**个人简介**

**李永生**，男，博士，三级教授，博士/硕士生导师，生物医学信息与工程学院党委副书记、院长。教育部霍英东青年科学奖获得者，海南省千人专项“领军人才”入选者，海南省拔尖人才，海南省“双百人才团队”后备带头人，海南医学院“热带生物医学信息学”A类重点学科后备带头人。目前主持国家自然科学基金3项、省自然科学基金3项，中国博士后特别资助和面上项目等10余项。主要研究成果获中华医学奖三等奖、省政府科学技术二等奖、省高校科学技术一等奖和二等奖等，获得省青年科技奖、校级十大杰出青年、校级科技人才奖、校级优秀科技工作者等荣誉称号。在美国MD安德森癌症研究中心及德州大学奥斯汀分校访问学习3年，获得美国MD安德森癌症研究中心授予的Harold C. and Mary L. Daily Endowment Fund和Ben F. Love Fellowship in Innovative Cancer Therapies奖项。

长期从事医学大数据生物信息学研究，深入研究人类重大疾病中基因型-表型关联这一基本而关键的科学问题，特别关注遗传变异分子标记识别及功能解析、非编码RNA表达调控机制和功能的研究。研究成果发表于《Nature Reviews Genetics》**（封面文章）**;《Cancer Cell》;《Trends in Biochemical Sciences》**（封面文章）**;《Hepatology》;《Nature Communications》**（ESI高被引论文）**;《Nucleic Acids Research》;《Molecular Cancer》;《Cell Reports》;《Cancer Research》;《Annals of Internal Medicine》**（ESI高被引论文）**等国际著名生命科学杂志，发表SCI论文70余篇，累计SCI影响因子400余点，H-index达到27, 谷歌学术总引用次数达2600余次，单篇最高引用300余次。

作为主要参加者编写国家级规划教材《生物信息学》（第二版、第三版编委）、人民卫生出版社教程《非编码微小分子RNA与心脏疾病》，受邀编写Springer出版社的《Systems Biology in Cancer Research and Drug Discovery》、《Functional Genomics》（第三版）、《Non-coding RNAs in Complex Diseases》及《Computational Epigenetics and Diseases》。担任《BMC Medicine》编辑顾问，《Frontiers in oncology》副主编，《Frontiers in genetics》、《Computational Biology and Bioinformatics》杂志编委，《Nucleic Acids Research》、《Life Sciences》、《Briefings In Bioinformatics》、《Molecular Therapy-Nucleic Acids》、《Journal of Molecular Biology》、《Nanoscale》、《International Journal of Biological Sciences》等10余家国际杂志审稿专家。

* **教育经历:**

1. 2009.9-2014.6, 哈尔滨医科大学, 生物物理学, 博士
2. 2004.9-2009.6, 哈尔滨医科大学, 生物信息, 学士, 大学本科

* **科研与学术工作经历:**

1. 2021.12–至今，海南医学院，生物医学信息与工程学院，党委副书记、院长
2. 2019.12–至今，海南医学院，生物医学信息与工程学院，教授
3. 2015.9–2019.12, 哈尔滨医科大学, 计算生物学教研室, 副教授，博导
4. 2014.7-2015.9, 哈尔滨医科大学, 计算生物学教研室, 讲师

* **留学经历:**

1. 2018.8–2019.10，美国德州大学奥斯汀分校，Dell医学院，四级研究员
2. 2016.9–2018.7, 美国德州大学MD安德森癌症研究中心，系统生物学系，博士后

* **主持及参与科研项目情况:**

1. 国家自然科学基金面上项目，恶性肿瘤关键遗传变异介导的RNA结合蛋白调控网络扰动模型构建与分析（31970646），2020年1月-2023年12月，项目负责人，在研；
2. 国家自然科学基金地区项目，基于多源数据融合的肿瘤免疫关键调控因子识别及作用机制研究（32060152），2021年1月-2024年12月，项目负责人，在研；
3. 海南省重点研发计划项目，基于单细胞测序解析热带病调控因子关键技术研究与应用（ZDYF2021SHFZ051），2021年9月-2023年9月，项目负责人，在研；
4. 海南省自然科学基金面上项目，基于多层次功能网络扰动的癌症热点突变优化筛选及功能预测模型研究（820MS053），2020年12月-2023年12月，项目负责人，在研；
5. 海南医学院国家级自然科学研究项目培育基金重点项目，重大疾病单细胞测序关键技术研究与应用（JBGS202103），2021年10月-2024年10月，项目负责人，在研；
6. 国家卫生健康委员会热带病防治重点实验室开放课题，融合多组学数据优选新冠感染关键RBP分子标记（2022NHCTDCKFKT31001），2021年12月-2023年12月，项目负责人，在研；
7. 国家自然科学基金青年项目，融合多组学数据优化筛选恶性肿瘤中表观失调非编码RNA及其功能研究（61502126）， 2016年1月-2018年12月，项目负责人，结题；
8. 中国博士后特别资助基金，复杂疾病中长链非编码RNA的识别及其调控机制研究（2016T90309），2016年6月-2019年4月，项目负责人，结题；
9. 中国博士后面上项目，恶性肿瘤表观失调长链非编码RNA的鉴定及其功能研究（2015M571436），2015年5月-2019年4月，项目负责人，结题；
10. 黑龙江省自然科学基金青年项目，恶性胶质瘤进展相关非编码RNA调控网络及耦合模块挖掘算法研究（QC2015020），2015年7月-2018年7月，项目负责人，结题；
11. 黑龙江省博士后基金，整合表观组和转录组识别乳腺癌亚型相关的非编码RNA标记（LBH-Z14134），2014年12月-2019年4月，项目负责人，结题；
12. 黑龙江省普通本科高等学校青年创新人才培养计划，基于RNA 结合蛋白调控网络扰动分析优化恶性肿瘤中关键调控因子，2017年10月-2019年12月，项目负责人，结题；
13. 哈尔滨医科大学于维汉院士杰出青年基金，2017年8月-2019年12月，项目负责人，结题；
14. 国家自然科学基金青年项目，基于多组学数据融合的泛癌中非编码RNA crosstalk模式研究（31601065），2017年1月-2019年12月，主要参与人，结题；
15. 国家自然科学基金重点项目，EGFR过表达协同PTEN缺失介导的免疫炎性网络促进胶质母细胞瘤恶性进展的分子机制（91229112），2013年1月-2015年12月，主要参与人，结题；
16. 国家自然科学基金培育项目，心血管疾病风险循环非编码RNA（miRNA/LncRNA)识别及其协同调控风险通路功能分析 (91439117) ，2015年1月-2017年12月，主要参与人，结题；
17. 哈尔滨医科大学伍连德青年科学基金：基于miRNA 协同调控网络的疾病miRNA和miRNA-mRNA耦合模块挖掘算法研究（WLD-QN1107），主要参与人，结题；
18. 黑龙江省研究生创新基金重点项目：融合甲基化组和互作组解析癌症关键的基因和功能通路（YJSCX2012-196HLJ），负责人，结题；

* **教学课题及教学论文：**

1. 海南医学院2020年校级教育科研课题，《海南自贸港建设背景下生物信息学专业课程体系改革的研究与实践》，2020年8月-2022年7月，主持，在研；

2. 《基于智慧教学+CDIO理念的大学生数学建模培训实践与研究》， 2019年6月-2021年6月，第2参与人，在研；

3. 《多学科交叉融合的生物信息学本科专业创新教学体系构建研究与实践》，2017年6月-2020年12月，第1参与人，在研；

4. 《面向生物医学大数据的生物信息专业教学体系改革的研究》，2019年6月-2020年12月，第1参与人，在研；

5. 《海南自贸港建设背景下生物信息学专业建设思考与洞见》，医学信息学，2021，李永生，徐娟

6. 《新医科背景下构建多学科交叉融合的生物信息学专业特色课程体系》，高教学刊，2020，徐娟，李永生，张云鹏，李霞，陈丽娜

7. 《关于生物分子网络课程教学模式的探讨》，科技创新导报，2017，徐娟，李永生，李霞，邵婷婷

8. 《关于生物信息学专业本科生培养方案改革的思考》，赤子，2017，徐娟，李永生，邵婷婷

9. 《任务教育法在医学院校计算机程序语言教学中的实践与探索》，高等医学教育，2015，李永生，徐娟

* **个人奖励情况:**

1. 2022年第18届霍英东教育基金会高等院校青年科学奖二等奖；
2. 2022年第十六届泛珠三角大学生计算机作品赛全国总决赛三等奖（指导教师）；
3. 2021年海南省千人专项领军人才入选者；
4. 2021年泛珠三角大学生计算机作品赛海南省一等奖（指导教师）；
5. 2020年海南医学院优秀共产党员；
6. 2020年海南省拔尖人才；
7. 2019年第十四届黑龙江省青年科技奖；
8. 2019年哈尔滨医科大学青年科技人才奖；
9. 2020年美国大学生数学建模竞赛二等奖（指导教师）；
10. 2019年第九届MathorCup高校数学建模竞赛二等奖（指导教师）；
11. 2019年黑龙江省数学建模竞赛二等奖（指导教师）；
12. 2018年哈尔滨医科大学十大杰出青年专家；
13. 2018年美国MD安德森癌症研究中心Ben F. Love Fellowship in Innovative Cancer Therapies奖；
14. Ebiomedicine杂志杰出审稿专家，2018年8月；
15. 2017年美国MD安德森癌症研究中心The Harold C. and Mary L. Daily Endowment Fund奖；
16. Life Science杂志杰出审稿专家，2016年11月；
17. 2015年哈尔滨医科大学优秀科技工作者；
18. 2014年哈尔滨医科大学生物信息学院优秀科技工作者；
19. 2014年黑龙江省优秀毕业生；
20. 2015年国家研究生奖学金一等奖；

* **科研奖励及软件著作权：**

1. 2022年度黑龙江省教学成果奖，“科教融合、全程多元、知行合一”的生物信息学专业创新教学体系研究与实践, 二等奖，排名第二；
2. 2022年度哈尔滨医科大学教学成果奖，“科教融合、全程多元、知行合一”的生物信息学专业创新教学体系研究与实践, 一等奖，排名第二；
3. 2020年度黑龙江省教学成果奖，“适应新医科发展理念，医工结合创办生物信息专业”，一等奖，排名第三；
4. 2020年度哈尔滨医科大学教学成果奖，“适应新医科发展理念，医工结合创办生物信息专业”，一等奖，排名第三；
5. 《基于生物数据融合的恶性肿瘤中miRNA-ceRNA复合协同调控模式的研究》，2019，黑龙江省高校科学技术奖，一等奖，排名第三；
6. 《癌风险miRNA及协同调控风险通路(pathway)识别》， 2015，中华医学科技奖，三等奖，排名第六；
7. 《癌风险miRNA及协同调控风险通路(pathway)识别方法研究》， 2015，黑龙江省政府科学技术奖（自然类），二等奖，排名第六；
8. 《癌风险miRNA及协同调控风险通路(pathway)识别方法研究》， 2015，黑龙江省高校科学技术奖，二等奖，排名第六；
9. 《恶性胶质瘤进展相关的miRNA识别以及功能分析》，哈尔滨市自然科学技术学术成果奖，排名第一，二等奖，2014-8
10. 《基于miRNA-miRNA功能协同调控网络剖析疾病miRNA的拓扑特性》，哈尔滨市自然科学技术学术成果奖，排名第三，一等奖，2012-8
11. 非编码RNA本体论软件, 2016R11L668233, 原始取得, 全部权利, 2015.9.22 (软件著作权)
12. e-MutPath：基于调控通路改变的关键突变识别分析平台，2021SR1046578, 原始取得, 全部权利, 2021.7.15(软件著作权)
13. DrAS-Net：基于网络的复杂疾病调控选择性剪接突变识别分析平台，2021SR0070974, 原始取得, 全部权利, 2021.1.14(软件著作权)
14. MERIT:复杂疾病遗传变异干扰RNA互作网络识别分析平台，2021SR0197169, 原始取得, 全部权利, 2021.2.4(软件著作权)
15. LncSpA:长链非编码RNA空间转录组在线分析平台，2022SR0880406, 原始取得, 全部权利, 2022.7.1(软件著作权)
16. ROI-Driver：重大疾病遗传变异功能结构优选分析平台，2022SR0986792, 原始取得, 全部权利, 2022.8.3(软件著作权)
17. HVPPI:人类-病毒蛋白互作网络在线分析平台，2022SR1167320, 原始取得, 全部权利, 2022.8.17(软件著作权)
18. TransLnc：长链非编码RNA多肽在线分析平台，2022SR1167319, 原始取得, 全部权利, 2022.8.17(软件著作权)

* **社会任职情况：**

国家自然科学基金评审专家；中国细胞生物学会功能基因组信息学与系统生物学理事；中国生物信息学会重大疾病组学信息学专委会副主任委员；中国抗癌协会肿瘤标志专业委员会委员；美国基因与癌症治疗协会会员；黑龙江省人工智能学会理事；中国计算机学会生物信息学专委会通讯委员；海南省免疫学会青年工作委员会主任委员；美国ACSR基金评审专家。

* **发表文章列表：**

1. Jiwei Zhang#, Tao Pan#, Weiwei Zhou#, Ya Zhang, Gang Xu, Qi Xu, Si Li, Yueying Gao, Zhengtao Wang\*, Juan Xu\*, **Yongsheng Li\***. Long noncoding RNA LINC01132 enhances immunosuppression and therapy resistance via NRF1/DPP4 axis in hepatocellular carcinoma. Journal of Experimental & Clinical Cancer Research, 2022. (**通讯作者, SCI影响因子12.658**)
2. Yangyang Cai#, Dezhong Lv#, Donghao Li#, Jiaqi Yin, Yingying Ma, Ya Luo, Limei Fu, Na Ding, **Yongsheng Li\***, Zhenwei Pan\*, Xia Li\*, Juan Xu\*. IEAtlas: an atlas of HLA-presented immune epitopes derived from non-coding regions. Nucleic Acids Research, 2022. **(并列通讯作者,SCI影响因子16.971)**
3. Dezhong Lv#, Kang Xu#, Changbo Yang, Yujie Liu, Ya Luo, Weiwei Zhou, Haozhe Zou, Yangyang Cai, Na Ding, Xia Li\*, Tingting Shao\*, **Yongsheng Li\*,** Juan Xu\*. PRES: a webserver for decoding the functional perturbations of RNA editing sites. Briefings in Bioinformatics, 2022. **(SCI影响因子11.622)**
4. Tao Pan#, Yueying Gao#, Gang Xu#, Ping Zhou#, Si Li, Jing Guo, Haozhe Zou, Qi Xu, Xiaoyan Huang\*, Juan Xu\*, **Yongsheng Li\***. Pan-cancer analyses reveal the genetic and pharmacogenomic landscape of transient receptor potential channels. NPJ Genome Medicine, 2022. **(SCI影响因子8.617)**
5. **Yongsheng Li**#, Sicong Xu#, Dahua Xu#, Tao Pan, Jing Guo, Shuo Gu, Qiuyu Lin, Xia Li\*, Kongning Li\*, Wei Xiang\*. Pediatric pan-central nervous system tumors methylomes analyses reveal immune-related lncRNAs. Frontiers in Immunology, 2022. **(SCI影响因子7.561)**
6. **Yongsheng Li**#**,** Yunpeng Zhang#, Tao Pan#, Ping Zhou#, Weiwei Zhou, Yueying Gao, Shaojiang Zheng\*, Juan Xu\*. Shedding light on the hidden human proteome expands immunopeptidome in cancer. Briefings in Bioinformatics, 2022. **(SCI影响因子11.622)**
7. Si Li#, Weiwei Zhou#, Donghao Li#, Tao Pan, Jing Guo, Haozhe Zou, Zhanyu Tian, Kongning Li, Juan Xu\*, Xia Li\*, **Yongsheng Li\***. Comprehensive characterization of human–virus protein-protein interactions reveals disease comorbidities and potential antiviral drugs. Computational and Structural Biotechnology Journal, 2022. **(通讯作者,SCI影响因子7.271)**
8. Lingli Li#, Hongyan Yi#, Zheng Liu#, Ping Long, Tao Pan, Yuanhua Huang, **Yongsheng Li\***, Qi Li\*, Yanlin Ma\*. Genetic correction of concurrent α- and β-thalassemia patient-derived pluripotent stem cells by the CRISPR-Cas9 technology. Stem Cell Res Ther, 2022. **(共同通讯,SCI影响因子6.832)**
9. Haozhe Zou#, Tao Pan#, Yueying Gao#, Renwei Chen#, Si Li, Jing Guo, Zhanyu Tian, Gang Xu, Juan Xu\*, Yanlin Ma\*, **Yongsheng Li\***. Pan-cancer assessment of mutational landscape in intrinsically disordered hotspots reveals potential driver genes.Nucleic Acids Research, 2022. **(通讯作者,SCI影响因子16.971)**
10. Chunjie Jiang\*, Shibiao Wan, Peng Hu, **Yongsheng Li,** Shengli Li\*. Editorial: Transcriptional Regulation in Metabolism and Immunology. Front Genet 2022. **(SCI影响因子4.599)**
11. Jasmine George, **Yongsheng Li**, Ishaque P Kadamberi, Deepak Parashar, Shirng-Wern Tsaih, Prachi Gupta, Anjali Geethadevi, Changliang Chen, Chandrima Ghosh, Yunguang Sun, Sonam Mittal, Ramani Ramchandran, Hallgeir Rui, Gabriel Lopez-Berestein, Cristian Rodriguez-Aguayo, Gustavo Leone, Janet S Rader, Anil K Sood, Madhusudan Dey, Sunila Pradeep, Pradeep Chaluvally-Raghavan\*. RNA-binding protein FXR1 drives cMYC translation by recruiting eIF4F complex to the translation start site. Cell Reports, 2021. **(SCI影响因子9.423)**
12. Tiantongfei Jiang#, Weiwei Zhou#, Zhenghong Chang#, Haozhe Zou, Jing Bai, Qisen Sun, Tao Pan, Juan Xu\*, **Yongsheng Li**\* and Xia Li\*. ImmReg: The regulon atlas of immune-related pathways across cancer types. Nucleic Acids Research, 2021. **(共同通讯,SCI影响因子16.971)**
13. Dezhong Lv, Zhenghong Chang, Yangyang Cai, Junyi Li, Liping Wang, Qiushuang Jiang, Kang Xu, Na Ding, Xia Li\*, Juan Xu\*, **Yongsheng Li**\*.TransLnc: a comprehensive resource for translatable lncRNAs extends immunopeptidome.Nucleic Acids Research, 2021. **(SCI影响因子16.971)**
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8. 《COMPUTATIONAL EPIGENETICS FOR BREAST CANCER》，2019年，Elsevier出版社

* **会议报告**

1. 2022年肿瘤生物信息学与临床科研培训班，大会报告，“如何“干湿结合”讲好肿瘤故事”；
2. 2022年福建省首届“医院医学实验室科研技能培训班”，大会报告，“如何结合生物信息讲好肿瘤故事”；
3. 2022年第一届智能健康与生物信息大会，线上，分会报告，“Integrative analysis reveals the functions of RNA binding proteins in cancer”；
4. 2021年第六届国际肿瘤精准医学高峰论坛，大会报告，“肿瘤系统免疫学：生物信息学方法与应用”；
5. 2021年中国细胞生物学学术年会，重庆，分会报告，“Characterization of single cell regulatory networks in cancer reveals oncogenic biomarkers”；
6. 2021生物信息学与智能信息处理学术会议，武汉，分会报告，“Pan-cancer characterization of immune-related regulons identifies potential oncogenic biomarkers”；
7. 2020年第五届CCF生物信息学会议，哈尔滨，分会报告，“Characterizing the function of genetic mutations based on regulatory network perturbations”；
8. 2020年第九届全国生物信息学与系统生物学学术大会，上海，分会报告，“Systematically Analyzing the Regulation of Immune Pathways Identifies Potential Oncogenic Biomarkers”；
9. 2020年第九届世界华人神经外科学术大会，武汉，分会报告，“Noncoding RNAs in Glioma: Biological functions and potential clinical applications”；
10. 2020年肿瘤转移相关的组学数据分析，在线会议，“基于生物大数据解析恶性肿瘤中免疫lncRNA分子标记功能”；
11. 2019年中国肿瘤标志物学术大会暨第十三届肿瘤标志物青年科学家论坛，武汉，分会报告，“From edgotype to phenotype: Revealing the functions of genetic variants by network biology”;
12. 中国生物工程学会2016年学术年会暨全国生物技术大会，哈尔滨，分会报告；