JUN ZHONG, Ph. D.

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RESEARCH INTERESTS

Computational Oncology (Gastrointestinal cancer, especially pancreatic cancer), Genome-Wide Association Study (GWAS), Transcriptome-Wide Association Study (TWAS), Population Genetics, Cohort Study, Polygenic Risk Scores (PRS), Cancer Drivers, Multi-Omics, AI-powered Risk Prediction Models, Drug Sensitivity Prediction Model.

PROFESSIONAL EXPERIENCE

Research Fellow (Full-time employee) …………………………………………………......2022 - present

National Cancer Institute, National Institute of Health, US

- Leading the bioinformatics analysis in the PanScan IV consortium, an international large-scale multi-ethnic pancreatic cancer cohort (total dataset includes > 1 million individuals, > 50 studies from > 20 countries), identifying novel pancreatic cancer susceptibility loci and fine-mapping in European and Asian populations.
- Building a trans-ancestry polygenic risk score (PRS) model for pancreatic cancer.
- Identifying noncoding somatic driver mutations for cancer using large-scale multi-omics datasets.

Postdoctoral Fellow……………………………………..………………...................................2017 - 2022

National Cancer Institute, National Institute of Health, US

Advisor: Laufey Amundadottir, Senior Investigator

- Data mining of large multi-omic datasets (International Cancer Genome Consortium (ICGC), UK Biobank, GTEx, ENCODE, 1KG Genomes Project, gnomAD, etc.)
- Transcriptome-wide association study (TWAS) identifies novel candidate susceptibility genes for pancreatic cancer.
- Fine-mapping of chr16q23.1, splicing quantitative trait locus (sQTL) analysis.
- Genome-wide association study (GWAS) for pancreatic cancer, meta-analysis.
- Building a PRS model for pancreatic cancer, absolute risk (AR) model.
- Identifying noncoding somatic driver mutations in regulatory elements for pancreatic cancer.
- High-resolution promoter capture C analysis to identify target genes of noncoding mutations.

Research Fellow (Full-time employee) ……………...………………...…………………………2014 - 2017

University of Chinese Academy of Sciences, CN

Research experience includes:

- Whole genome sequencing (WGS) analysis by PacBio single-molecule real-time (SMRT) technology.
- Precision methylome characterization by PacBio SMRT technology.
- Identification of ^{m6}A sequence motifs and corresponding methyltransferase (MTase) genes.
- Pan-genome and single nucleotide polymorphism (SNP) deserts analyses.
- Building a high-performance bioinformatic server.

EDUCATION

Ph. D Bioinformatics……………………………………………………………….…………...2014

University of Chinese Academy of Sciences, CN

Dissertation: Genome sequencing, assembly, and comparative analysis of *Penicillium chrysogenum* and miniature *Sus scrofa.*

- Whole genome sequencing analysis by and next generation sequencing (NGS) (Roche 454 and

Illumina Hiseq 2000) and Sanger (ABI 3730).

- Building a first high-quality genome sequence of industrial high-penicillin strain of *Penicillium chrysogenum*
- Genomic study on the high-yield mechanism of *Penicillium chrysogenum*
- Building a genome reference and identification of genome-wide genetic diversity for miniature *Sus scrofa.*

B. S Biotechnology……………………………..………………………………….……………2009
South-Central University for Nationalities, CN
General molecular biology and bioinformatic training.

PROFESSIONAL SERVICE FOR JOURNALS

Editorial Service:

- Editorial Board Member in *BMC Medicine*……………...…………….………………………… 2024 - present
- Youth Editor in *The Innovation*……………...……………………………………...………2022 - 2024
- Associate Editor in *Frontiers in Oncology*……...………………………………………..2021 - 2023

Journal Reviewer Service (selected):
Gastroenterology, Nature Communications, The Innovation, Journal of Hematology & Oncology, Genome Biology, BMC Medicine, eLife, Genomics Proteomics & Bioinformatics, Med, Molecular Oncology, Cancer Letters. 71 peer reviews and 28 editorial records have already been certified by Web of Science.

Conference/Award Reviewer Service:
American Society of Human Genetics (ASHG) annual meeting……………………………………….2024
NIH DCEG Fellows Award for Research Excellence competition (DFARE) ……………………………2019

FUNDING

- DCEG Intramural Research Award ($50,000), National Cancer Institute………………...…………..2021
  Principal Investigator | Uncovering the dark matter of pancreatic cancer: searching for noncoding somatic driver mutations in regulatory elements
- NCI Director's Innovation Award ($10,000), National Cancer Institute………………...…………...2020
  Key Participant | Examining the interplay between PDAC risk and stress response
- DCEG BRG Funding ($846,513), National Cancer Institute, NIH……...........………..........................2019
  Lead Participant | Genome-Wide Association Study (GWAS) for Pancreatic Cancer - PanScan IV
- National Natural Science Foundation of China (¥204,000) (Grant No. 31601047)…………………....2016
  Principal Investigator | Genetic diversity and core-genome evolution mechanism of *Mycobacterium tuberculosis* Beijing Lineage
- National Natural Science Foundation of China (¥150,000) (Grant No. 31370855)…………………....2014
  Participant | A study on a new method of low-abundance gene mutation enrichment based on artificial simulated nucleic acid
- National Natural Science Foundation of China (¥200,000) (Grant No. 31200978)…………………....2013
  Participant | A study of the mechanism of miR-21 in cancer cells based on Ribo-minus deep transcriptome sequencing

AWARDS AND HONORS

- National Institute of Health Cancer Research Training Award …..........……………………….2017 - 2022
- Fellows Award for Research Excellence (FARE), NIH (Top 25%)……………….…………………2021

- Reviewers' Choice Abstract Award at American Society of Human Genetics (ASHG) annual meeting (Top 10%) ……………………………………...………………………………..………...2020
- Fellows Award for Research Excellence (FARE), NIH (Top 25%)……………………….…………………2020
- Summer Research Mentor Award, NIH………………………………………………….…………………...2019
- Best Paper Award in the Twelfth Asia Pacific Bioinformatics Conference………….………………………2014
- Merit Student, University of Chinese Academy of Sciences (Top 15%) ……………..……………...2011
- Merit Student, University of Chinese Academy of Sciences (Top 15%) ……………..…………….. 2010

TEACHING/MENTORSHIP

- Courtney D. Dill, **Ph. D candidate** from Morehouse School of Medicine
  Project: *Uncovering the dark matter of pancreatic cancer by assessing noncoding regulatory variations.*
  Role: Summer Internship Mentor (2019). Mentored Courtney on cancer genomic research, guiding her through bioinformatic design, data analysis and poster preparation.
- Yusuph M. Mavura, **M.S candidate** from Georgia Institute of Technology
  Project: *Genome-wide association study to identify risk loci for pancreatic cancer in Asians.*
  Role: Summer Internship Mentor (2018). Supervised Yusuph's research on GWAS data analysis, helping him develop a foundation for statistical methods.
- Tingting Yang and Ximiao Jia, **Ph. D candidates**, University of Chinese Academy of Sciences
  Project: *The methylome and pan-genome analysis of Mycobacterium tuberculosis complex*
  Role: Research Mentor (2014 – 2016). Guided graduate students through advanced genomic techniques, helping design the pan-genome study, troubleshooting and providing feedback on the data interpretation.
- 5 **Master candidates**, University of Chinese Academy of Sciences
  Course: Perl programming in Bioinformatics
  Role: Instructor (2016). Created this course and taught students to use Perl for the data mining.
- 60 **attendees**, University of Chinese Academy of Sciences and other universities/institutes
  Course: Genome Science Training Course
  Role: Assistant Instructor (2013). Helped students learned cutting-edge genomic skills and programming.

PUBLICATIONS IN PREPRINTS

(# co-first author, § co-corresponding author)

1. **Zhong J**(#,§), O'Brien A(#), Patel M, Eiser D, Mobaraki M, Collins I, Wang L, Guo K, TruongVo T, Jermusyk A, O'Neill M, D Dill CD, Wells AD, Leonard ME, Pippin JA, Grant SFA, Zhang T, Andresson T, Connelly KE, Shi J, Arda HE, Hoskins JW, Amundadottir LT(§). Large-scale multi-omic analysis identifies noncoding somatic driver mutations and nominates ZFP36L2 as a driver gene for pancreatic ductal adenocarcinoma. ***medRxiv.*** 2024. (under review in ***Gut***)
2. Connelly KE, Hullin K, Abdolalizadeh E, **Zhong J**, Eiser D, O'Brien A, Collins I, Das S, Duncan G, Pancreatic Cancer Cohort Consortium, Pancreatic Cancer Case-Control Consortium, Chanock S, Stolzenberg-Solomon RZ, Klein A, Wolpin BM, Hoskins JW, Andresson T, Smith JP, Amundadottir LT(§). Allelic effects on KLHL17 expression likely mediated by JunB/D underlie a PDAC GWAS signal at chr1p36.33. ***medRxiv.*** 2024. (under review/revision in ***Nature Communications***)
3. Wang L, Baek S, Prasad G, Wildenthal J, Guo K, Sturgill D, Truongvo T, Char E, Pegoraro G, McKinnon K, Pancreatic Cancer Cohort Consortium (including **Zhong J**), Pancreatic Cancer Case-Control Consortium, Hoskins JW, Amundadottir LT, Arda HE. Predictive Prioritization of Enhancers Associated with Pancreas Disease Risk. ***bioRxiv.*** 2024. (under review/revision in ***Cell Genomics***)

PUBLICATIONS IN JOURNALS

($^{\#}$ co-first author, § co-corresponding author)

1. Klein A, **Zhong J**, Landi M, Zhang T. Sherlock-Genome: An R Shiny application for genomic analysis and visualization. ***BMC genomics.*** 2025, 26(1):44.
2. **Zhong J**$^{(\S)}$, Amundadottir LT$^{(\S)}$. Uncovering dark matter in cancer by identifying epigenetic drivers. ***Trends in Genetics.*** 2024, 40(3): 211-212.
3. Ni Z, Kundu P, McKean DF, Wheeler W, Albanes D, Andreotti G, Antwi SO, Arslan AA, Bamlet WR, Beane Freeman LE, Berndt SI, Bracci PM, Brennan P, Buring JE, Chanock SJ, Gallinger S, Gaziano JM, Giles GG, Giovannucci EL, Goggins MG, Goodman PJ, Haiman CA, Hassan MM, Holly EA, Hung RJ, Katzke V, Kooperberg C, Kraft P, Le Marchand L, Li D, McCullough ML, Milne RL, Moore SC, Neale RE, Oberg AL, Patel AV, Peters U, Rabe KG, Risch HA, Shu XO, Smith Byrne K, Visvanathan K, Wactawski-Wende J, White E, Wolpin BM, Yu H, Zeleniuch-Jacquotte A, Zheng W, **Zhong J**, Amundadottir LT, Stolzenberg-Solomon RZ, Klein AP. Genome-wide analysis to assess if heavy alcohol consumption modifies the association between SNPs and pancreatic cancer risk. ***Cancer Epidemiol Biomarkers Prev***. 2024, 33 (9): 1229–1239.
4. **Zhong J**$^{(\S)}$, Shi J$^{(\S)}$, Amundadottir LT$^{(\S)}$. Artificial intelligence and improved early detection for pancreatic cancer. ***The Innovation***. 2023, 4(4):100457. (**Highlighted** in the cover legend of Volume 4, Issue 4: New Cool, AI for pancreatic cancer).
5. Lindström S, Wang L, Feng H, Majumdar A, Huo S, Macdonald J, Harrison T, Turman C, Chen H, Mancuso N, Bammler T; Breast Cancer Association Consortium (BCAC); Gallinger S, Gruber SB, Gunter MJ, Le Marchand L, Moreno V, Offit K; Colorectal Transdisciplinary Study (CORECT), Colon Cancer Family Registry Study (CCFR), Genetics And Epidemiology Of Colorectal Cancer Consortium (GECCO); De Vivo I, O'Mara TA, Spurdle AB, Tomlinson I; Endometrial Cancer Association Consortium (ECAC); Fitzgerald R, Gharahkhani P, Gockel I, Jankowski J, Macgregor S, Schumacher J, Barnholtz-Sloan J, Bondy ML, Houlston RS, Jenkins RB, Melin B, Wrensch M, Brennan P, Christiani DC, Johansson M, Mckay J, Aldrich MC, Amos CI, Landi MT, Tardon A; International Lung Cancer Consortium (ILCCO); Bishop DT, Demenais F, Goldstein AM, Iles MM, Kanetsky PA, Law MH; Ovarian Cancer Association Consortium (OCAC); Amundadottir LT, Stolzenberg-Solomon R, Wolpin BM; Pancreatic Cancer Cohort Consortium (PanScan, including **Zhong J**); Klein A, Petersen G, Risch H; Pancreatic Cancer Case-Control Consortium (PanC4), The PRACTICAL Consortium; Chanock SJ, Purdue MP, Scelo G, Pharoah P, Kar S, Hung RJ, Pasaniuc B, Kraft P. Genome-wide analyses characterize shared heritability among cancers and identify novel cancer susceptibility regions. ***JNCI: Journal of the National Cancer Institute***. 2023, 115(6):712-732.
6. King SD, Veliginti S, Brouwers MCGJ, Ren Z, Zheng W, Setiawan VW, Wilkens LR, Shu XO, Arslan AA, Beane Freeman LE, Bracci PM, Canzian F, Du M, Gallinger SJ, Giles GG, Goodman PJ, Haiman CA, Kogevinas M, Kooperberg C, LeMarchand L, Neale RE, Visvanathan K, White E, Albanes D, Andreotti G, Babic A, Berndt SI, Brais LK, Brennan P, Buring JE, Rabe KG, Bamlet WR, Chanock SJ, Fuchs CS, Gaziano JM, Giovannucci EL, Hackert T, Hassan MM, Katzke V, Kurtz RC, Lee IM, Malats N, Murphy N, Oberg AL, Orlow I, Porta M, Real FX, Rothman N, Sesso HD, Silverman DT, Thompson IM, Wactawski-Wende J, Wang X, Wentzensen N, Yu H, Zeleniuch-Jacquotte A, Yu K, Wolpin BM, Duell EJ, Li D, Hung RJ, Perdomo S, McCullough ML, Freedman ND, Patel AV, Peters U, Riboli E, Sund M, Tjønneland A, **Zhong J**, Van Den Eeden SK, Kraft P, Risch HA, Amundadottir LT, Klein AP, Stolzenberg-Solomon RZ, Antwi SO. Genetic Susceptibility to Nonalcoholic Fatty Liver Disease and Risk for Pancreatic Cancer: Mendelian Randomization. ***Cancer Epidemiol Biomarkers Prev***. 2023, 32(9):1265-1269.

7. Jermusyk A[(#)], **Zhong J**[(#)], Connelly KE[(#)], Gordon N[(#)], Perera S, Abdolalizadeh E, Zhang T, O'Brien A, Hoskins JW, Collins I, Eiser D, Yuan C; PanScan Consortium; PanC4 Consortium, Risch HA, Jacobs EJ, Li D, Du M, Stolzenberg-Solomon RZ, Klein AP, Smith JP, Wolpin BM, Chanock SJ, Shi J, Petersen GM, Westlake CJ, Amundadottir LT. A 584 bp deletion in CTRB2 inhibits chymotrypsin B2 activity and secretion and confers risk of pancreatic cancer. ***The American Journal of Human Genetics,*** 2021, 108(10):1852-1865.

8. Hoskins JW, Chung CC, O'Brien A, **Zhong J**, Connelly K, Collins I, Shi J, Amundadottir LT. Inferred expression regulator activities suggest genes mediating cardiometabolic genetic signals. ***PLoS Computational Biolgy***, 2021, 17(11):e1009563.

9. Julián-Serrano S, Yuan F, Wheeler W, Benyamin B, Machiela MJ, Arslan AA, Beane-Freeman LE, Bracci PM, Duell EJ, Du M, Gallinger S, Giles GG, Goodman PJ, Kooperberg C, Marchand LL, Neale RE, Shu XO, Van Den Eeden SK, Visvanathan K, Zheng W, Albanes D, Andreotti G, Ardanaz E, Babic A, Berndt SI, Brais LK, Brennan P, Bueno-de-Mesquita B, Buring JE, Chanock SJ, Childs EJ, Chung CC, Fabiánová E, Foretová L, Fuchs CS, Gaziano JM, Gentiluomo M, Giovannucci EL, Goggins MG, Hackert T, Hartge P, Hassan MM, Holcátová I, Holly EA, Hung RI, Janout V, Kurtz RC, Lee IM, Malats N, McKean D, Milne RL, Newton CC, Oberg AL, Perdomo S, Peters U, Porta M, Rothman N, Schulze MB, Sesso HD, Silverman DT, Thompson IM, Wactawski-Wende J, Weiderpass E, Wenstzensen N, White E, Wilkens LR, Yu H, Zeleniuch-Jacquotte A, **Zhong J**, Kraft P, Li D, Campbell PT, Petersen GM, Wolpin BM, Risch HA, Amundadottir LT, Klein AP, Yu K, Stolzenberg-Solomon RZ. Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. ***The American Journal of Clinical Nutrition***, 2021, 114(4), 1408–1417.

10. **Zhong J,** Jermusyk A, Wu L, Hoskins JW, Collins I, Mocci E, Zhang M, Song L, Chung CC, Zhang T, Xiao W, Albanes D, Andreotti G, Arslan AA, Babic A, Bamlet WR, Beane-Freeman L, Berndt S, Borgida A, Bracci PM, Brais L, Brennan P, Bueno-de-Mesquita B, Buring J, Canzian F, Childs EJ, Cotterchio M, Du M, Duell EJ, Fuchs C, Gallinger S, Gaziano JM, Giles GG, Giovannucci E, Goggins M, Goodman GE, Goodman PJ, Haiman C, Hartge P, Hasan M, Helzlsouer KJ, Holly EA, Klein EA, Kogevinas M, Kurtz RJ, LeMarchand L, Malats N, Männistö S, Milne R, Neale RE, Ng K, Obazee O, Oberg AL, Orlow I, Patel AV, Peters U, Porta M, Rothman N, Scelo G, Sesso HD, Severi G, Sieri S, Silverman D, Sund M, Tjønneland A, Thornquist MD, Tobias GS, Trichopoulou A, Van Den Eeden SK, Visvanathan K, Wactawski-Wende J, Wentzensen N, White E, Yu H, Yuan C, Zeleniuch-Jacquotte A, Hoover R, Brown K, Kooperberg C, Risch HA, Jacobs EJ, Li D, Yu K, Shu XO, Chanock SJ, Wolpin BM, Stolzenberg-Solomon RZ, Chatterjee N, Klein AP, Smith JP, Kraft P, Shi J, Petersen GM, Zheng W, Amundadottir LT. A Transcriptome-Wide Association Study (TWAS) Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. ***JNCI: Journal of the National Cancer Institute***, 2020, 112(10):1003-1012. (**Highlighted** by an editorial in *JNCI*: Identifying Novel Genetic Markers Through a Transcription-Wide Association Study: Can This Be a Path to Reducing the Burden of Pancreatic Cancer?)

11. Zhang YD, Hurson AN, Zhang H, Choudhury PP, Easton DF, Milne RL, Simard J, Hall P, Michailidou K, Dennis J, Schmidt MK, Chang-Claude J, Gharahkhani P, Whiteman D, Campbell PT, Hoffmeister M, Jenkins M, Peters U, Hsu L, Gruber SB, Casey G, Schmit SL, O'Mara TA, Spurdle AB, Thompson DJ, Tomlinson I, De Vivo I, Landi MT, Law MH, Iles MM, Demenais F, Kumar R, MacGregor S, Bishop DT, Ward SV, Bondy ML, Houlston R, Wiencke JK, Melin B, Barnholtz-Sloan J, Kinnersley B, Wrensch MR, Amos CI, Hung RJ, Brennan P, McKay J, Caporaso NE, Berndt SI, Birmann BM, Camp NJ, Kraft P, Rothman N, Slager SL, Berchuck A, Pharoah PDP, Sellers TA, Gayther SA, Pearce CL, Goode EL, Schildkraut JM, Moysich KB, Amundadottir LT, Jacobs EJ, Klein AP, Petersen GM, Risch HA, Stolzenberg-Solomon RZ, Wolpin BM, Li D, Eeles RA, Haiman CA, Kote-Jarai Z, Schumacher FR, Al Olama AA, Purdue MP, Scelo G, Dalgaard MD, Greene MH, Grotmol T, Kanetsky PA, McGlynn KA,

Nathanson KL, Turnbull C, Wiklund F; Breast Cancer Association Consortium (BCAC); Barrett's and Esophageal Adenocarcinoma Consortium (BEACON); Colon Cancer Family Registry (CCFR); Transdisciplinary Studies of Genetic Variation in Colorectal Cancer (CORECT); Endometrial Cancer Association Consortium (ECAC); Genetics and Epidemiology of Colorectal Cancer Consortium (GECCO); Melanoma Genetics Consortium (GenoMEL); Glioma International Case-Control Study (GICC); International Lung Cancer Consortium (ILCCO); Integrative Analysis of Lung Cancer Etiology and Risk (INTEGRAL) Consortium; International Consortium of Investigators Working on Non-Hodgkin's Lymphoma Epidemiologic Studies (InterLymph); Ovarian Cancer Association Consortium (OCAC); Oral Cancer GWAS; Pancreatic Cancer Case-Control Consortium (PanC4); Pancreatic Cancer Cohort Consortium (PanScan) (including **Zhong J**); Prostate Cancer Association Group to Investigate Cancer Associated Alterations in the Genome (PRACTICAL); Renal Cancer GWAS; Testicular Cancer Consortium (TECAC), Chanock SJ, Chatterjee N, Garcia-Closas M. Assessment of Polygenic Architecture and Risk Prediction based on Common Variants Across Fourteen Cancers. ***Nature Communications,*** 2020, 11:3353.

12. Lin Y, Nakatochi M, Hosono Y, Ito H, Kamatani Y, Inoko A, Sakamoto H, Kinoshita F, Kobayashi Y, Ishii H, Ozaka M, Sasaki T, Matsuyama M, Sasahira N, Morimoto M, Kobayashi S, Fukushima T, Ueno M, Ohkawa S, Egawa N, Kuruma S, Mori M, Nakao H, Adachi Y, Okuda M, Osaki T, Kamiya S, Wang C, Hara K, Shimizu Y, Miyamoto T, Hayashi Y, Ebi H, Kohmoto T, Imoto I, Kasugai Y, Murakami Y, Akiyama M, Ishigaki K, Matsuda K, Hirata M, Shimada K, Okusaka T, Kawaguchi T, Takahashi M, Watanabe Y, Kuriki K, Kadota A, Okada R, Mikami H, Takezaki T, Suzuki S, Yamaji T, Iwasaki M, Sawada N, Goto A, Kinoshita K, Fuse N, Katsuoka F, Shimizu A, Nishizuka SS, Tanno K, Suzuki K, Okada Y, Horikoshi M, Yamauchi T, Kadowaki T, Yu H, **Zhong J**, Amundadottir LT, Doki Y, Ishii H, Eguchi H, Bogumil D, Haiman CA, Le Marchand L, Mori M, Risch H, Setiawan VW, Tsugane S, Wakai K, Yoshida T, Matsuda F, Kubo M, Kikuchi S, Matsuo K. Genome-wide association meta-analysis identifies *GP2* gene risk variants for pancreatic cancer. ***Nature Communications,*** 2020, 11:3175.
13. Huang H(#), Ding N(#), Yang T(#), Li C(#), Jia X(#), Wang G(#), **Zhong J**, Zhang J, Jiang G, Wang S, Zong Z, Jing W, Zhao Y, Xu S, Chen F. Cross-sectional Whole-genome Sequencing and Epidemiological Study of Multidrug-resistant *Mycobacterium tuberculosis* in China. ***Clinical Infectious Diseases***, 2019, 69(3):405-413.
14. Klein AP, Wolpin BM, Risch HA, Stolzenberg-Solomon RZ, Mocci E, Zhang M, Canzian F, Childs EJ, Hoskins JW, Jermusyk A, **Zhong J**, Chen F, Albanes D, Andreotti G, Arslan AA, Babic A, Bamlet WR, Beane-Freeman L, Berndt SI, Blackford A, Borges M, Borgida A, Bracci PM, Brais L, Brennan P, Brenner H, Bueno-de-Mesquita B, Buring J, Campa D, Capurso G, Cavestro GM, Chaffee KG, Chung CC, Cleary S, Cotterchio M, Dijk F, Duell EJ, Foretova L, Fuchs C, Funel N, Gallinger S, M Gaziano JM, Gazouli M, Giles GG, Giovannucci E, Goggins M, Goodman GE, Goodman PJ, Hackert T, Haiman C, Hartge P, Hasan M, Hegyi P, Helzlsouer KJ, Herman J, Holcatova I, Holly EA, Hoover R, Hung RJ, Jacobs EJ, Jamroziak K, Janout V, Kaaks R, Khaw KT, Klein EA, Kogevinas M, Kooperberg C, Kulke MH, Kupcinskas J, Kurtz RJ, Laheru D, Landi S, Lawlor RT, Lee IM, LeMarchand L, Lu L, Malats N, Mambrini A, Mannisto S, Milne RL, Mohelníková-Duchoňová B, Neale RE, Neoptolemos JP, Oberg AL, Olson SH, Orlow I, Pasquali C, Patel AV, Peters U, Pezzilli R, Porta M, Real FX, Rothman N, Scelo G, Sesso HD, Severi G, Shu XO, Silverman D, Smith JP, Soucek P, Sund M, Talar-Wojnarowska R, Tavano F, Thornquist MD, Tobias GS, Van Den Eeden SK, Vashist Y, Visvanathan K, Vodicka P, Wactawski-Wende J, Wang Z, Wentzensen N, White E, Yu H, Yu K, Zeleniuch-Jacquotte A, Zheng W, Kraft P, Li D, Chanock S, Obazee O, Petersen GM, Amundadottir LT. Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. ***Nature Communications***, 2018, 9:556.

15. Yang T(#), **Zhong J**(#), Zhang J(#), Li C(#), Yu X(#), Xiao J, Jia X, Ding N, Ma G, Wang G, Yue L, Liang Q, Sheng Y, Sun Y, Huang H, Chen F. Pan-genomic study of *Mycobacterium tuberculosis* reflecting the primary/secondary genes, generality/individuality, and the interconversion through copy number variations. ***Frontiers in Microbiology***, 2018, 9:1886.
16. Zhang L(#), **Zhong J**(#), Liu H, Xin K, Chen C, Li Q, Wei Y, Wang Y, Chen F(*), Shen X(*). Complete genome sequence of the drought resistance-promoting endophyte *Klebsiella* sp. LTGPAF-6F. ***Journal of Biotechnology,*** 2017, 246: 36-39.
17. Zhu L(#), **Zhong J**(#), Jia X(#), Liu G(#), Kang Y(#), Dong M, Zhang X, Li Q, Yue L, Li C, Fu J, Xiao J, Yan J, Zhang B, Lei M, Chen S, Lv L, Zhu B, Huang H(*), Chen F(*). Precision methylome characterization of *Mycobacterium tuberculosis* complex (MTBC) using PacBio single-molecule real-time (SMRT) technology. ***Nucleic Acids Research,*** 2016, 44, 730-743.
18. Hao L(#), Xia L(#), Huang D(#), Yang L(#), Xu X(#), Yan W(#), Zhang Y(#), Zou D(#), Liu S(#), Sang J, Deng W, Wang Y, Cheng H, Ma L, Yuan F, **Zhong J**, Li Q, Wu S, He Z, Luo Y, Wang X, Ji Z, Wang X, Xue Y, Chen L, Xiao J, Zhao W, Chen F, Zhang H(*), He H(*), Hu S(*), Zhang Z(*). Information Commons for Rice (IC4R). ***Nucleic Acids Research***, 2016, 44(D1):D1172-D1180.
19. Wang FQ(#), **Zhong J**(#), Zhao Y, Xiao J, Liu J, Dai M, Zheng G, Zhang L, Yu J, Wu J(*), Duan B(*). Genome sequencing of high-penicillin producing industrial strain of *Penicillium chrysogenum*. ***BMC Genomics*** 2014, 15 S1:S11.
20. Ling Y(#), Jin Z(#), Su M, **Zhong J**, Zhao Y, Yu J(*), Wu J(*), Xiao J(*). VCGDB: a dynamic genome database of the Chinese population. ***BMC Genomics*** 2014, 15:265.
21. Wu J, Xiao J, Wang L, **Zhong J**, Yin H, Wu S, Zhang Z, Yu J. Systematic analysis of intron size and abundance parameters in diverse lineages. ***Sci China Life Sci***, 2013, 56: 1–7.

PUBLICATIONS IN CONFERENCES

1. Patel MB, O'Brien A, **Zhong J**, Collins I, Hoskins JW, Chanock SJ, Antwi SO, Stolzenberg-Solomon RZ, Klein AP, Wolpin BM, Lindström S, Arda HE, Brown KM, Connelly KE, Amundadottir LT, Jezek M. The functional characterization of pancreatic ductal adenocarcinoma GWAS risk variants in primary pancreatic cells – A pilot study [abstract]. In: Proceedings of the AACR Special Conference in Cancer Research: Advances in Pancreatic Cancer Research; 2024 Sep 15-18; Boston, MA. Philadelphia (PA): AACR; Cancer Res 2024; 84(17 Suppl_2):Abstract nr A018.
2. O'Brien A, Kong, Patel M, Connelly KE, Xu M, Collins I, **Zhong J**, Hoskins J, Ho M, Papenburg B, Iles MM, Law MH, Landi M, Stolzenber-Solomon R, Wolpin BM, Klein AP, Orr N, Chanock SJ, Lindström S, Stern M, Prokunina-Olsson L, Choi J, Brown KM, Amundadottir LT. Unraveling pancreatic cancer susceptibility at 5p15.33: Functional characterization of a novel VNTR element [abstract]. In: Proceedings of the AACR Special Conference in Cancer Research: Advances in Pancreatic Cancer Research; 2024 Sep 15-18; Boston, MA. Philadelphia (PA): AACR; Cancer Res 2024; 84(17 Suppl_2):Abstract nr C055.
3. O'Brien A, Hoskins JW, Eiser DR, Connelly KE, **Zhong J**, Andresson T, Collins I, Pancreatic Cancer Cohort Consortium, Pancreatic Cancer Case-Control Consortium, Chanock SJ, Klein AP, Arda HE, Amundadottir LT. Uncovering the functional variants and target genes of the 7q32 pancreatic cancer risk locus [abstract]. In: Proceedings of the American Association for Cancer Research Annual Meeting 2022; 2022 Apr 8-13. Philadelphia (PA): AACR; Cancer Res 2022; 82(12_Suppl):Abstract nr 1475.

4. Jermusyk A, **Zhong J**, Gordon N, Connelly K, Perera S, Abdolalizadeh E, Zhang T, O'Brien A, Hoskins J, Collins I, Eiser D, Yuan C, Risch G, Jacobs EJ, Li D, Du M, Stolzenberg-Solomon R, Klein AP, Smith J, Wolpin BM, Chanock SJ, Shi J, Petersen GM, Westlake C, Amundadottir LT. An exception to the rule:

A coding functional variant at a pancreatic cancer GWAS locus [abstract]. In: Proceedings of the AACR Virtual Special Conference on Pancreatic Cancer; 2020 Sep 29-30. Philadelphia (PA): AACR; Cancer Res 2020; 80(22 Suppl):Abstract nr IA-11.

5. **Zhong J** , Jermusyk A, Wu L, Hoskins JW, Collins I, Zhang M, Lei S, Chung CC, Zhang T, Xiao W, Stolzenberg-Solomon R, Klein AP, Wolpin BM, Shu XO, Chanock SJ, Olson S, Chatterjee N, Smith J, Shi J, Kraft P, Petersen GM, Zheng W, Amundadottir LT. Large-scale transcriptome-wide association study identifies novel candidate susceptibility genes for pancreatic cancer [abstract]. In: Proceedings of the American Association for Cancer Research Annual Meeting 2019; 2019 Mar 29-Apr 3; Atlanta, GA. Philadelphia (PA): AACR; Cancer Res 2019; 79(13 Suppl):Abstract nr 1591.

MANUSCRUPT IN PREPARATION

1. **Zhong J**, Albanes D, Andreotti G, Arslan AA, Beane-Freeman L, Berndt SI, Buring JE, Campa D, Canzian F, Chanock SJ, Chen Y, Colorado-Yohar SM, Eliassen A, Gaziano J, Giles GG, Goodman PJ, Haiman CA, Johansson M, Katzke V, Kooperberg C, Kraft P, Kogevinas M, Lee I, LeMarchand L, Malats N, Matsuda K, Morisaki T, Okada Y, Kamatani Y, Muto K, Nagai A, Sagiya Y, Kumasaka N, Furukawa Y, Yamanashi Y, Murakami Y, Nakamura Y, Obara W, Yamaji K, Takahashi K, Asai S, Takahashi Y, Higashiue S, Kobayashi S, Yamaguchi H, Nagata Y, Wakita S, Nito C, Iwasaki Y, Murayama S, Yoshimori K, Miki Y, Obata D, Higashiyama M, Masumoto A, Koga Y, Koretsune Y, Männistö S, McCullough ML, Milne R, Moore SC, Mucci L, Panico S, Patel AV, Peters U, Porta M, Real FX, Sesso HD, Shu X, Stampfer MJ, Tobias GS, Visvanathan K, Weiderpass E, Wentzensen N, White E, Yuan C, Zheng W, Wactawski-Wende J, Stolzenberg-Solomon RZ, Wolpin BM, Amundadottir LT. A multi-ancestry genome-wide association study identifies novel risk loci and a multi-factorial risk prediction model for pancreatic cancer.
2. Zhang T, Hua X, Mohindroo C, Wang X, Dutta D, Liu J, Wang J, Li S, Antwi SO, Arslan AA, Freeman LEB, Bracci PM, Canzian F, Du M, Gallinger S, Goodman PJ, Katzke V, Kooperberg C, Marchand LL, Milne RL, Neale RE, Patel AV, Perdomo S, Shu XO, Visvanathan K, Eeden SKVD, White E, Zheng W, Albanes D, Andreotti G, Bamlet WR, Brennan P, Buring JE, Chanock SJ, Yu Chen Y, Darst B, Ferrari P, Giovannucci EL, Goggins M, Haiman C, Hassan M, Holly EA, Hung RJ, Jones MR, Kraft P, Kurtz RC, Malats N, Moore S, Ng K, Oberg AL, Orlow I, Peters U, Porta M, Rabe KG, Real FX, Rothman N, Sánchez MJ, Sesso HD, Silverman DT, Southey MC, Um C, Yarmolinsky, Yu JH, Yuan C, **Zhong J**, Wolpin BM, Risch HA, Amundadottir LT, Klein AP, Yu K, Zhang H, Stolzenberg-Solomon RA. Different types of diabetes and pancreatic ductal adenocarcinoma risk: A Mendelian randomization and pathway/gene-set analysis.

PRESENTATIONS

Invited speaker:

1. **Identifying noncoding somatic driver mutations in pancreatic cancer**. Presented in the NCI DCEG Early Career Scientist seminar, virtually, March 2023.
2. **Pancreatic Cancer Cohort Consortium (PanScan IV) Update**. Presented in the Pancreatic Cancer Case-Control Consortium (PanC4) annual meeting, virtually, December 2022.
3. **Identifying noncoding somatic driver mutations in regulatory elements for pancreatic cancer**. Presented (Platform) at the American Society of Human Genetics (ASHG) annual meeting, Los Angeles, October 2022.
4. **Pancreatic Cancer Cohort Consortium (PanScan) IV GWAS update.** Presented in the FinnGen Scientific Committee/Analysis group meeting, virtually, January 2022.

5. **PanScan update and preliminary results for PANDoRA and Asian GWAS scans.** Presented in the PanScan cohort consortium annual meeting, virtually, October 2021.
6. **Uncovering the dark matter of pancreatic cancer: noncoding somatic driver mutations in regulatory elements.** Presented in the CRL (Consolidated Research Laboratory) seminar series, Division of Cancer Epidemiology and Genetics (DCEG, NCI), virtually. September 2020.
7. **Large-scale Transcriptome-Wide Association Study (TWAS) Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer.** Presented at the 11th Annual Division of Cancer Epidemiology and Genetics (DCEG, NCI) Fellows' Training Symposium, Bethesda, MD. April 2019.
8. **A Transcriptome-Wide Association Study (TWAS) Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer**. Presented at the LTG (Laboratory of Translational Genomics) seminar, Division of Cancer Epidemiology and Genetics (DCEG, NCI), Gaithersburg, MD. February 2019.
9. **Genome sequencing of high-penicillin producing industrial strain of *Penicillium chrysogenum*.** Presented at the twelfth Asia Pacific Bioinformatics Conference, Shanghai, China. January 2014. (**Best Paper Award** in the conference)

Posters (selected):

1. **Zhong J**, Eiser D, Brien A, Connelly K, Hoskins J, Jermusyk A, Collins I, Shen T, Zhao Y, Li Wang3, Guo K, TruongVo T, Wildenthal J, McKinnon K, Wells A, Grant S, Arda E, Shi J, Amundadottir L. *Uncovering the dark matter of pancreatic cancer: identifying driver mutations in noncoding gene regulatory elements.* Presented at the American Society of Human Genetics virtual meeting (ASHG), October 2020. **[Reviewers' Choice award, top 10%]**
2. **Zhong J**, Jermusyk A, Wu L, Hoskins J, Collins I, Zhang M, Lei S, Chung C, Zhang T, Xiao W, Stolzenberg-Solomon R, Klein A, Wolpin B, Shu X, Chanock S, Olson S, Chatterjee N, Smith J, Jianxin Shi, Kraft P, Petersen G, Zheng W, Amundadottir L. *Large-scale transcriptome-wide association study (TWAS) identifies novel candidate susceptibility genes for pancreatic cancer*. Presented at the American Association for Cancer Research Annual Meeting (AACR), Atlanta, GA. March 2019.
3. **Zhong J**, Wu L, Jermusyk A, Hoskins J, Collins I, Zhang M, Lei S, Chung C, Zhang T, Xiao W, PanScan, PanC4, Stolzenberg-Solomon R, Klein A, Wolpin B, Brown K, Shu X, Chanock S, Olson S, Chatterjee N, Petersen G, Smith J, Shi J, Kraft P, Zheng W, Amundadottir L. A *Transcriptome-wide association study for pancreatic cancer.* Presented at the American Society of Human Genetics annual meeting (ASHG), San Diego, CA. October 2018.

PROFESSIONAL MEMBERSHIP/ROLE

- Member in American College of Medical Genetics and Genomics (ACMG) ……………………….2024
- Gold member in American Association for the Advancement of Science (AAAS)……………2023 - 2024
- Member in American Society of Human Genetics (ASHG)………………...…………..2017, 2022 - 2025
- Associate Member in American Association for Cancer Research (AACR)…….2018 - 2020, 2024 - 2025
- Member in Tumor Microenvironment Group of the AACR………………………………..2018 - 2019
- Planning Committee Member in 10th Annual NCI DCEG Fellows' Training Symposium…….2017 - 2018

COURSE/WORKSHOP/TRAINING (selected)

- **Learning Python for Data Science: What to Learn and Why?** NIH Library, NIH.......................2023
- **Mentoring Across Differences**. Research Workforce Development, Office of Intramural Research, NIH...2022
- **Statistical Analysis of Research Data (SARD) course.** National Cancer Institute, NIH..................2021

- **Teamwork**. Office of Postdoc Services & Career Services Center, Office of Intramural Training and Education, NIH..2021
- **Grant Writing**. Office of Intramural Training & Education, NIH..2021
- **Understanding the NIH Grant Peer Review Process**. NIH..2021
- **Grants and Grantsmanship Workshop**. Division of Cancer Epidemiology and Genetics, National Cancer Institute, NIH..2020 - 2021
- **Translational Research in Clinical Oncology Training Course** (26 lessons). National Cancer Institute, NIH..2020
- **Visualization with R workshop.** Foundation for Advanced Education in the Sciences, NIH............2020
- **Python Programming for Scientists Series**. NIH..2020