Qian; Wang, Shuyuan; Yu, Xuexin; Liu, Dianming; Yang, Qian; Dai, Hong; Jiang, Wei(*); Ling, Hong(*), Accurate prediction and elucidation of drug resistance based on the robust and reproducible chemoresponse communities, <i>Int J Cancer</i>, 2017.11.16, 142(7): 1427~1439. 3. Yang, Qian(#); Wang, Shuyuan(#); Dai, Enyu; Zhou, Shunheng; Liu, Dianming; Liu, Haizhou; Meng, Qianqian; Jiang, Bin (*); Jiang, Wei(*), Pathway enrichment analysis approach based on topological structure and updated annotation of pathway, <i>Briefings in Bioinformatics</i>, 2017.8.16, 2017. 4. Jiang, Wei(#); Mitra, Ramkrishna(#); Lin, Chen-Ching; Wang, Quan; Cheng, Feixiong; Zhao, Zhongming(*), Systematic dissection of dysregulated transcription factor-miRNA feed-forward loops across tumor types., <i>Briefings in Bioinformatics</i>, 2016.11, 17(6): 996~1008. 5. Zhang, Yan(#); Liu, Dianming; Wang, Lihong; Wang, Shuyuan; Yu, Xuexin; Dai, Enyu; Liu, Xinyi; Luo, Shanshan(*); Jiang, Wei(*), Integrated systems approach identifies risk regulatory pathways and key regulators in coronary artery disease, <i>J Mol Med (Berl)</i>, 2015.12, 93(12): 1381~1390. 6. Lv, Yingli(#); Wang, Shuyuan; Meng, Fanlin; Yang, Lei; Wang, Zhifeng; Wang, Jing; Chen, Xiaowen; Jiang, Wei(*); Li, Yixue(*); Li, Xia(*), Identifying novel associations between small molecules and miRNAs based on integrated molecular networks, <i>Bioinformatics</i>, 2015.11.15, 31(22): 3638~3644. 7. Dai, Enyu(#); Lv, Yingli(#); Meng, Fanlin; Yu, Xuexin; Zhang, Yan; Wang, Shuyuan; Liu, Xinyi; Liu, Dianming; Wang, Jing; Li, Xia(*); Jiang, Wei(*), CREAM: a database for chemotherapy resistance-associated miRSNP, <i>Cell Death & Disease</i>, 2014.5, 5. 8. Jiang, Wei(#); Zhang, Yan(#); Meng, Fanlin; Lian, Baofeng; Chen, Xiaowen; Yu, Xuexin; Dai, Enyu; Wang, Shuyuan; Liu, Xinyi; Li, Xiang; Wang, Lihong(*); Li, Xia(*), Identification of active transcription factor and miRNA regulatory pathways in Alzheimer's disease, <i>Bioinformatics</i>, 2013.10.15, 29(20): 2596~2602. 9. Liu, Xinyi(#); Wang, Shuyuan(#); Meng, Fanlin; Wang, Jizhe; Zhang, Yan; Dai, Enyu; Yu, Xuexin; Li, Xia(*); Jiang, Wei (*), SM2miR: a database of the experimentally validated small molecules' effects on microRNA expression, <i>Bioinformatics</i>, 2013.2.1, 29(3): 409~411. 10. Li, Xia(#)(*); Jiang, Wei(#); Li, Wei(#); Lian, Baofeng(#); Wang, Shuyuan; Liao, Mingzhi; Chen, Xiaowen; Wang, Yanqi u; Lv, Yingli; Wang, Shuyuan; Yang, Lei, Dissection of human MiRNA regulatory influence to subpathway, <i>Briefings in Bioinformatics</i>, 2013.12.15, 14(6): 1427~1439. 		姓名:	姜伟	性别:	男	职务:		职称:	教授	导师类别:	硕士生导师	办公室:	自动化学院2号楼404-1室	研究领域:	1. 非编码RNA靶向药物预测;	2. 肿瘤耐药性分子机制研究;	电话:		Email:	bioccjw@126.com
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