1. **导师的个人情况概括**

**王珍珍**，女，1980.01，中共党员，博士，三级教授，博士导师，海南医学院药物组学信息学教研室主任、科研团队PI。2003年到哈尔滨医科大学生物信息科学与技术学院工作，2005年攻读硕士学位，2011年获博士学位，2012年进入哈尔滨医科大学基础医学院病原微生物博士后工作站，2016年到纽约西奈山医学院微生物系从事博士后研究工作，2018年人才引进到海南医学院院工作。主要从事非编码RNA（miRNA, lncRNA, circRNA）在复杂疾病中的作用机制的研究；P53肿瘤抑制因子在泛癌中的分子致病机制的研究；利用4SU-seq数据识别病毒转染后基因的转录、合成、降解的动态性变化；基于单细胞测序识别肿瘤微环境中的免疫信号；RNA-seq数据处理及pipeline的搭建。

近年来在《CELL》,《Briefings in Bioinformatics》,《Journal of Experimental & Clinical Cancer Research》,《Scientific Reports》等杂志发表SCI论文21篇，以第一、共一和通讯作者身份，发表SCI论文9篇， SCI单篇最高影响因子30.409，SCI累计影响因子100余点，主持国家自然青年科学、地区基金，海南省面上项目、黑龙江省自然科学基金、黑龙江省教育厅项目，黑龙江省卫生厅项目等多项课题。参与国自然重大、面上、青年基金及黑龙江省各级、各类项目共7项。作为学业指导教师、毕业设计指导教师、研究生导师共培养27名本科生，3名硕士研究生，其中2名学生获本科优秀毕业论文，多名本科生在本科阶段发表SCI论文。独立主讲《分子生物软件工程 》、《生物医学网络平台分析 》、《生物网络医学资源》等11门生物信息学专业基础及专业课程，教学效果优秀，多次被评为校级“我心目中的好老师”。

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**2.研究方向**

生物信息学，基于深度学习的系统生物学，主要关注单细胞测序的研究内容，及利用利用免疫特征挖掘肿瘤微环境特征。

**3.发表的学术论文和专著**

1. A Rialdi**#**, J Hultquist, D Jimenez-Morales, Z Peralta, L Campisi, R Fenouil, N Moshkina, **Z. Z. Wang**, B Laffleur, RM Kaake, M. J. McGregor, K. Haas, E Pefanis, R. A. Albrecht, L.Pache, S.Chanda, J. Jen, J. Ochando, M. Byun, U. Basu, A. Garcia-Sastre, N. Krogan**#**, H. van Bakel**#**, I. Marazzi**\***, 'The RNA Exosome Syncs IAV-RNAPII Transcription to Promote Viral Ribogenesis and Infectivity', **Cell** **5** **(2017**), 169(4):679-692 e614.
2. Wang, Xin, Hongjiu Wang, Dan Liu, Na Wang, Danni He, Zheyu Wu, Xu Zhu, Xiaoling Wen, Xuhua Li, Jin Li and **Zhenzhen Wang\***. "Deep Learning Using Bulk Rna-Seq Data Expands Cell Landscape Identification in Tumor Microenvironment." **Oncoimmunology (2022)**,11, no. 1 : 2043662-2043662.
3. Wang, L., W. Xie, K. Li, **Z. Wang**, X. Li, W. Feng and J. Li. "Dyspia: A Novel Dysregulated Pathway Identification Analysis Method." **Front Genet (2021):** 647653.
4. Wang, X., S. He, J. Li, J. Wang, C. Wang, M. Wang, D. He, X. Lv, Q. Zhong, H. Wang and **Z. Wang**. "Pulsetd: Rna Life Cycle Dynamics Analysis Based on Pulse Model of 4su-Seq Time Course Sequencing Data." **PeerJ(2020**): e9371.
5. L. Cheng**#**, H. Yang**#**, H. Zhao**#**, . Pei, H. Shi, J. Sun, Y. Zhang**\***, **Z. Z. Wang\*** and M Zhou**\*** 'MetSigDis: a manually curated resource for the metabolic signatures of diseases', **Briefings in bioinformatics, 1 (2019)**,20(1):203-209.通讯作者
6. H. Shi**\*#**, J. Li**#**, Q. Song**#**, L. Cheng, H. Sun, W. Fan, J. Li, **Z. Z. Wang\***, and G. Zhang**\***, 'Systematic identification and analysis of dysregulated miRNA and transcription factor feed-forward loops in hypertrophic cardiomyopathy', **Journal of cellular and molecular medicine**, **1** **(2019**), 23(1):306-316.
7. SY. He**#**, WJ. Xi**#**, X. Wang, CH. Xu, L. Cheng, SY. Liu, QQ. Meng, B. Li, Y. Wang, HB. Shi**\***, HJ. Wang**\*** and **Z. Z. Wang\***, 'Identification of a Combined RNA Prognostic Signature in Adenocarcinoma of the Lung. Medical science monitor', **International medical journal of experimental and clinical research, 5 (2019)**, 25:3941-3956.
8. H. Shi**\*#**, G. Zhang**#**, M. Zhou, L. Cheng, H. Yang, J. Wang, J. Sun**\***, and **Z. Z. Wang\***, 'Integration of Multiple Genomic and Phenotype Data to Infer Novel Mirna-Disease Associations', **PLoS One**, 11 (**2016**), e0148521.
9. Y. Hu, Y. Zhang, J. Ren, Y. Wang**\***, **Z. Z. Wang\***, and J. Zhang**\***, 'Statistical Approaches for the Construction and Interpretation of Human Protein-Protein Interaction Network', **Biomed Res Int**, 2016 (**2016**), 5313050.
10. H. J. Wang**#**, M. Zhou**#**, L. Jia**#**, J. Sun, H. B. Shi, S. L. Liu**\***, and **Z. Z. Wang\***, 'Identification of Aberrant Chromosomal Regions in Human Breast Cancer Using Gene Expression Data and Related Gene Information', **Med Sci Monit**, 21 (**2015**), 2557-66.
11. L. Cheng**#**, H. Shi**#**, **Z. Z. Wang #**, Y. Hu, H. Yang, C. Zhou, J. Sun**\***, and M. Zhou**\***, 'Intnetlncsim: An Integrative Network Analysis Method to Infer Human Lncrna Functional Similarity', **Oncotarget**, 7 (**2016**), 47864-74.
12. M. Zhou**#**, H. Zhao**#**, **Z. Z. Wang #**, L. Cheng, L. Yang, H. Shi, H. Yang, and J. Sun**\***, 'Identification and Validation of Potential Prognostic Lncrna Biomarkers for Predicting Survival in Patients with Multiple Myeloma', **J Exp Clin Cancer Res**, 34 (**2015**), 102.
13. J. Sun**#**, X. Chen**#**, **Z. Z. Wang#**, M. Guo, H. Shi, X. Wang, L. Cheng, and M. Zhou**\***, 'A Potential Prognostic Long Non-Coding Rna Signature to Predict Metastasis-Free Survival of Breast Cancer Patients', **Sci Rep**, 5 (**2015**), 16553.
14. H. K. Wang**#**, **Z. Z. Wang#** X. Li**\***, B. S. Gong, L. Feng and Y. Zhou. "A Robust Approach Based on Weibull Distribution for Clustering Gene Expression Data." **Algorithms Mol Biol**, (**2011**) ,14.
15. **Z. Z. Wang#**, B. S. Gong**#**, H. K. Wang,**#** H. J. Wang, M. Zhou, Q. H. Wang, X. Chen, T. Liu, and X. Li**\***, 'Microrna Regulation Constrains the Organization of Target Genes on Mammalian Chromosomes', **FEBS Lett**, 585 (**2011**), 1897-904.
16. M. Zhou**#**, W. Xu**#**, X. Yue**#**, H. Zh**ao, Z. Z. Wang,** H. Shi, L. Cheng, and J. Sun**\***, 'Relapse-Related Long Non-Coding Rna Signature to Improve Prognosis Prediction of Lung Adenocarcinoma', **Oncotarget**, 7 **(2016**), 29720-38.
17. M. Zhou**#**, X. Wang**#**, H. Shi, L. Cheng, **Z. Z. Wang**, H. Zhao, L. Yang, and J. Sun**\***, 'Characterization of Long Non-Coding Rna-Associated Cerna Network to Reveal Potential Prognostic Lncrna Biomarkers in Human Ovarian Cancer', **Oncotarget**, 7 (**2016**), 12598-611.
18. J. Sun**\***, L. Cheng**#**, H. Shi**#**, Z. Zhang, H. Zhao, **Z. Z. Wang**, and M. Zhou**\***, 'A Potential Panel of Six-Long Non-Coding Rna Signature to Improve Survival Prediction of Diffuse Large-B-Cell Lymphoma', **Sci Rep**, 6 (**2016**), 27842.
19. H. Shi**#**, G. Zhang**#**, J. **Z. Z. Wang.** Wang, X. Liu, L. Cheng, and W. Li**\***, 'Studying Dynamic Features in Myocardial Infarction Progression by Integrating Mirna-Transcription Factor Co-Regulatory Networks and Time-Series Rna Expression Data from Peripheral Blood Mononuclear Cells', **PLoS One**, 11 (**2016**), e0158638.
20. L. Cheng**\***, Y. Jiang, **Z. Z. Wang**, H. Shi, J. Sun, H. Yang, S. Zhang, Y. Hu**\***, and M. Zhou**\***, 'Dissim: An Online System for Exploring Significant Similar Diseases and Exhibiting Potential Therapeutic Drugs', **Sci Rep**, 6 (**2016**), 30024.
21. M. Zhou, X. Wang, J. Li, D. Hao, **Z. Z. Wang**, H. Shi, L. Han**\***, H. Zhou**\***, and J. Sun**\***, 'Prioritizing Candidate Disease-Related Long Non-Coding Rnas by Walking on the Heterogeneous Lncrna and Disease Network', **Mol Biosyst**, 11 (**2015**), 760-9.
22. G. Zhang**#**, H. Shi, L**#**. Wang, M. Zhou, **Z. Z. Wang**, X. Liu, L. Cheng, W. Li**\***, and X. Li**\***, 'Microrna and Transcription Factor Mediated Regulatory Network Analysis Reveals Critical Regulators and Regulatory Modules in Myocardial Infarction', **PLoS One**, 10 (**2015**), e0135339.
23. M. Zhou**#**, L. Han**#**, J. Zhang, D. Hao, Y. Cai, **Z. Z. Wang**, H. Zhou**\***, and J. Sun**\***, 'A Computational Frame and Resource for Understanding the Lncrna-Environmental Factor Associations and Prediction of Environmental Factors Implicated in Diseases', **Mol Biosyst**, 10 (**2014**), 3264-71.
24. J. Sun**#**, H. Shi**#**, **Z. Z. Wang**, C. Zhang, L. Liu, L. Wang, W. He, D**\***. Hao, S. Liu**\***, and M. Zhou**\***, 'Inferring Novel Lncrna-Disease Associations Based on a Random Walk Model of a Lncrna Functional Similarity Network', **Mol Biosyst**, 10 (**2014**), 2074-81.
25. J. Sun**#**, M. Zhou**#**, Z. T. Mao, D. P. Hao, **Z. Z. Wang**, and C. X. Li**\***, 'Systematic Analysis of Genomic Organization and Structure of Long Non-Coding Rnas in the Human Genome', **FEBS Lett**, 587 (**2013**), 976-82.
26. J. Sun**#**, B. Gao**#**, M. Zhou**\*#**, **Z. Z. Wang**, F. Zhang, J. E. Deng, and X. Li**\***, 'Comparative Genomic Analysis Reveals Evolutionary Characteristics and Patterns of Microrna Clusters in Vertebrates', **Gene**, 512 (**2013**), 383-91
27. **获得的学术成果奖励（标注名次）**

无

**5.获得的发明专利（标注名次）**

无

**6.主持过的科研项目（项目名称；项目编号；级别；经费；起止日期）**

**主持的课题：**

1. 国家自然科学基金委（地区基金）：基于深度学习的肿瘤微环境景观检测及免疫亚型识别方法的研究（32160179），35万，2022.01-2025.12。
2. 海南省自然科学基金青年基金项目：融合多组学数据识别肿瘤免疫亚型及其T细胞障碍机制，5万，2021.04-2023.12
3. 海南医学院引进人才科研启动金项目（XRC202107）：基于深度学习的肿瘤微环境景观检测，25万，2021.01-2025.12
4. 国家自然科学基金委（青年科学基金）：基于遗传变异驱动的个性化分子网络识别复杂疾病亚型（31701159），22万，2018.01-2020.12
5. 黑龙江省科技厅（黑龙江省自然青年基金）：应用新一代测序数据识别癌基因组的染色体变异谱(QC2013C019)，5万，2013.01-2020.15
6. 黑龙江省教育厅（科技面上)：应用表达谱及基因整合信息挖掘肝癌染色体变异区域的研究 (12521307)，1万，2011.01-2013.12
7. 黑龙江省卫生厅（计划项目)：应用基因的融合信息识别乳腺癌中变异的染色体区域 (2011-252) 2011.01-2013.12

**8.学术兼职**

黑龙江省科学技术协会会员，黑龙江省生物信息学学会会员。