**附：公示内容**

**1.推荐奖种:** 中华医学科技奖医学科学技术奖

**2.项目名称:** 癌症个性化遗传分子图谱重构及早期风险预警平台研究

**3.推荐单位：**哈尔滨医科大学

**4.推荐意见**

癌症已经成为严重危害人类生命健康的一类重大疾病。利用癌症生物医学大数据资源重构癌症个性化遗传分子图谱，对于探索癌症发病机理、发现癌诊断与预后标记、发现药靶及药物作用通路具有重要意义。本研究利用癌症生物医学大数据资源完成了癌症个性化遗传分子图谱的重构，并基于遗传谱、转录谱等多组学数据开发了癌症精准诊断和治疗的新方法，构建了癌症早期风险预警平台，对预测癌症患病风险，提高诊断及预后预测准确率，实施个性化医疗等具有重大意义和社会效益。

李霞教授及课题组主要成员长期从事癌症相关的生物信息学研究，主持多项863项目和973项目和国家自然科学基金项目，发表代表性SCI论文20篇，累计SCI影响因子超过150，总引用次数400次，开发的生物信息学平台得到超过55个国家的1万余次访问。该项目按照要求进行了公示，且公示结果无异议，特推荐该项目申报。

**5.项目简介**

癌症已经成为严重危害人类生命健康、制约社会经济发展的一类重大疾病。中国的癌症发病率和死亡率一直居高不下，从2010年开始已经成为主要的致死原因。本项目在国家973计划、国家863计划和国家自然科学基金等项目的资助下，利用癌症生物医学大数据资源完成了癌症个性化遗传分子图谱的重构，基于遗传谱、转录谱等多组学数据开发了癌症精准诊断和治疗的新方法，并构建了癌症早期风险预警平台，完成的工作主要包括：1）建立了癌症大数据资源库和遗传分子图谱数据库；2）开发了基于多组学数据融合的癌症个性化多态位点识别算法；3）挖掘和解析了干扰非编码RNA调控的癌症风险多态位点；4）开发了癌症发病风险的早期预警平台和在线生物信息学分析平台。

**6.客观评价**

研究成果对预测癌症个体患病风险和实施癌症个性化医疗具有重大意义和社会效益。共发表SCI 论文20篇，累计影响因子超过150，总引用次数超过400次，其中影响因子>10的SCI论文2篇，1篇论文被评为ESI高被引论文。

**7.推广应用情况**

在成果转化方面，开发了在线的癌症遗传图谱分析和早期预警平台，目前该平台得到超过55个国家的1万余次访问，受到国际著名期刊的多次引用和正面评论，产生了很好的学术影响和社会效益，培养了大批生物信息学高级人才。

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**9.完成人情况**

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