杨亚东

联系方式

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个人主页

https://genegps.com

技能

Cancer genomics
Epigenomics
Bioinformatics
Machine learning
Leadership and teamwork

求职意向

生物信息总**监**
目前年薪：72~75万
期望年薪：90~100万

个人介绍

在基因组学、生物医学、生物信息学等多个领域具有丰富的成果、科研和管理工作经验。在 *Genomics*,*Briefings in Bioinformatics*,*Genomics, Proteomics & Bioinformatics* 等国际知名学术期刊发表 SCI 论文近 50 篇，被引超过 1600 余次，h-index 17；建设了国家生物信息中心 GSA, GliomaDB 等多个大型数据系统，开发了基于外周血转录组的肿瘤早筛算法 rankDetect 并获得相关发明专利、基于多组学的肿瘤免疫疗效预测等多个算法。参与编写精准医学基础系列中的转录组学内容《转录组学与精准医学》。曾参与组学大数据中心和知识库构建与服务技术 ("863")、精准医学大数据处理和利用的标准化技术体系建设 ("精准医学")、精准医学大数据管理和共享技术平台 ("精准医学") 等科研项目。在生物科技公司主导生物信息渠道从基础设施建设、软件工程到算法开发、肿瘤分子诊断标志物发现等工作。

工作履历

—— 生物信息总监，博尔诚（北京）科技有限公司， 北京
2021.2- 当前日期

团队 8 人，汇报对象：研究院院长

主要负责癌症早筛、卒中预后、心肌病预后等产品标志物的研发。建立完整的甲基化分析流程，包括基于单体型的甲基化分析、片段组、甲基化熵等；建立完整的机器学习体系，并基于多维度信息建立六癌模型，实现了二分类和组织溯源功能。基于甲基化数据筛选肺癌、食管癌、肝癌、膀胱癌等血浆标志物，并推动肝癌和膀胱癌进入注册检。共提交标志物、算法等专利 74 篇，已公开 26 项。发表 SCI 论文 1 篇。

—— 生物信息高级经理，上海仁东医学检验所有限公司， 北京/上海
2018.6- 2021.2

团队 5 人，汇报对象：CTO
主要负责肿瘤伴随诊断领域研究和产品开发，包括誉衡生物药赛帕利单抗（Anti-PD-1）Ib 期生物标志物数据分析项目；头颈鳞癌、膀胱癌、黑色素瘤、肺癌等免疫治疗标志物开发和疗效预测算法研发；肠癌 MRD 产品、膀胱癌分型等产品研发。构建 tTMB、bTMB、基因表达、肿瘤免疫浸润等指标与免疫治疗效果的在线数据库和分析平台。发表文章 3 篇，会议摘要 11 篇。

—— 助理研究员，中国科学院北京基因**组**研究所， 北京
2011.7-2015.9

以基础研究为主，主要方向包括造血干细胞分化、白血病的转录组和 miRNA 研究，iPSC 基因组研究，乳腺癌筛查算法开发，组学数据库建设，以关键作者身份开发国家生物信息中心基因组序列数据库 GSA，对标 NCBI 的 SRA 库，目前已先后被威利、爱思唯尔、施普林格·自然等全球主要出版集团认可。发表文章 39 篇，发表会议**摘要 2 篇**，获**得**专**利 2 篇**。

教育经历

—— 基因**组**学博士，中国科学院大学，北京
2015.9- 2018.7
—— 基因**组**学**硕**士， 中国科学院北京基因**组**研究所， 北京
2008.8- 2011.7
—— 生物工程学士，北京工商大学，北京
2004.9- 2008.7

附录一：已发表文章

1 Gao Y, Yang C, He N, Wang J, **Yang Y*.** Integration of TMB and tumor heterogeneity identify an immunologic subtype of melanoma with favorable survival. Oct 2020**,** ***Frontiers in Oncology*** **(IF: 4.84)**

2 Zhou X[#], **Yang Y[#]**, Ma P, Wang Na, Yang D, Tu Q, Sun B, Xiang T, Zhao X, Hou Z*, Fang X*. TRIM44 is indispensable for glioma cell proliferation and cell cycle progression through AKT/p21/p27 signaling pathway. ***Journal of Neuro-Oncology***, November 2019, 145(2), pp 211 – 222 **(IF: 3.129)**

3 **Yang Y[#]**, Zhang T[#], Qu H, Xie B, Fang X*. Platform-independent approach for cancer detection from gene expression profiles of peripheral blood cells. ***Brief Bioinform***. 2019 Mar 20. pii: bbz027. doi: 10.1093/bib/bbz027. [Epub ahead of print] **(IF: 9.5)**

4 **Yang Y**, Sui Y, Xie B, Qu H, Fang X*. GliomaDB: a Database of Integrating Glioma Precision Medicine Data. ***Genomics Proteomics Bioinformatics.*** 2018. [Epub ahead of print] **(IF: 6.597)**

5 Wang Y[#], Song F[#], Zhu J[#], Zhang S[#], **Yang Y[#]**, Chen T, Tang B, Dong L, Ding N, Zhang Q, Bai Z, Dong X, Chen H, Sun M, Zhai S, Sun Y, Yu L, Lan L, Xiao J, Fang X, Lei H, Zhang Z, Zhao W (2017) GSA: Genome Sequence Archive. ***Genomics Proteomics Bioinformatics*** 15 (1):14-18. doi:10.1016/j.gpb.2017.01.001 **(IF: 6.597)**

6 **Yang Y**, Ding N, Dong X, Fang X. miRNome Analysis of CML Cells. ***Methods Mol Biol.*** 2016;1465:207-17. doi: 10.1007/978-1-4939-4011-0_17. **(Springer book)**

7 Dong C[#], **Yang Y[#]**, Li S, Yang Y, Zhang X, Fang X, Yan J, Cong B. Whole genome nucleosome sequencing identifies novel types of forensic markers in degraded DNA samples. ***Sci Rep***. 2016 May 18;6:26101. **(IF: 4.011)**

8 **Yang Y**, Dong X, Xie B, Ding N, Chen J, Li Y, Zhang Q, Qu H, Fang X*. Databases and Web Tools for Cancer Genomics Study. ***Genomics Proteomics Bioinformatics.*** 2015 Feb;13(1):46-50. **(IF: 6.597)**

9 Zhao M[#], Lei C[#], **Yang Y[#]**, Bu X, Ma H, Gong H, Liu J, Fang X, Hu Z, Fang Q. Abraxane, the Nanoparticle Formulation of Paclitaxel Can Induce Drug Resistance by Up-Regulation of P-gp. ***PLoS One.*** 2015 Jul 16;10(7):e0131429. **(IF: 2.776)**

10 Xiong Q[#], **Yang Y[#]**, Wang H, Li J, Wang S, Li Y, Yang Y, Cai K, Ruan X, Yan J, Hu S*, Fang X*. Characterization of miRNomes in acute and chronic myeloid leukemia cell lines. ***Genomics Proteomics Bioinformatics***. 2014 Apr;12(2):79-91. **(IF: 6.597)**

11 **Yang Y[#]**, Wang H[#], Chang KH[#], Qu H, Zhang Z, Xiong Q, Qi H, Cui P, Lin Q, Ruan X, Yang Y, Li Y, Shu C, Li Q, Wakeland EK, Yan J, Hu S*, Fang X*. Transcriptome Dynamics during Human Erythroid Differentiation and Development. ***Genomics***. 2013;102(5-6):431-41. **(IF: 3.16)**

12 Su RJ[#], **Yang Y[#]**, Neises A, Payne KJ, Wang J, Viswanathan K, Wakeland EK, Fang X*, Zhang XB*. Few single nucleotide variations in exomes of human cord blood induced pluripotent stem cells. ***PLoS One*** 2013; 8: e59908. **(IF: 2.776)**

13 Xu Z, Cheng S, Qiu X, Wang X, Hu Q, Shi Y, Liu Y, Lin J, Tian J, Peng Y, Jiang Y, **Yang Y**, Ye J, Wang Y, Meng X, Li Z, Li H, Wang Y. A Pipeline for Sample Tagging of Whole Genome Bisulfite Sequencing Data Using Genotypes of Whole Genome Sequencing. Jun 2023, ***BMC Genomics*** **(IF: 4.4)**

14 Jiang J, Jin Z, Zhang Y, Peng L, Zhang Y, Zhu Z, Wang Y, Tong D, **Yang Y**, Wang J, Yang Y, Xiao K. Robust prediction of immune checkpoint inhibition therapy for non-small cell lung cancer. Apr 2021, ***Frontiers in Immunology*** **(IF: 8.78)**

15 Du Z, Ma L, Qu H, Chen W, Zhang B, Lu X, Zhai W, Sheng X, Sun Y, Li W, Lei M, Qi Q, Yuan N, Shi S, Zeng J, Wang J, **Yang Y**, Liu Q, Hong Y, Dong L, Zhang Z, Zou D, Wang Y, Song S, Liu F, Fang X, Chen H, Liu X, Xiao J, Zeng C. Whole genome analyses of Chinese population and de novo assembly of a northern Han genome. ***Genomics Proteomics Bioinformatics***. 2019 Jun;17(3):229-247. doi: 10.1016/j.gpb.2019.07.002

16 Xie B, Yuan Z, **Yang Y**, Sun Z, Zhou S, Fang X. MOBCdb: a comprehensive database integrating multi-omics data on breast cancer for precision medicine. ***Breast Cancer Res Treat*** 2018. [Epub ahead of print]

17 Zhao X, **Yang Y**, Qu H, Fang X. Applications of machine learning in clinical decision support in the omic era[J]. ***Hereditas(Beijing)***, 2018, 40(9): 693-703.

18 Li Y, Zhang Q, Du Z, Lu Z, Liu S, Zhang L, Ding N, Bao B, **Yang Y**, Xiong Q, Wang H, Zhang Z, Qu H, Jia H, Fang X. MicroRNA 200a inhibits erythroid differentiation by targeting PDCD4 and THRB. ***Br J Haematol.*** 2017 Jan;176(1):50-64. doi: 10.1111/bjh.14377. Epub 2016 Oct 13.

19 Zhang Q, Ding N, Zhang L, Zhao X, **Yang Y**, Qu H, Fang X. Biological Databases for Hematology Research. ***Genomics Proteomics Bioinformatics***. 2016 Dec;14(6):333-337. doi: 10.1016/j.gpb.2016.10.004. Epub 2016 Dec 11.

20 Zhang T, **Yang Y**, Fang X. Identification of alternative splicing from RNA-Seqdata and its role in precision medicine. ***Journal of Developmental Medicine(Electronic Version)***, 2016, 4(2): 78-85.

21 Xie B, **Yang Y**, Ding N, Fang X. Identification of disease targets for precision medicine by integrative analysis of multi-omics data. ***HEREDITAS(Beijing)*** . 2015; 37(7): 655-663

22 李艳明, **杨亚东**, 张昭军, 方向东*. 精准医学大数据的分析与共享. **中国医学前沿杂志**, 2015; 7(6): 4-10

23 Li Y, Liu S, Sun H, **Yang Y**, Qi H, Ding N, Zheng J, Dong X, Qu H, Zhang Z, Fang X. MiR-218 Inhibits Erythroid Differentiation and Alters Iron Metabolism by Targeting ALAS2 in K562 Cells. ***Int J Mol Sci.*** 2015 Nov 26;16(12):28156-68.

24 Ding N, Wang S, Yang Q, Li Y, Cheng H, Wang J, Wang D, Deng Y, **Yang Y**, Hu S, Zhao H, Fang X. Deep sequencing analysis of microRNA expression in human melanocyte and melanoma cell lines. ***Gene***. 2015 Nov 1;572(1):135-45.

25 Liang F, Qu H, Lin Q, **Yang Y**, Ruan X, Zhang B, Liu Y, Yu C, Zhang H, Fang X, Hao X. Molecular biomarkers screened by next-generation RNA sequencing for non-sentinel lymph node status prediction in breast cancer patients with metastatic sentinel lymph nodes. ***World J Surg Oncol.*** 2015 Aug 28;13:258.

26 Hu Y, Xiong Q, **Yang Y**, Wang H, Shu C, Xu W, Fang X, Hu S. Integrated analysis of gene expression and microRNA regulation in three leukemia-related lymphoblastic cell lines. ***Gene***. 2015 Jun 10;564(1):39-52.

27 Wang H, Li Y, Wang S, Zhang Q, Zheng J, **Yang Y**, Qi H, Qu H, Zhang Z, Liu F, Fang X. Knockdown of transcription factor forkhead box O3 (FOXO3) suppresses erythroid differentiation in human cells and zebrafish. ***Biochem Biophys Res Commun***. 2015 May 15;460(4):923-30.

28 Dong C, **Yang Y**, Yan J, et al. Evaluation of the protective capabilities of nucleosome STRs obtained by large-scale sequencing. ***Electrophoresis***. 2015;36(14):1640-1650. doi:10.1002/elps.201400537

29 Zhao H#, Li Y#, Wang S#, **Yang Y**, Wang J, Ruan X, Yang Y, Cai K, Zhang B, Cui P, Yan J, Zhao Y, Wakeland EK3, Li Q, Hu S*, Fang X*. Whole Transcriptome RNA-seq Analysis: Tumorigenesis and Metastasis of Melanoma. ***Gene***. 2014 Sep 15;548(2):234-43.

30 Wang Y#, Zhang Z#, Chi Y, Zhang Q, Xu F, Yang Z, Meng L, Yang S, Yan S, Mao A, Zhang J, **Yang Y**, Wang S, Cui J, Liang L, Ji Y, Han ZB, Fang X*, Han ZC*. Long-term cultured mesenchymal stem cells frequently develop genomic mutations but do not undergo malignant transformation. ***Cell Death Dis*** 2013; 4: e950

31 Xiong Q#, Zhang Z#, Chang KH#, Qu H, Wang H, Qi H, Li Y, Ruan X, Yang Y, **Yang Y**, Li Y, Sandstrom R, Sabo PJ, Li Q, Stamatoyannopoulos G, Stamatoyannopoulos JA, Fang X*. Comprehensive characterization of erythroid-specific enhancers in the genomic regions of human Kruppel-like factors. ***BMC Genomics***. 2013 Aug 28;14:587.

32 Wang H#, Hu H#, Zhang Q, **Yang Y**, Li Y, Hu Y, Ruan X, Yang Y, Zhang Z, Shu C, Yan J, Wakeland EK, Li Q, Hu S*,

Fang X*. Dynamic transcriptomes of human myeloid leukemia cells. ***Genomics*** 2013; 102: 250-6

33 Chang KH[#], Fang X[#], Wang H, Huang A, Cao H, **Yang Y**, Bonig H, Stamatoyannopoulos JA, Papayannopoulou T*. Epigenetic Modifications and Chromosome Conformations of the Beta Globin Locus throughout Development. ***Stem Cell Rev.*** 2013; 9(4):397-407.

34 Ma L, Nie L, Liu J, Zhang B, Song S, Sun M, Yang J, **Yang Y**, Fang X, Hu S, Zhao Y*, Yu J*. An RNA-seq-based Gene Expression Profiling of Radiation-induced Tumorigenic Mammary Epithelial Cells. ***Genomics Proteomics Bioinformatics.*** 2012; 10(6): 326-35.

35 Li Y[#], Wang H[#], Yang B[#], Yang J, Ruan X, **Yang Y**, Wakeland EK, Li Q, Fang X*. Influence of Carbon Monoxide on Growth and Apoptosis of Human Umbilical Artery Smooth Muscle Cells and Vein Endothelial Cells. ***Int J Biol Sci.*** 2012; 8(10): 1431 – 1446.

附录二：已发表会议

1 Ma J, He N, Wang J, Wang L, Jin G, Lin R, Yang Y. CD8A and HAPLN3 expression profiling to reveal an immunologic subtype of bladder cancer with favorable survival. 2020. Journal of Clinical Oncology. American Society of Clinical Oncology

2 Fu, Zhichao and Liu, Shenghua and Wang, Jianfei and Zhang, Yiqun and Yang, Yadong and Xu, Tianyuan and Anil, Shrestha and Yan, Yang and Li, Cheng and Zheng, Zongtai and others. Transcriptome analysis of low-risk and high-risk non-muscular invasive bladder cancer patients to reveal disease progression related genes. 2020. Journal of Clinical Oncology. American Society of Clinical Oncology

3 Yang, Chunhe and Zhao, Guodong and Wang, Jianfei and Wang, Lingyu and Jin, Ge and Lin, Rongbo and Yang, Yadong. Integration of TMB and tumor heterogeneity identify an immunologic subtype of melanoma with favorable survival. 2020. Journal of Clinical Oncology. American Society of Clinical Oncology

4 Wang, Kun and Yang, Yadong and Zhang, Xiaoyu and Li, Juan and Bao, Quan and Wang, Hongwei and Jin, Kemin and Liu, Ming and Liu, Wei and Yan, Xiaoluan and others. Prognostic impact of mutation profiling in Chinese patients with colorectal liver metastases. 2020. Journal of Clinical Oncology. American Society of Clinical Oncology

5 Wang, Hai and Yang, Yadong and Hongzhu, QU and Ruan, Xiuyan and Zhang, Zhaojun and Xiong, Qian and Qi, Heyuan and Stamatoyannopoulos, George and Stamatoyannopoulos, John A and Fang, Xiangdong. unctional Analysis of FOXO3A Involved in Erythroid Differentiation. 2012. Blood. American Society of Hematology

6 He, Ning and Wang, Jianfei and Wang, Lingyu and Jin, Ge and Lin, Rongbo and Yang, Yadong. Metabolism of tumor cell in tumor micro environment assist immune escape. 2020. Journal of Clinical Oncology. American Society of Clinical Oncology

7 Yu, Yao and Lin, Rongbo and He, Ning and Yang, Yadong and Jin, Ge and Wang, Jianfei. Correlation of tumor mutational burden, tumor microenvironment and alterations of driver genes in patients with NSCLC: A retrospective analysis. 2019. Journal of Clinical Oncology. American Society of Clinical Oncology

8 He, Ning and Zhang, Yiqun and Yang, Yadong and Wang, Jianfei. Multi-omics prognosis predictive model of metastatic urothelial carcinoma (mUCs) with immunotherapy. 2021. Journal of Clinical Oncology. American Society of Clinical Oncology

9 Zhang, Yiqun and Zhao, Guodong and He, Ning and Wang, Lingyu and Wang, Jianfei and Jin, Ge and Lin, Rongbo and Yang, Yadong. Robust prediction of immune checkpoint inhibition therapy for non-small cell lung cancer. 2020. Journal of Clinical Oncology. American Society of Clinical Oncology

10 Jia, Yuanyuan and He, Ning and Yang, Yadong and Huang, Yuliang and Zhang, Xiaoyu and Fu, Zhichao and Xu, Xiaohong and Cao, Jianjun and Wang, Jianfei. Tumor mutation burden and immune microenvironment analysis of urothelial carcinoma. 2021. Journal of Clinical Oncology. American Society of Clinical Oncology

11 Li, Yanming and Liu, Shuge and Hongzhu, QU and Yang, Yadong and Ding, Nan and Ruan, Xiuyan and Stamatoyannopoulos, George and Fang, Xiangdong. PDCD2 Knockdown Promoted Induced Erythroid Differentiation in TF-1 Cells. 2014. Blood. American Society of Hematology

12 Yang, Ping and Ji, Guanghui and Jiang, Qionghui and Lu, Zejun and Yu, Yao and Yang, Yadong and Jin, Ge. Mutation profiles in circulating tumor DNA (ctDNA) to predict the efficacy of sorafenib treatment in patients with advanced hepatocellular carcinoma (HCC). 2019. Journal of Clinical Oncology. American Society of Clinical Oncology

13 Fu, Zhichao and Liu, Shenghua and Wang, Jianfei and He, Ning and Yang, Yadong and Xu, Tianyuan and Anil, Shrestha and Yan, Yang and Li, Cheng and Zheng, Zongtai and others. RNA-seq analysis of non-muscular

invasive bladder cancer to reveal different gene expression profiles between smoking and non-smoking patients. 2021. Journal of Clinical Oncology. American Society of Clinical Oncology

附录三：已公开专利

1	CN116949173A	用于肺癌筛查的标志物、探针组合物及其应用	吴宁宁；彭勇飞；王小奇；**杨亚东**；李永君；魏闯；张聪
2	CN116926191A	用于肺腺癌筛查的标志物、探针组合物及其应用	郭媛媛；吴宁宁；刘栓平；田继超；魏闯；张聪；李永君；**杨亚东**
3	CN116891891A	用于预测脑卒中复发的甲基化标志物及其应用	彭勇飞；户秋稳；田继超；王小奇；叶建伟；**杨亚东**；韩晓亮；叶志海；王建铭
4	CN116875695A	用于肺癌检测的甲基化标志物、引物探针组合物及其应用	聂海珍；吴宁宁；王秀秀；**杨亚东**；汪亚林；古双臻；陈丽娟；郭媛媛；李永君；吴振；周光朋
5	CN116790756A	用于检测肺癌的组合物及其用途	聂海珍；吴宁宁；王秀秀；**杨亚东**；汪亚林；古双臻；陈丽娟；魏闯；刘栓平；李永君；吴振；周光朋
6	CN116798606A	用于检测甲状腺癌的系统	陈树超；关晋霞；吴宁宁；**杨亚东**；郭媛媛；魏闯；李永君；陈丽娟；王晶；王元昊；吴振；周光朋
7	CN116779025A	用于癌症筛查的系统	彭勇飞；**杨亚东**；李永君；王小齐；郭媛媛；田继超
8	CN116732180A	用于检测甲状腺癌的组合物及其用途	陈树超；关晋霞；吴宁宁；**杨亚东**；张欢跃；刘栓平；李永君；陈丽娟；王晶；王元昊；吴振；周光朋
9	CN116705153A	确定 SNP 检测区域的方法和对测序样本进行校正的方法	王小奇；许喆；仇鑫；户秋稳；田继超；彭勇飞；**杨亚东**；叶建伟；程丝；林金嬉；李昊；叶志海；李子孝；王拥军
10	CN116676389A	用于肺癌筛查的标志物、探针组合物及其应用	吴宁宁；韩晓亮；王小奇；连明；魏闯；张聪；**杨亚东**
11	CN116312739A	基于甲基化测序的标志物筛选方法、癌症检测方法及装置	连明；李永君；**杨亚东**；彭勇飞；关晋霞；韩晓亮；王建铭
12	CN115961028A	用于检测肺癌的标志物及其用途和系统	田继超；**杨亚东**；李永君；关晋霞；魏闯；张聪
13	CN115896258A	一种用于癌症筛查的方法及用于癌症筛查的系统	王小奇；**杨亚东**；李永君；吴宁宁；郭媛媛；彭勇飞
14	CN114974430A	用于癌症筛查的系统及其方法	田继超；**杨亚东**；李永君；王小奇；彭勇飞；连明
15	CN114606319A	用于检测肺癌的标志物、试剂盒及系统	关晋霞；**杨亚东**；李永君；刘栓平；彭勇飞；吴宁宁
16	CN114540497A	用于膀胱癌筛查的标志物、探针组合物及其应用	连明；韩晓亮；王小奇；刘栓平；魏闯；张聪；**杨亚东**
17	CN114507734A	用于甲状腺癌筛查的标志物、探针组合物及其应用	关晋霞；韩晓亮；连明；王小奇；郭媛媛；张聪；**杨亚东**
18	CN114395628A	用于结直肠癌筛查的标志物、探针组合物及其应用	吴宁宁；韩晓亮；连明；王小奇；刘栓平；魏闯；**杨亚东**
19	CN114369663A	用于肝癌筛查的标志物、探针组合物及其应用	彭勇飞；韩晓亮；郭媛媛；魏闯；连明；王小奇；**杨亚东**
20	CN114369661A	用于乳腺癌筛查的标志物、探针组合物及其应用	连明；韩晓亮；王小奇；**杨亚东**；田继超；刘栓平；叶志海
21	CN114317740A	用于胃癌筛查的标志物、探针组合物	王小奇；**杨亚东**；李永君；吴宁宁；郭媛媛；关晋霞

		及其应用	
22	CN114317737A	用于肺癌筛查的组合物及其应用	吴宁宁; **杨亚东**; 李永君; 关晋霞; 魏闯; 连明
23	CN114317735A	用于肺癌筛查的组合物及其应用	**杨亚东**; 吴宁宁; 李永君; 刘栓平; 王小奇; 韩晓亮; 王建铭
24	CN114317734A	用于肺癌筛查的组合物及其应用	吴宁宁; 李永君; **杨亚东**; 田继超; 彭勇飞; 张聪; 韩晓亮; 王建铭
25	CN114317732A	用于肺癌筛查的组合物及其应用	吴宁宁; 李永君; **杨亚东**; 郭媛媛; 韩晓亮; 王建铭
26	CN114231635A	用于肺癌筛查的标志物、探针组合物及其应用	吴宁宁; 韩晓亮; 王小奇; 连明; 魏闯; 张聪; **杨亚东**
27	CN113403380A	一种复杂疾病相关 SNP 位点引物组合物及应用	方向东; 单广乐; **杨亚东**; 隋阳; 辛子娟
28	CN107766695A	一种获取外周血基因模型训练数据的方法及装置	方向东; **杨亚东**; 张韬